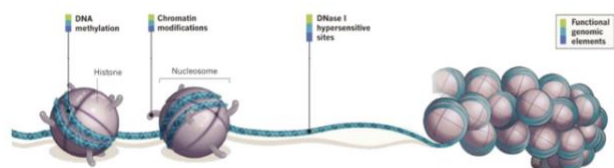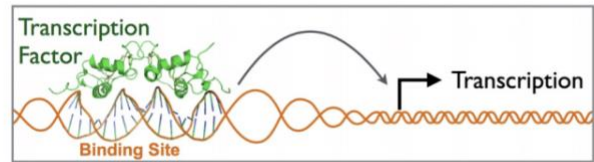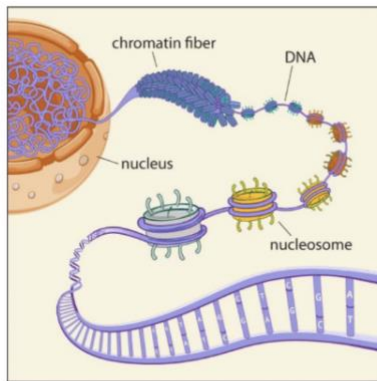# Lec 18 - note

1155138415 Leung Tak Sum

==Epigenetics==

1) Gene expression regulation: structure and environment

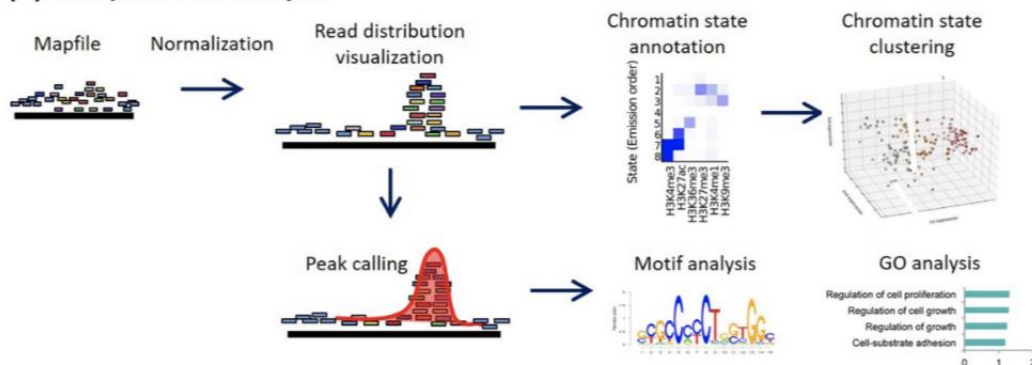

Sequencing protocols: FAIRE-seq, DNase-seq, ATAC-seq, MNase-sequencing, ChIP-seq
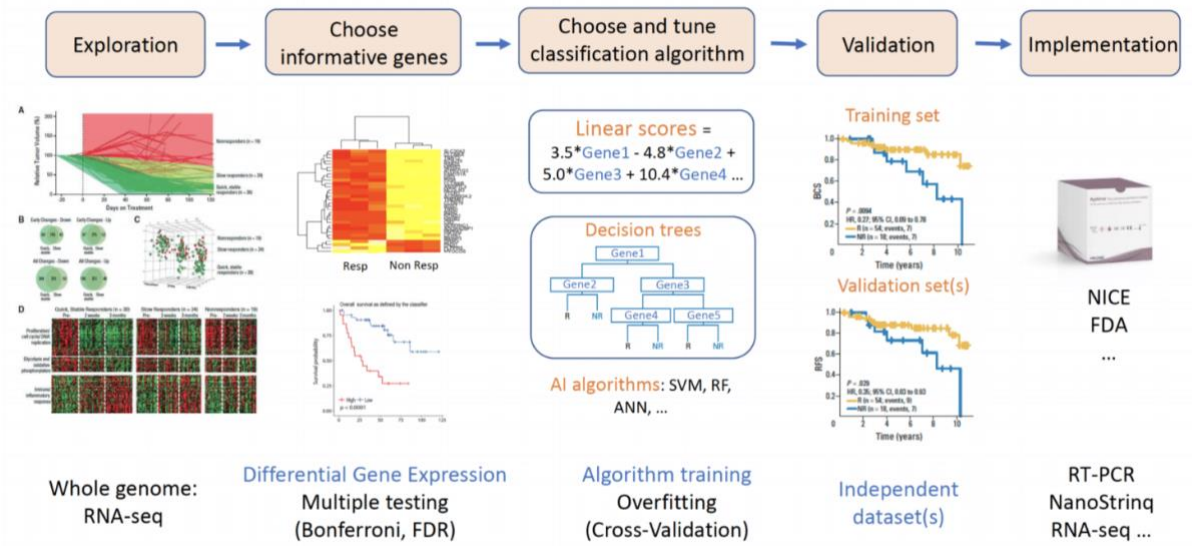
2) Data analytics pipeline

Peak calling: Peak shape vs random background, output-BED file (chromosome, start, end, label…)

Histone makes and chromatin accessibility: enhancer, promoter, gene

1) Why single cell?

Tumor micro-environment
Produce different population ⟹ define heterogeneity, identify rare cell population, cell population dynamics

2) What is single-cell RNA-seq?
Single cell sequencing examines the sequence information from individual cells with optimized next-generation sequencing (NGS) technologies, providing a higher resolution of cellular differences and a better understanding of the function of an individual cell in the context of its microenvironment

3) What can single-cell sequencing do?
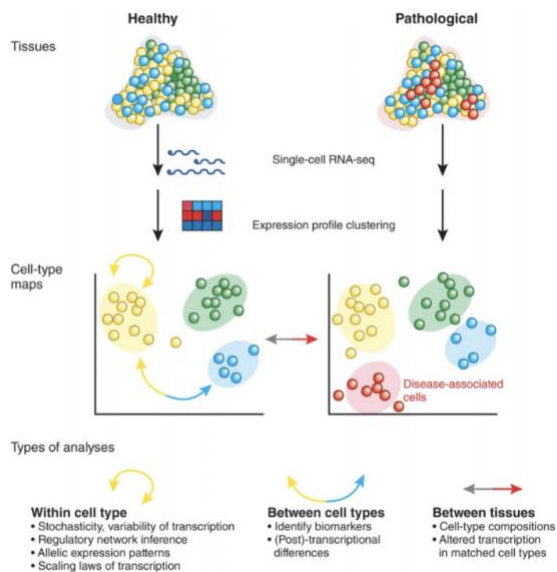
➢ Understanding heterogeneous tissues
➢ Identification and analysis of rare cell types
➢ Changes in cellular composition
➢ Dissection of temporal changes
➢ Example of applications:
  • Differentiation paths
  • Cancer heterogeneity
  • Neural cell classification
  • Embryonic development
  • Drug treatment response