单细胞测序数据介绍

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专 业: 22级 数学

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提纲

- > 单细胞单组学
- > 单细胞多组学
- > 空间转录组学
- > 空间多组学



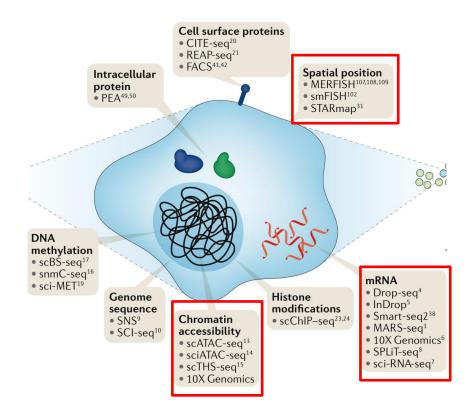
单细胞单组学

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单细胞单组学 single cell sequencing

Single-cell sequencing (SCS) technology allows researchers to study *cell heterogeneity* at different levels of gene regulation.

- Single cell RNA-seq
- Single cell DNA-seq
- **■** Single cell epigenomics
- Single cell multi-omics
- Single cell omics integrated with spatial transcriptomics



Stuart T. et al. Nat. Rev. Genet. (2019)



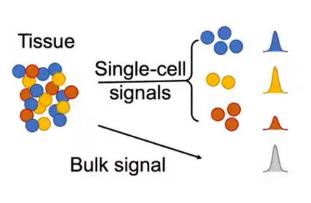
单细胞单组学 scRNA-seq and scATAC-seq

- **Single cell expression**(Compared with bulk-seq).
- Single cell RNA sequencing(scRNA-seq),

$$\mathbf{X} = (x_{ij})_{m \times n} \in \mathbb{N}^{m \times n}$$
.

Single cell ATAC sequencing(scATAC-seq),

$$\mathbf{X} = (x_{ij})_{m \times n} \in \{0, 1\}^{m \times n}$$
.



	gene 1	gene 2		gene n	
cell 1	3	0		0	
cell 2	0	0		14	
÷	÷	:	٠	:	
cell m	0	1		13	

	peak 1	peak 2	 peak n
cell 1	1	0	 0
cell 2	0	0	 1
:	÷	:	 :
cell m	0	1	 0



单细胞单组学 features of single cell omic data

Challenges

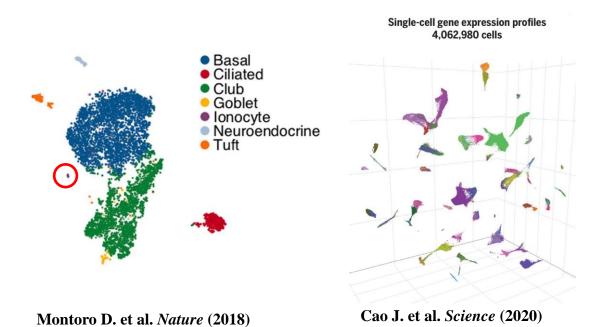
- ☐ High dimensional data (e.g. thousands of genes).
- ☐ High missing data. (e.g. specific expression in each cell).
- ☐ Strong noisy data. (e.g. high amplification bias).
- ☐ Dropout events.

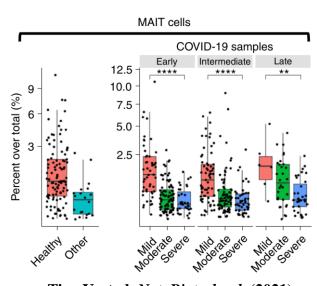
dataset	organ	platform	cell types	cells	zero percentage
Adam	Kidney	Drop-seq	8	3660	92.33%
Bach	Gammary Gland	10x	8	23184	88.04%
Chen	Brain	Drop-seq	46	12089	93.74%
Klein	Embryonic Stem Cell	inDrop	4	2717	65.58%

Chen L. et al. NAR Genom. Bioinform. (2020)

单细胞单组学 pros of SCS

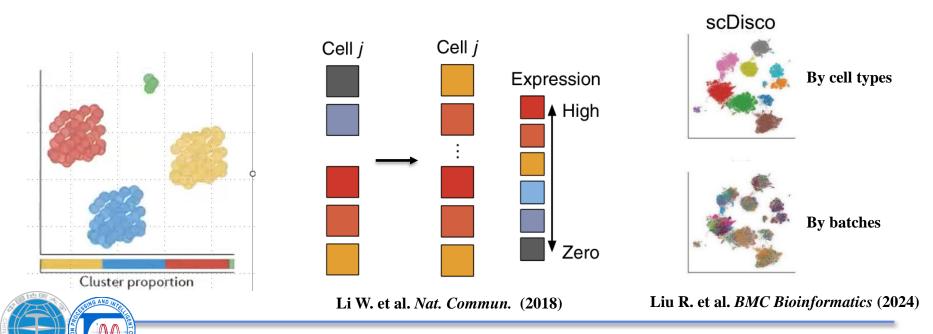
- Discovery of rare cell type,
- Cellular atlas construction,
- Understanding of pathological immunity.





单细胞单组学 problems in scRNA-seq(scATAC-seq)

- *Clustering*, separate cells to different clusters.
- *Imputation*, decline dropout events.
- *Integration*, correct batch effects.
- *Annotation*, labeling clusters to cell types.

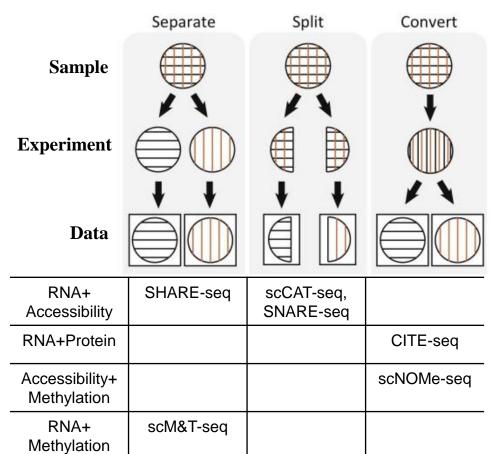


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单细胞多组学 single cell multimodal omics

Simultaneously obtain multimodal data (aka paired data).



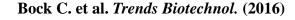
Pros.
1 1 1 1 1 1 1 1 1

- More information.
- ☐ Deeper insights.

Cons:

- More complicated.
- More noise and lower quality.

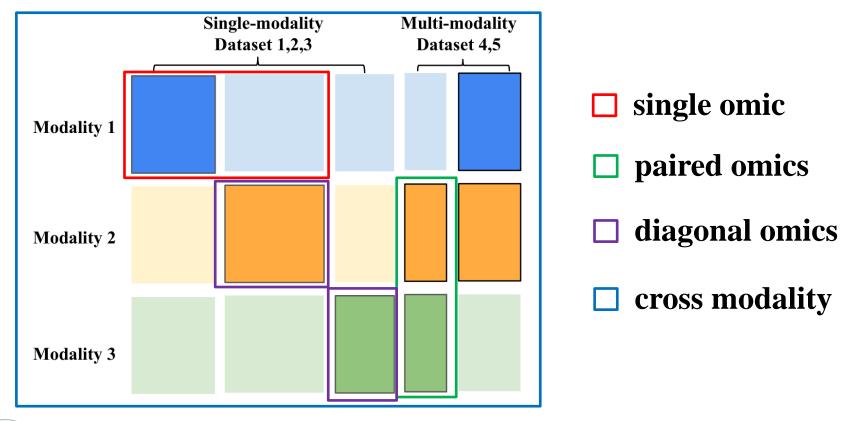
modality	technology	Avg. counts	Non-zeros
Multi-modal	sci-CAR	1600	2.19%
scRNA-seq	10X RNA	7589	9.65%
scATAC-seq	10X ATAC	15902	6.81%





单细胞多组学 integration task

- Single omic integration: batch effect.
- Multiple omics integration: different feature spaces + different distributions





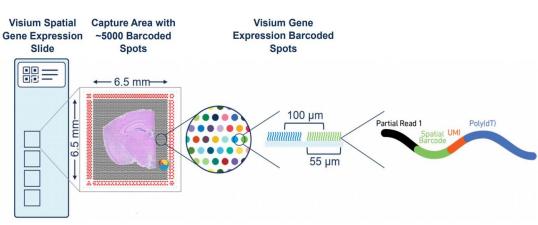
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空间转录组学 spatial transcriptomics

Spatial Transcriptomics (ST) profiles gene expression while retaining *spatial information*.

- > Image based: high resolution, low depth;
- > Sequencing based: high throughput, (low) resolution.
 - Slide-seq (v1, 2019; v2, 2021)
 - 10x Visium (2019)
 - <u>HDST</u> (2019)
 - <u>Stereo-seq</u> (2022)



https://www.10xgenomics.com/



空间转录组学 comparing with scRNA-seq







Bulk RNA-seq

scRNA-seq

ST

Avg. expr. of cells

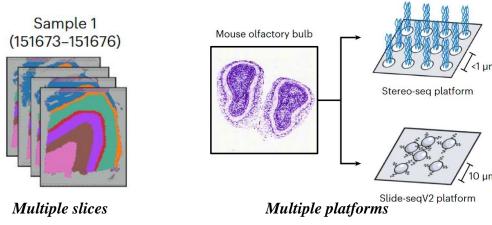
expr. of single cell

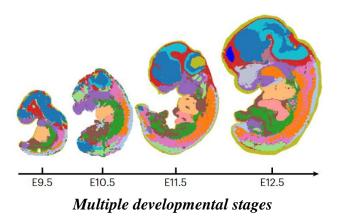
Spot expression +locations+(histology)



空间转录组学 integration of ST data

- *Clustering*. Identify different spatial domains.
- *Integration*. Integrate multiple samples.
- *Deconvolution*. Decipher cell type proportions in each spot.
- *Highly variable gene (HVG) detection*. Detect HVGs of specific domain.





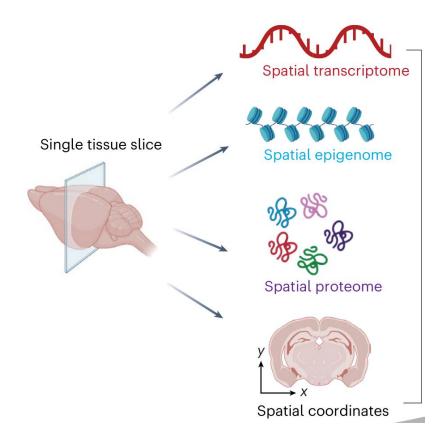
Zhou X. et al. Nat. Comput. Sci. (2023)

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空间多组学 spatial multi-omics

■ Spatial locations + multi-omics data.



Long Y. et al. Nat. Methods (2024)

Video links

See these videos for more details:

- Jin W. <u>https://www.youtube.com/watch?v=1SfRob9Y-4g</u>
- Cao Z. https://www.youtube.com/watch?v=cJ_II_UzXbc&t=4579s
- Li R. <u>https://www.youtube.com/watch?v=7026mRoJbMQ&t=127s</u>
- **Li Y.** https://www.youtube.com/watch?v=CE-T-L1EX51&t=4298s
- **Jin S**. <u>https://www.youtube.com/watch?v=GNU0SwVr948&t=1032s</u>
- Tian Y. https://www.youtube.com/watch?v=4b4lrY7DJIo

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