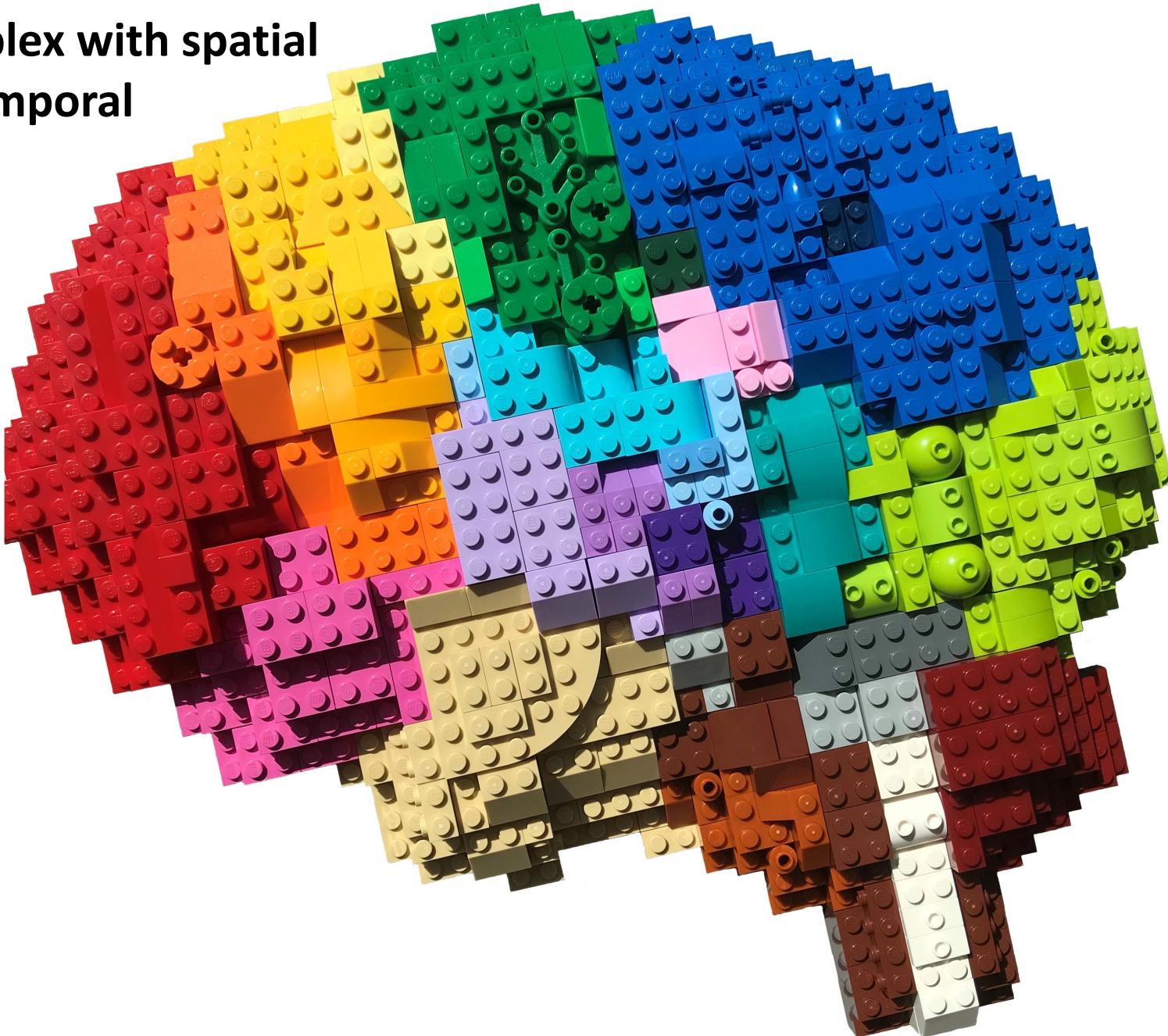


SINGLE CELL
RNA-
SEQUENCING

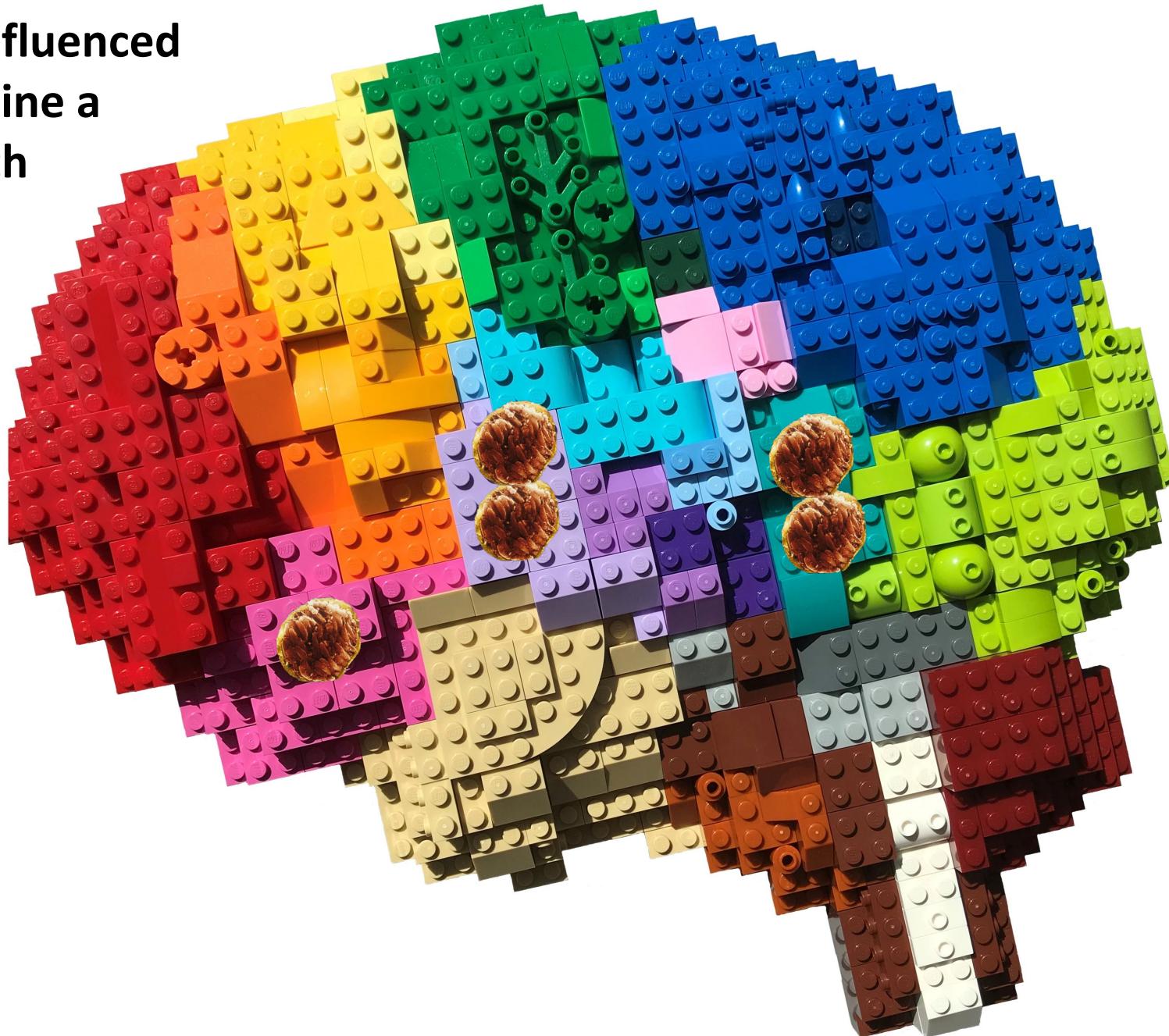
scRNaseq

**Systems are complex with spatial
functional and temporal
dimensions**



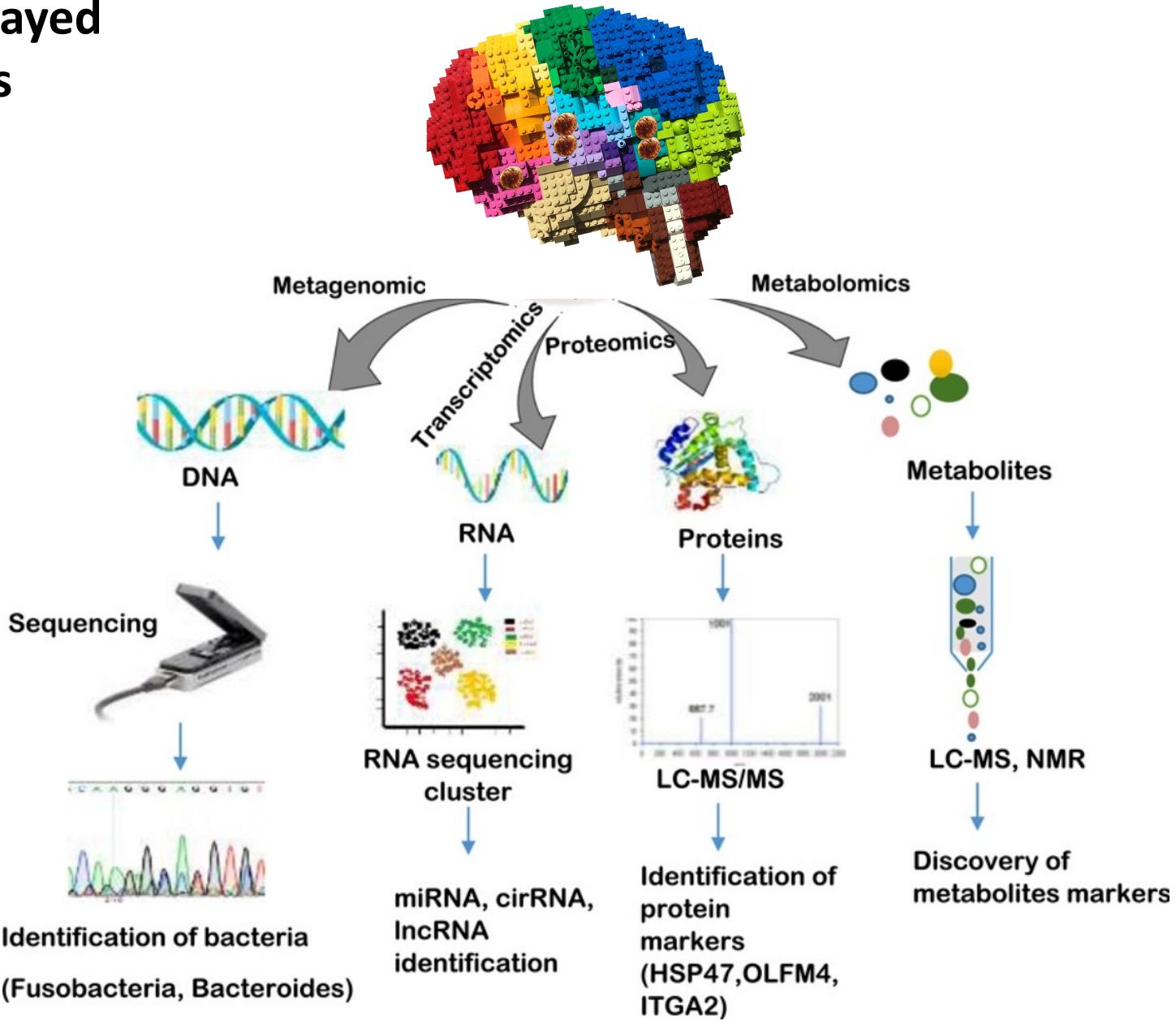
Adapted from @BoXia7

Systems can be influenced
by disease – imagine a
brain infected with
Toxoplasma



Adapted from @BoXia7

Systems can be assayed using various omics techniques



**Traditionally most
techniques assay the
“bulk” status of a system**



**What is changing in the
total brain that is infected
with *Toxoplasma***

Adapted from @BoXia7

**Single cell
omics allows
you to assay
the sub-
systems**

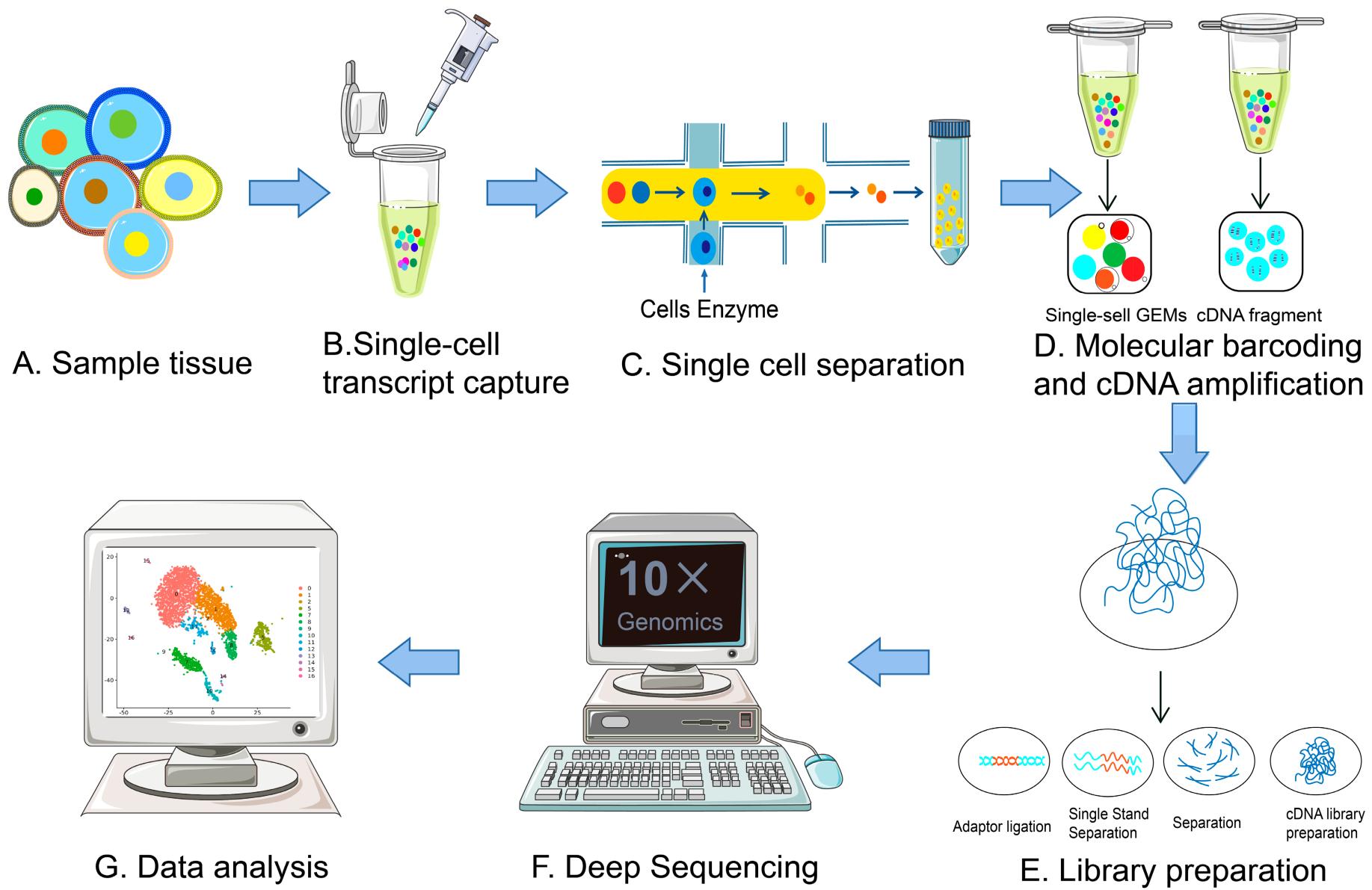


Adapted from @BoXia7

- Which cells are infected?
- What is changing in the infected cells?
- What is changing in the uninfected cells?
- What is the changing in the parasites and is this influenced by the type of cell they are interacting with?

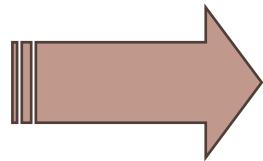


Adapted from @BoXia7

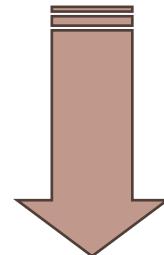


Single cell omics data is highly dimensional

	Cell1	Cell2	Cell3	Cell4	Cell5	Cell6	Cell7	Cell8	Cell9
Gene 1	12		10	34	9	4	5		33
Gene 2	4		7	5	99	55	6	5	3
Gene 3		4	5		87	55		4	33
Gene 4	5	6	3	6	4	5	45	3	24
Gene 5	60	77	3	77	5	44	3	34	2
Gene 6	70	8		8		6		34	
Gene 7	5	23		9		55	3		14



**Thousands
of cells**



**Thousands
of genes**

**The more data the better, right?
The problem is the more dimensional the data becomes
you risk introducing noise and making it harder to
visualize and understand the data.**

Dimentionality reduction

The concept behind dimensionality reduction is that high-dimensional data are dominated by a small number of simple variables. This way, we can find a subset of variables to represent the same level of information in the data or transform the variables into a new set of variables without losing much information.

Main algorithms

- Principal Component Analysis (PCA)
- t-Distributed Stochastic Neighbour Embedding (t-SNE)
- Uniform Manifold Approximation and Projection (UMAP)

