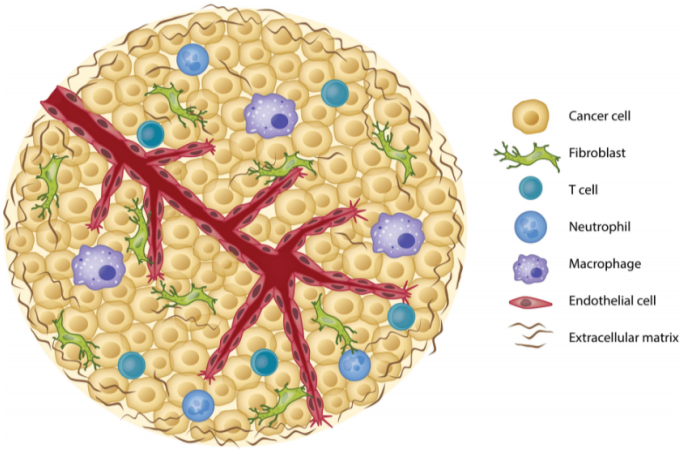
Course Code : BMEG 3105
Course Title : Data Analytics for Personalized Genomics and Precision medicine
Lecture Topic: Single Cell sequencing
Scribed by Kyaw Saw Lin (1155173213@link.cuhk.edu.hk)

Contents

- Why single cell
- What is single cell RNA sequencing
- How to get single cell sequencing

Why

Usually, collected samples are from tissues in which there are lots of cells. Therefore, RNA we got came from different cells.

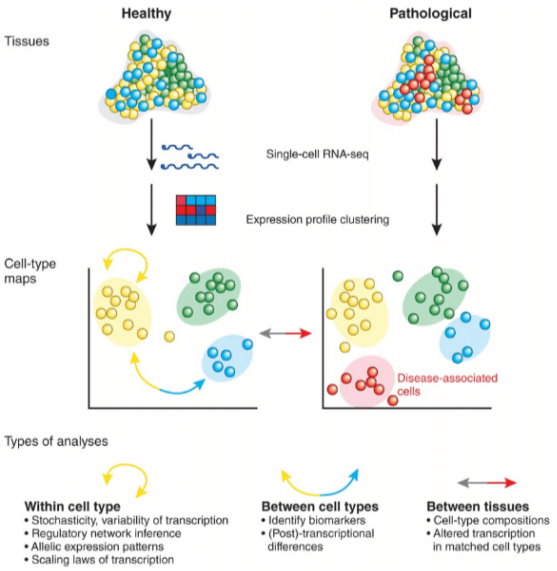


RNA sequence extracted from this cell will be a mixture of gene expression from different cells. So the resulting gene expression matrix reflects the cells in this region, not just cancer cells.

This technique is called bulk RNA-seq and just measures tissue level difference. it still can differentiate between cancer tissue and normal tissue but with low resolution.

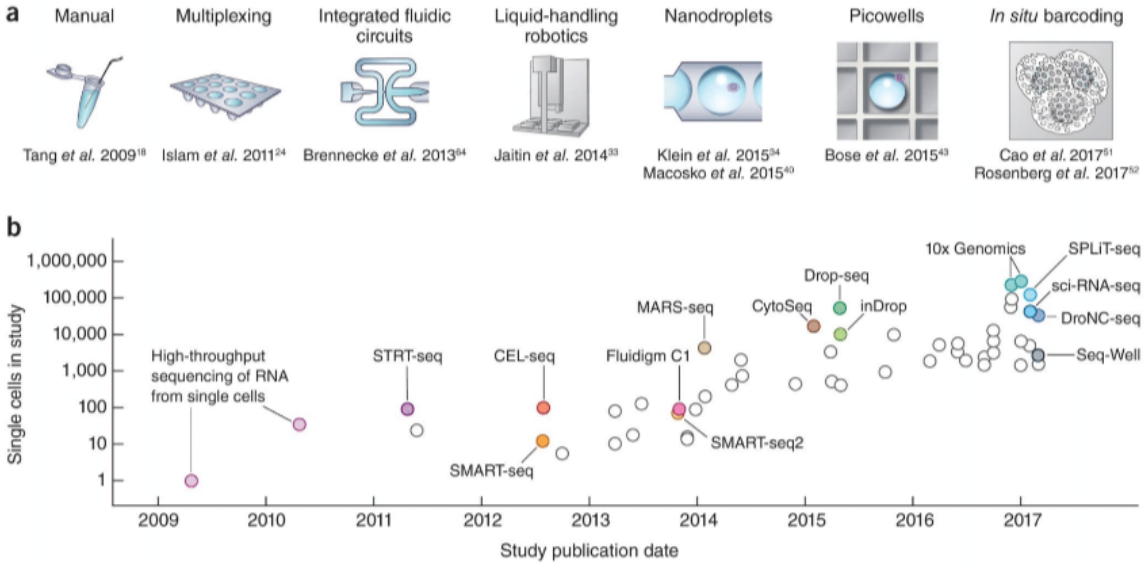
scRNA-seq (single cell RNA-seq) can measure heterogeneity, identify cell population and study cell dynamic - which can help us understand how cancer develops.

What



We cluster the gene expression matrix of the different cells and do the clustering. That way we can discover new cell clusters which can be disease associated cell groups. The difference can be within the cells, between the cells and between the tissues.

How



There are numerous ways to separate and identify single cells as follows. After that we do the sequencing and then do the data analytics.