Data-driven precision medicine approaches to cancer

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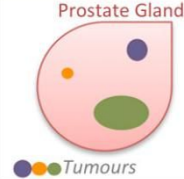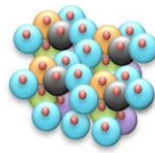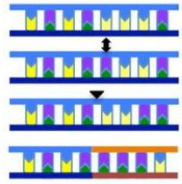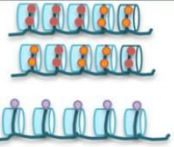
# Cancer Background

- Mass of cells
- Heterogeneity

Types of heterogeneity

Patient	Tumour	Cellular	Genomic	Epigenetic
Different primary tumours in different patients. Different metastatic tumours in different locations.	Different tumours in the same prostate of a single patient (multi-focal disease). Recurrent tumours that have been altered or selected for by treatment.	Different cell types within each tumour mass. These range from stem cells to terminally differentiated cells.	Different mutations (small nucleotide polymorphisms, insertions, deletions or genome rearrangements).	Different methylation and acetylation patterns between the same genes in the same cells, between normal and cancer cells and between different cancer cells.

Single Cell Sequences

- Seurat - R toolkit for single cell genomics
- Filter based on QC metrics (ex: total number of molecules detected in a cell)
- Identify highly variable features
- Determine dimensionality of dataset (look at p-values)
- Cluster Cells
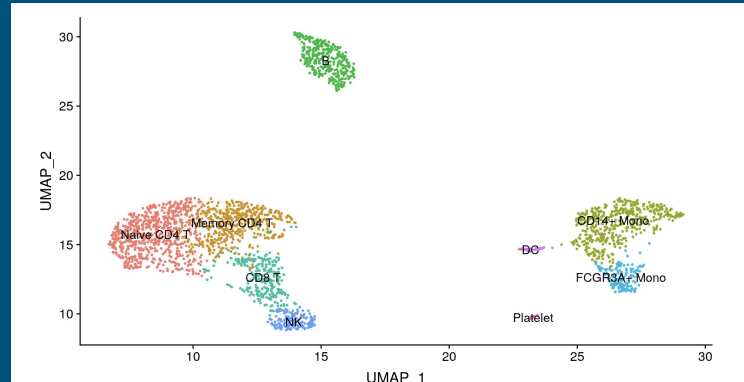
Patient Data

- Look at DNA
- Compare treatment success
- Gene expression difference

Application

- Identify tumor/aggressiveness
- More effective treatment

Acknowledgements

Thank you