

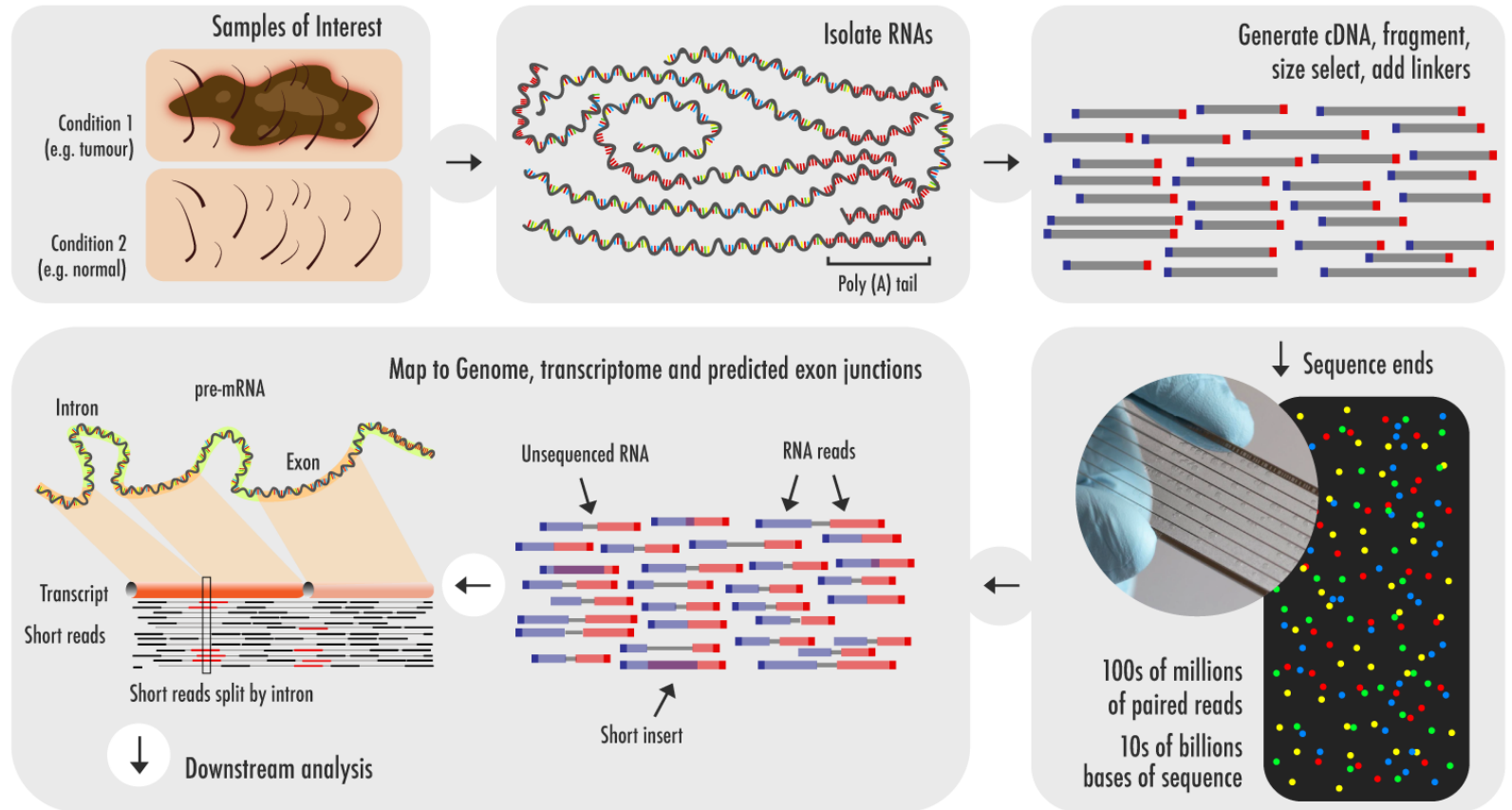
Single-Cell RNA Sequencing in Cancer

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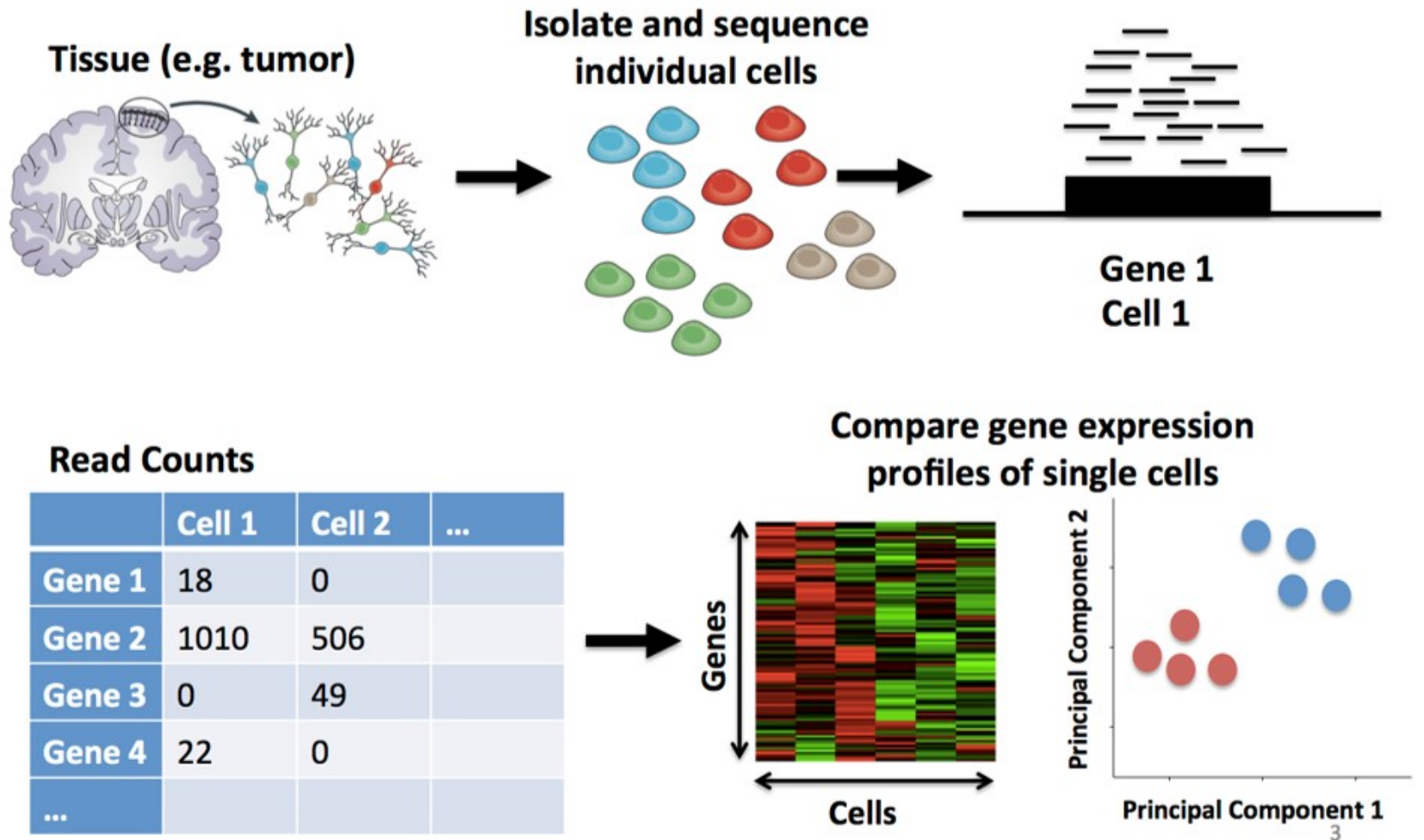
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RNA Sequencing(RNA-seq)



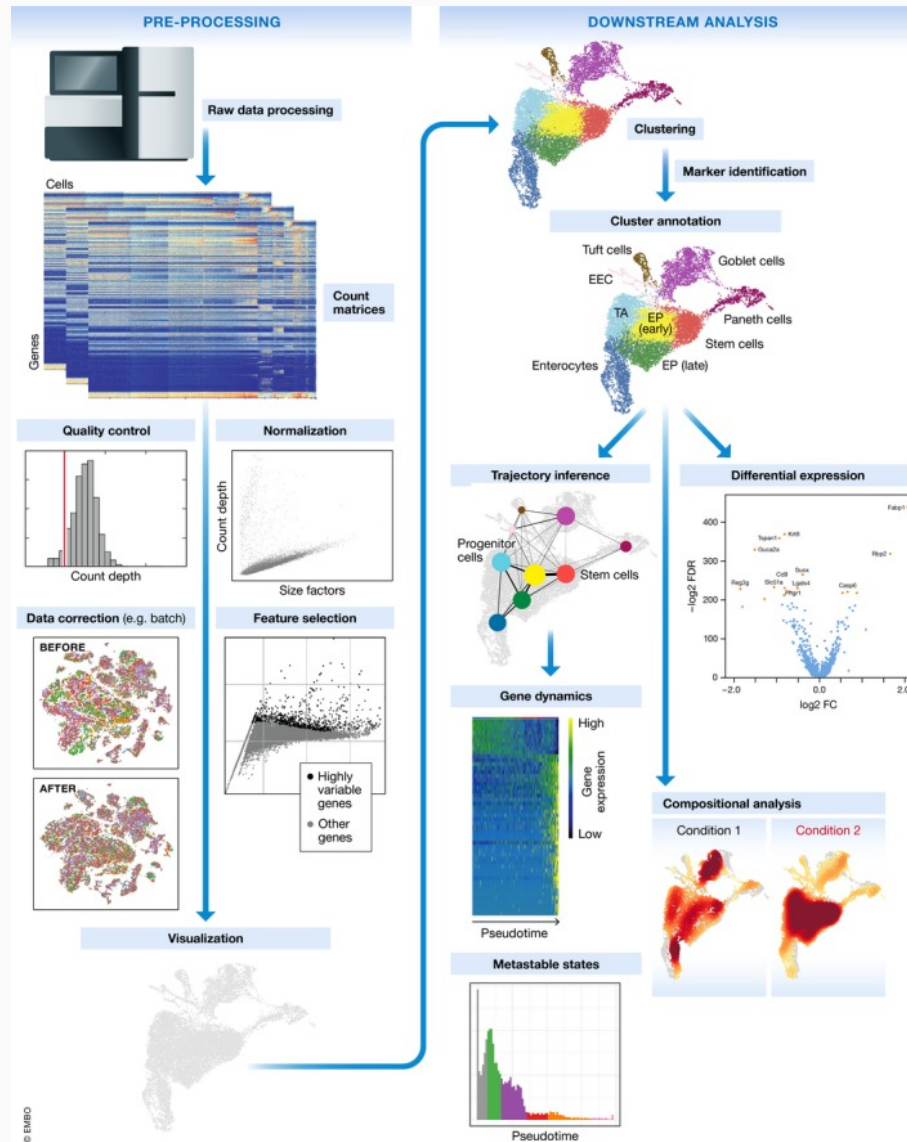
Single-cell RNA Sequencing(scRNA-seq)



Expression Intra-tumor Heterogeneity (eITH)

- caused by genomic instability
- governs many critical facets of tumor biology
 - tumor progression
 - metastasis
 - resistance to treatment
- driven by subsets of tumor cells -> crucial to learn single cell level genomic information

Bioinformatics Analysis

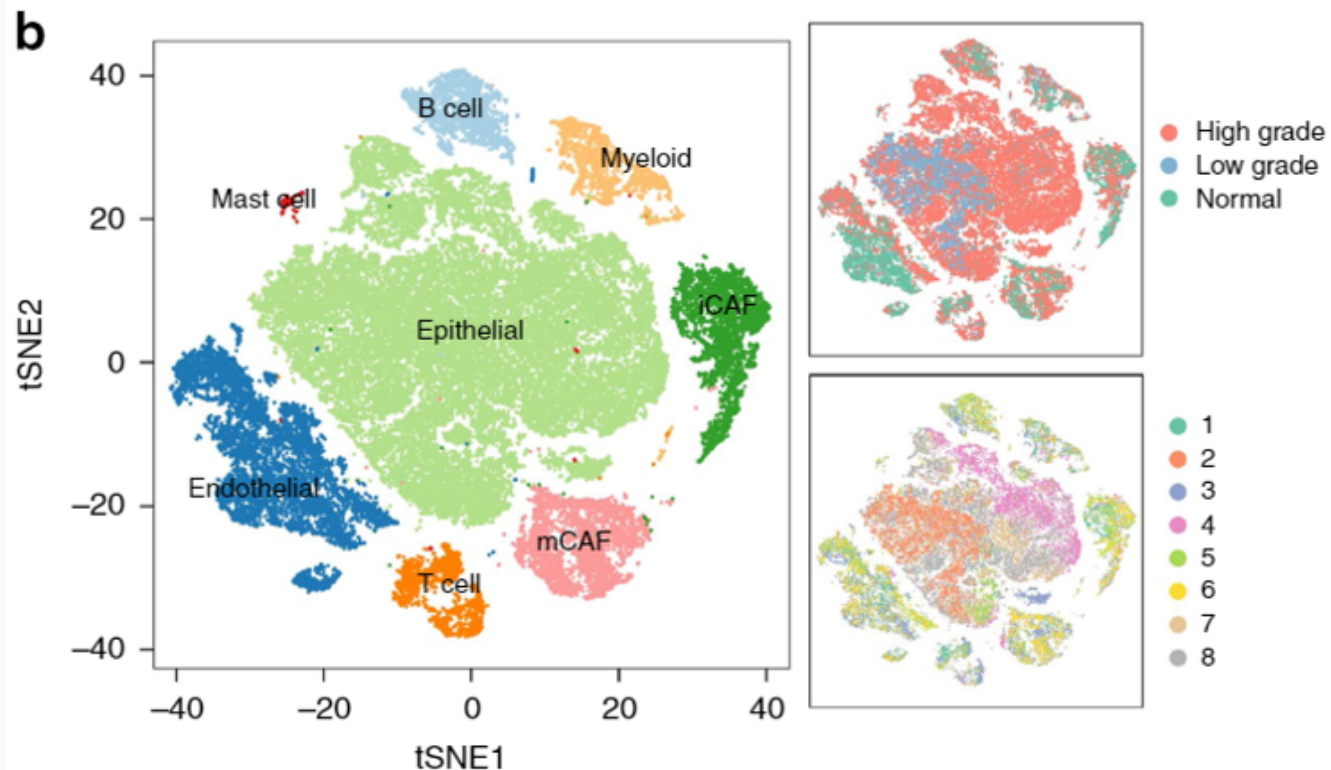


Example: bladder urothelial carcinoma

- one of the most prevalent uro-genital malignant disease
- healthy cells(urothelial cells) in the bladder lining change and grow out of control
- designing new treatment strategies for BC is challenging
 - one of the least immune infiltrated cancers
 - poor response to anti-PD1 therapy

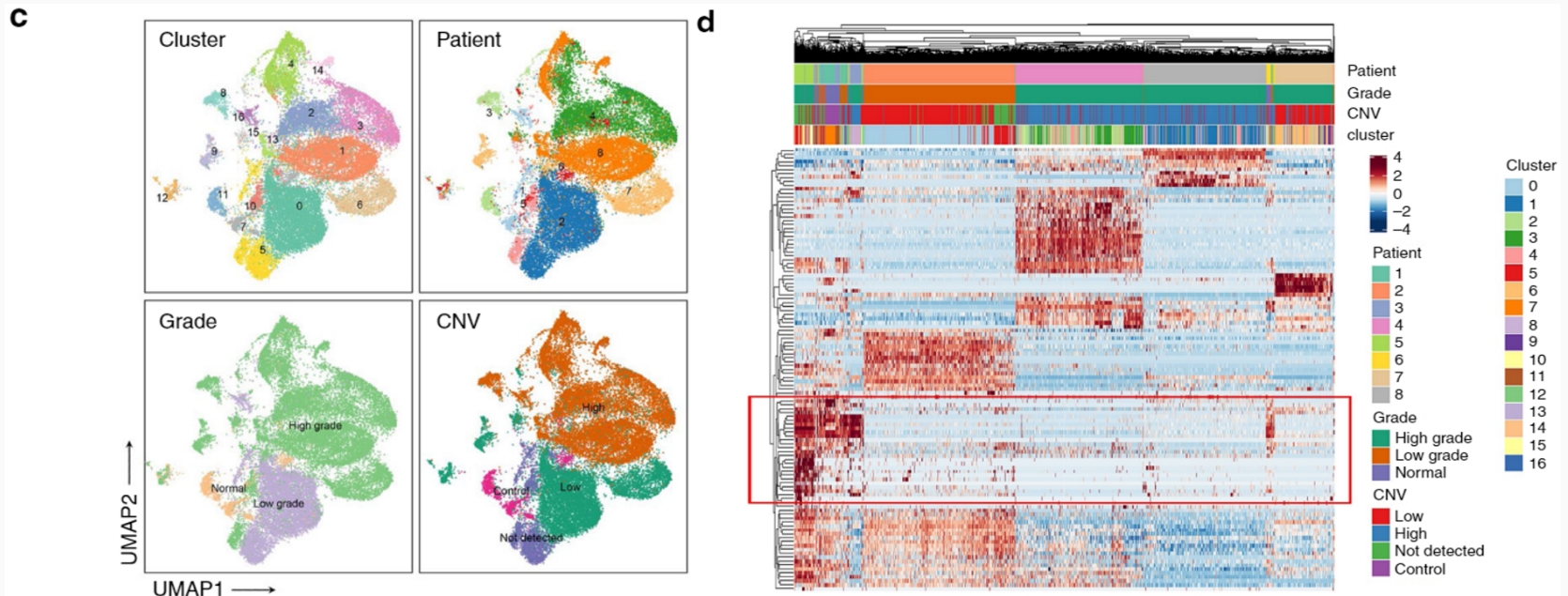
Example: bladder urothelial carcinoma[4]

- overall
- 2 low-grade bladder urothelial tumors; 6 high-grade bladder urothelial tumors; 3 adjacent normal mucosae
- iCAFs: inflammatory cancer-associated fibroblasts; mCAF: myo-CAFs



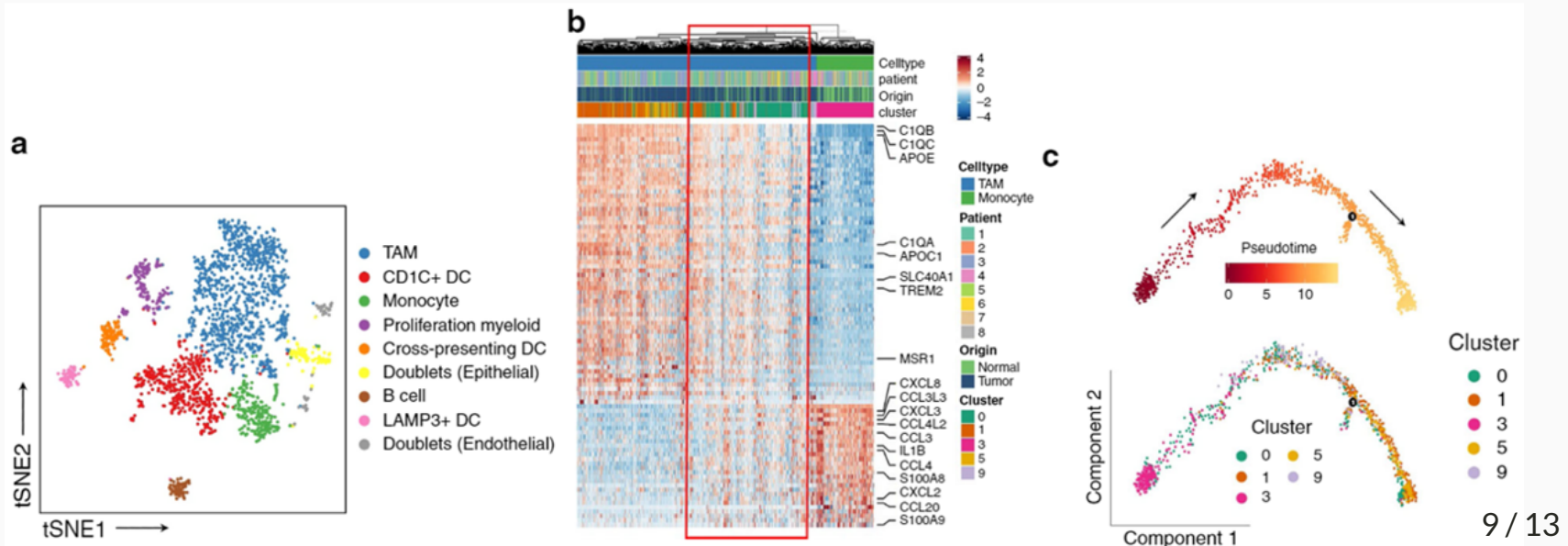
Example: bladder urothelial carcinoma [4]

- EPCAM+ epithelial cells(EPCs)
- CNVs accumulated in most high-grade tumor-derived EPCs
- showed high heterogeneity among clusters
- some cells from tumor tissue possessed almost no CNV and showed a similar expression pattern to normal EPCs -> non-malignant EPCs.



Example: bladder urothelial carcinoma[4]

- myeloid cells
- monocytes recruited into the tumor region were reprogrammed into tumor-associated macrophages(TAMs)
 - monocytes mostly originated from normal mucosal tissues, while TAMs were enriched in BC tissues
 - the transcriptomes of these two cell types exhibited continual changes
 - confirmed by trajectory analysis

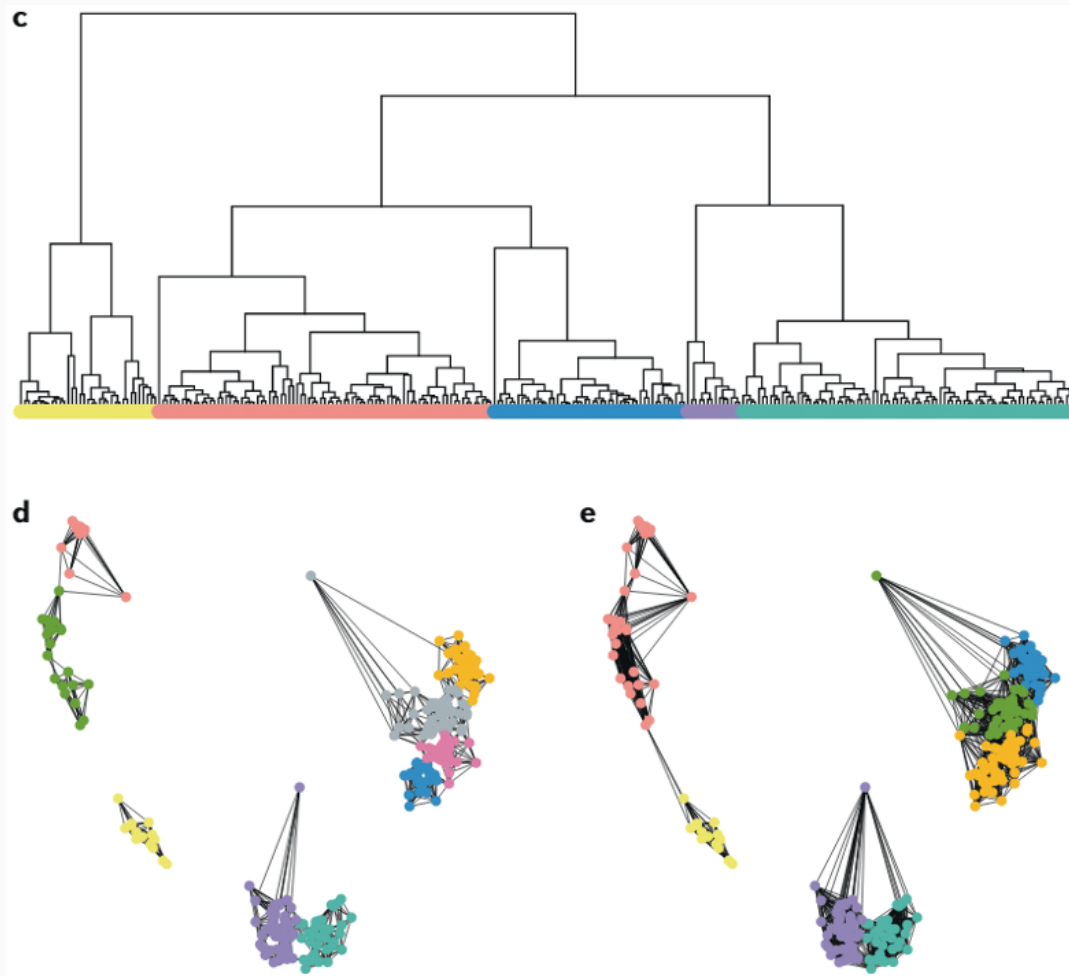


Thanks!

References

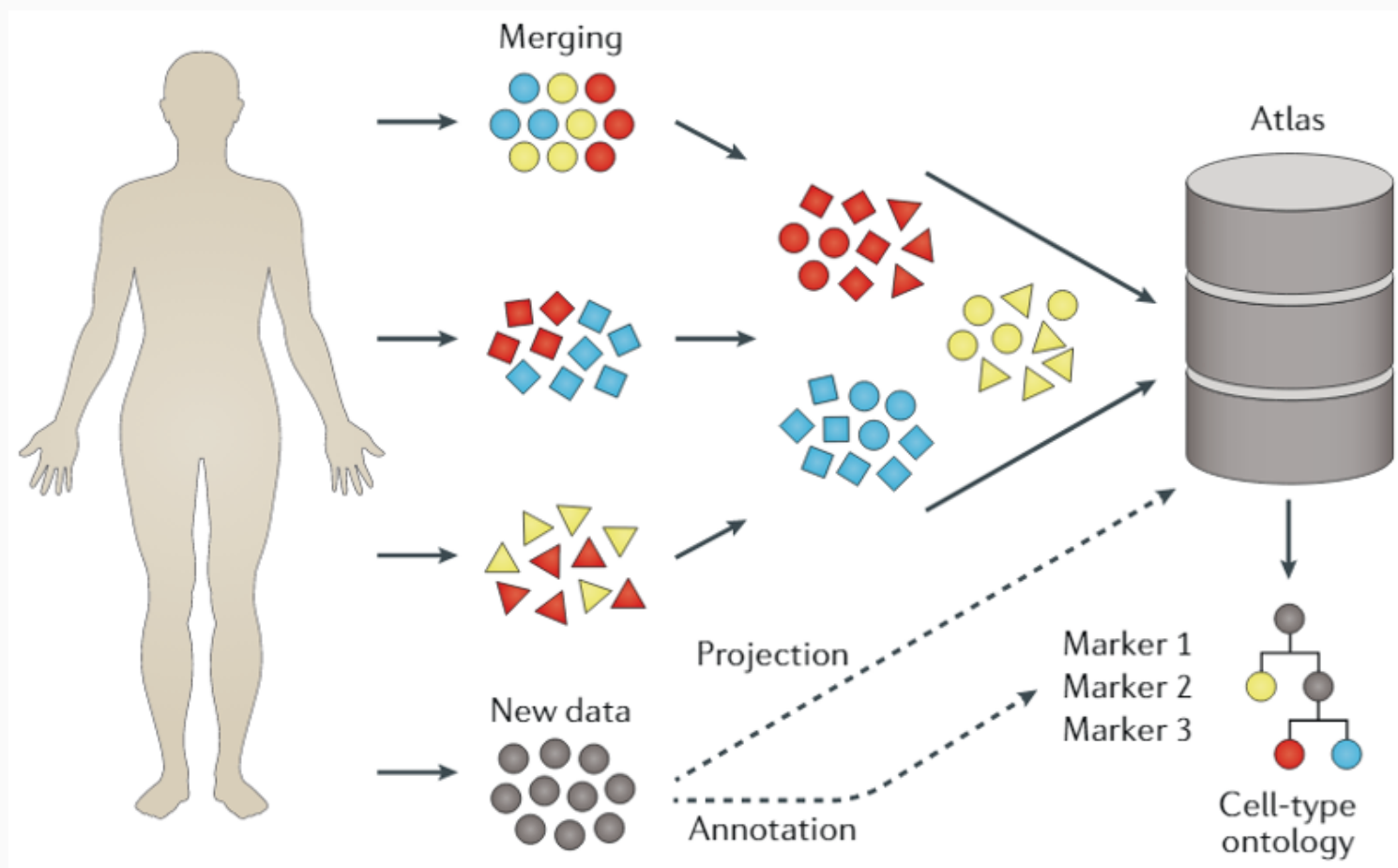
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- [2] M. Li, Z. Zhang, L. Li, et al. "An algorithm to quantify intratumor heterogeneity based on alterations of gene expression profiles". In: *Communications biology* 3.1 (2020), pp. 1-19.
- [3] V. Y. Kiselev, T. S. Andrews, and M. Hemberg. "Challenges in unsupervised clustering of single-cell RNA-seq data". In: *Nature Reviews Genetics* 20.5 (2019), pp. 273-282.
- [4] Z. Chen, L. Zhou, L. Liu, et al. "Single-cell RNA sequencing highlights the role of inflammatory cancer-associated fibroblasts in bladder urothelial carcinoma". In: *Nature communications* 11.1 (2020), pp. 1-12.

Bioinformatics Analysis: clustering



"Challenges in unsupervised clustering of single-cell RNA-seq data."

Bioinformatics Analysis: clustering



"Challenges in unsupervised clustering of single-cell RNA-seq data."