

# Single Cell RNA-seq Copilot In-school Evaluation Form - Feedback quiz

Thank you again for joining this experiment.

\* 表示必填問題

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1。 電子郵件 \*

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2。 Which group were you assigned? \*

單選。

- ☐ Without AI group, Control
- ☐ With AI group, Experimental
- ☐ No Search or Internet

3。 Clarification: There is always the possibility of tampering from an outside source \*  
when using the internet for collecting information. While the confidentiality of your responses will be protected once the data are downloaded from the internet, there is always a possibility of hacking or other security breaches that could threaten the confidentiality of your responses. Please know that you are free to decide not to answer any question.

I have read the consent information above and agree to participate and allow information collection during the research.

單選。

- ☐ Yes
- ☐ No

4 ° Do you have any experience in bioinformatics? \*

單選。

- ☐ No, I have no idea what bioinformatics is.
- ☐ Beginner, I know what tools they use and how.
- ☐ Intermediate, I have done some analysis
- ☐ Advanced, I am professional in bioinformatics

### Multiple Choice Questions

These questions are related to single cell sequencing. Please answer them to the best of your knowledge.

Some of them have MORE THAN ONE answer.

5 ° What is single cell RNA sequencing (scRNA-seq)? \*

1 分

(可複選)

- ☐ It is a technique that examines the nucleic acid sequence information from individual cells
- ☐ It is a technique used to extract genes from cells
- ☐ It is a technique mainly used to get RNA sequence of COVID patients
- ☐ It is a technique that tests the numbers of cells expressing certain genes

6 ° What can we know about from the expression matrix of a tissue? \*

2 分

(可複選)

- ☐ Gene expression level of different genes in each cell of the tissue
- ☐ Translation level (protein level) of each cell of the tissue
- ☐ Overall gene expression level of a tissue
- ☐ The total number of cell organelles
- ☐ The number of chromosomes

7. Why do we need to do quality control (selecting cells based on some parameters)? \* 2 分

(可複選)

- ☐ To choose cells that expresses certain genes only
- ☐ To normalize the cells
- ☐ To eliminate unqualified, dead cells which might contaminate or interfere with the expression of our target, healthy cells.
- ☐ To exclude cells expressing more than a threshold percentage of mitochondria genes
- ☐ To select the cells expressing genes at the highest level

8. What is the next step of quality control? \* 1 分

(可複選)

- ☐ Normalization
- ☐ Clustering
- ☐ Annotation
- ☐ Sequencing

9. Why do we need to reduce the dimensions of the data? \* 2 分

(可複選)

- ☐ To visualize the multidimensional gene expression data on a 2D graph
- ☐ Since gene expression is in three dimensional space, we need to reduce it to 2D for better data representation.
- ☐ To make the data more accessible (readable, or explainable)
- ☐ We need to reduce the dimensions of the data because it gives no useful information
- ☐ To unify the RNA expression level of cells in the same type

10 ° Which of the following is NOT an application of scRNA-seq analysis? \* 2 分

(可複選)

- ☐ Revealing the composition of different cell types and functions within highly organized tissues
- ☐ Engineering new proteins
- ☐ Identifying rare/ new cell types
- ☐ Studying the gene expression pattern of cancer cells
- ☐ Treating tumors or cancer cells

11 ° What can you know from the annotated graph of simple single cell RNA sequencing? \* 1 分

(可複選)

- ☐ The percentage of each type of cells
- ☐ The types of cells in the tissue
- ☐ The possibility of cancer
- ☐ The distribution (location) of cells in the tissue (2D)

12 ° How do algorithms annotate cells (classifying cells into known cell types)? 2 分

(可複選)

- ☐ By calculating the number of genes, number of cells, and match them by manually
- ☐ By finding the highly expressed gene of cells and match with marker genes of certain cell types.
- ☐ By comparing the query data with bench dataset
- ☐ By generating the total number of cells that express one gene

13 ° What is the full name of PCA and what does it do? \*

1 分

(可複選)

- ☐ Principal Component Analysis, finding the major expressing genes of the data and represent them in fewer dimension graphs
- ☐ Primary Causes Analysis, finding the major expressing genes of the data and represent them in fewer dimension graphs
- ☐ Primary I Causes Analysis, transforming high-dimensional data into fewer dimensions and still keeping the pattern and trend of the data
- ☐ Principal Component Analysis, transforming high-dimensional data into fewer dimensions and still keeping the pattern and trend of the data

14 ° Which of these is a down-stream analysis after annotation? \*

1 分

單選。

- ☐ Unsupervised Clustering
- ☐ Trajectory Analysis
- ☐ Dimensional Reduction
- ☐ Normalization

15 ° Which are the ways to annotate cells? \*

2 分

(可複選)

- ☐ Positive and negative cell marker set
- ☐ Use reference dataset
- ☐ Labeling
- ☐ Batch effect removal

16 ° Which computational method is often used for dimensionality reduction in scRNA-seq data? \* 1 分

單選。

- ☐ Polymerase chain reaction (PCR)
- ☐ UMAP (Uniform Manifold Approximation and Projection)
- ☐ In-situ hybridization
- ☐ Western Blotting

17 ° Which one is CORRECT? \* 1 分

單選。

- ☐ We can know about gene expression level with single cell sequencing data
- ☐ Cells do not need to be isolated in single cell sequencing
- ☐ Only RNA of mammalian cells can be sequenced
- ☐ GO enrichment is not a type of down stream analysis of single cell sequencing

18 ° Why do we need to select cells with low levels of mitochondrial genes? 1 分

單選。

- ☐ Mitochondria DNA does not regulate the gene expression of the cell
- ☐ Cells with high levels of mitochondrial genes are often indicative of low-quality cells
- ☐ Mitochondrial genes have a low level of expression
- ☐ Cells with these genes are bacteria, not our target cells

### User feedback

If you were in the **Control group or No Internet group**, you ought not answer the questions below except the first one.

19 ° On the scale of 1 to 10, how hard do you think it is for you to learn scRNA-seq? \*

單選。

	1	2	3	4	5	6	7	8	9	10	
Very	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	Very Hard

20 ° On the scale of 1 to 10, how much do you think the scRNA-seq analysis copilot helped you to learn scRNA-seq?

單選。

	1	2	3	4	5	6	7	8	9	10	
Little	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	Very much

21 ° How can the AI chatbot be optimized?

(可複選)

- ☐ Add more features, functions
- ☐ Add references to the responses
- ☐ Add more default datasets
- ☐ 其他 : \_\_\_\_\_

22 ° Any comments or advice

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Thank you!





