Integration: Single-cell RNA and Single-cell RNA

Group 5

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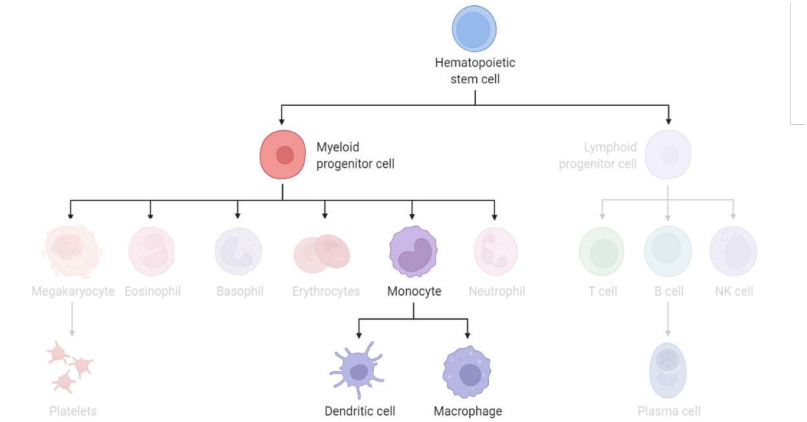
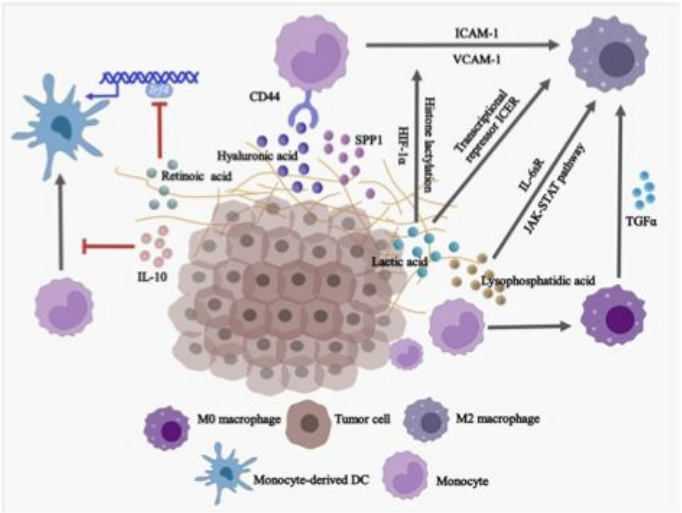
Monocytes can **differentiate** into **macrophages** or **dendritic cells**





The **TME** (tumoural factors) play a role in driving the **differentiation of monocytes into pro-tumoral/anti-tumoral** monocyte-derived cells (macrophages/DCs), contributing to tumor development

TME: Tumor Microenvironment

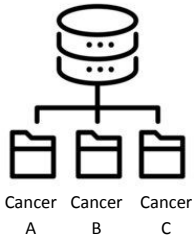
How do **monocyte populations** vary across **different cancer types**, and how does this variation contribute to their **differentiation into pro-tumoral or anti-tumoral phenotypes**, impacting tumor progression?

HOW?

Analyze a collection of **scRNA-seq datasets** for **monocytes** from **different cancer samples**

Dataset collection

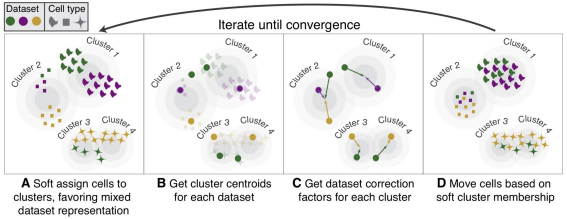
Raw scRNA-seq datasets (monocytes)



Data preprocessing

- CellRanger
- QC
- Filtering out low-quality cells
- Normalization
- …

Integration



Characterize monocytes subpopulations

I.e., based on marker gene expression and known monocyte subsets (e.g., classical, intermediate, non-classical, DC-like cells…etc.)

Differential Gene Expression Analysis

Downstream analysis

Functional Annotation and Pathway Analysis

Mapping GEX signatures of monocytes to known anti-/pro-tumour signals

Criteria

- Human data
- Monocytes
- Monocytes isolated from cancer patient samples

Raw scRNA-seq datasets (monocytes)

Breast Cancer	**Lung Cancer**	**Melanoma**
Ding et al. (2023)	Sun et al. (2024)	Smalley et al. (2021)
Brechbuhl et al. (2020)	Chen et al. (2021)	Lozano et al. (2022)
	Chan et al. (2021)	Rad Pour et al. (2021)