實作作業說明

書面報告繳交期限：工作坊結束後 1 個月內

口頭報告: 時間：2025/8/30 (六) 10:00-16:00 (待定); **地點:** 成大醫學院 六樓 82-0624

本實作請下載**「線上公開的皮膚相關 scRNA-seq 資料」** 進行完整分析。

課程設計 9+1 項 *Checkpoints*，其中 **第 0, 5–8 項為必答**，其餘可視需求選答。請於分析與撰寫報告時，依序回應下列問題並提出具體佐證（圖表、統計量或文獻）：

#	檢核主題	檢查點與關鍵問題
0	資料來源與預處理記錄	· 請詳細紀錄資料來源與樣本說明、分析流程、R 及套件版本與參數設定。
1	品質管制（QC）設定	· 閾值與過濾策略是否合理？ · 是否可能過度過濾而排除關鍵細胞？
2	主成分數量（PCs）選擇	· 依據哪些指標或概念決定 PC 數？
3	批次效應校正	· 整合後是否改善 batch effect 且保留生物訊號？ · 若為跨平台／實驗室／物種整合，需注意哪些問題？
4	群集解析度調整	· 最終採用的解析度是否合理?如何判斷過高或過低？ · 是否使用量化指標進行解析度優化？
5	細胞類型標註 (必答)	· 標註結果是否符合已知生物學知識？ · 是否有值得關注的細胞族群變化或新穎細胞族群?
6	差異表達基因（DEG）(必答)	· 目前使用的篩選門檻與統計方法是否恰當？為什麼? · 這些 DEG 是否與既有的疾病機轉、治療靶點、或細胞功能相關？是否提供新見解？
7	功能富集與細胞通訊 (必答)	· 富集分析與通訊網絡揭示何種機制假設？ · 與臨床或病理的連結為何？
8	結果整合 (必答)	· 各分析結果間是否具有一致性？是否可整合為一個生物機制假說或模型？
9	軌跡分析（若適用）	· 如何界定起點（root）？ · 起點選擇對軌跡推論結果造成何種影響？

提交格式

- 書面報告：Word 或 PDF，附完整程式碼、主要圖表與關鍵結果說明
- 口頭報告：10 分鐘簡報＋5 分鐘 Q&A

Practical Assignment Instructions

Oral Presentation:

Date: August 30, 2025 (Saturday), 10:00–16:00 (TBD)

Venue: Room 82-0624, 6th Floor, College of Medicine, National Cheng Kung University

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Assignment Description:

Participants are required to download a **publicly available skin-related scRNA-seq dataset** and conduct a complete analysis.

The assignment includes **9+1 checkpoints**, where **Checkpoints 0 and 5–8 are mandatory**, and the rest are optional based on your analysis needs.

Please respond to the following checkpoints in order, with **supporting evidence** such as plots, statistical metrics, or references.

#	Topic	Checkpoints & Key Questions
0	Data Source and Preprocessing	• Record dataset source, sample information, analysis workflow, R and package versions, and parameter settings in detail.
1	Quality Control (QC) Settings	• Are the filtering thresholds and strategies reasonable? • Could essential cell populations be excluded due to over-filtering?
2	Selection of Principal Components (PCs)	• What indicators or concepts were used to determine the number of PCs?
3	Batch Effect Correction	• Does the integration effectively reduce batch effects while preserving biological signals? • For cross-platform/lab/species integration, what issues arise?
4	Clustering Resolution Adjustment	• Is the chosen resolution appropriate? How do you determine if it is too high or low? • Did you use quantitative metrics to optimize resolution?
5	Cell Type Annotation (**Required**)	• Do the annotations match known biological knowledge? • Are there notable population shifts or novel cell types?

#	Topic	Checkpoints & Key Questions
6	Differential Gene Expression (**Required**)	• Are the current thresholds and statistical methods appropriate? Why? • Do the DEGs relate to disease mechanisms, therapeutic targets, or cell functions?
7	Functional Enrichment & Cell-Cell Communication (**Required**)	• What mechanistic hypotheses do enrichment and communication analyses suggest? • How do these findings connect to clinical or pathological features?
8	Integration of Results (**Required**)	• Are the findings consistent across analyses? • Can the results be synthesized into a coherent biological model or hypothesis?
9	Trajectory Analysis (if applicable)	• How is the root state defined? • How does the root selection affect the inferred trajectory?

Submission Format

- **Written Report:**
  Submit as a Word or PDF file, including the full analysis code, key plots, and explanations of major findings.
- **Oral Presentation:**
  10-minute presentation followed by 5 minutes of Q&A.