Sprint2 : Machine learning and bacth effect correction

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Non-Hodgkin B-cell lymphomas take their origin in Germinal center reaction
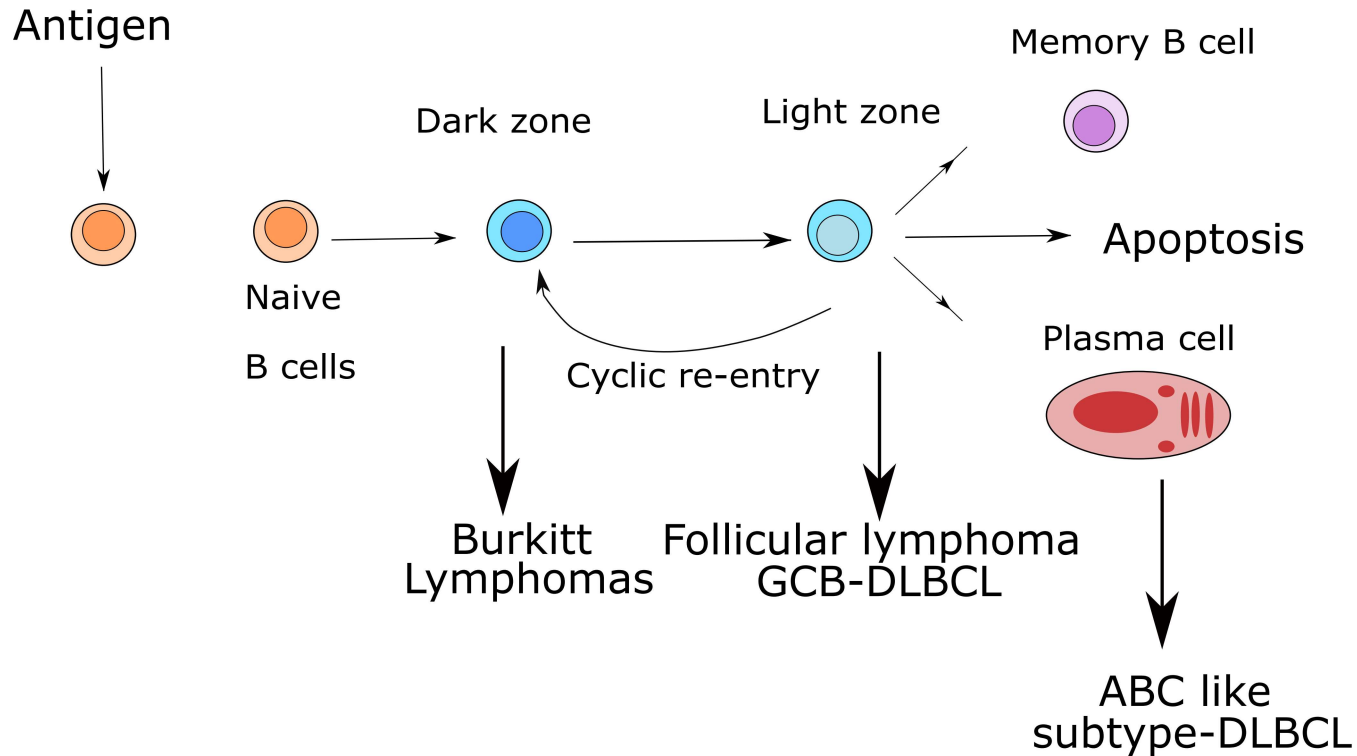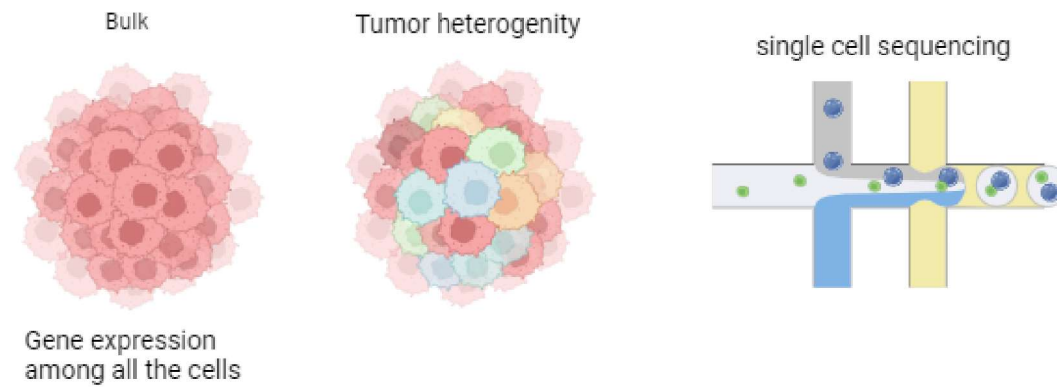

Figure 1: Origin of NHBCL

Single cell technology allows for a finer description of the tumor

Figure 2: Single cell technology

Dataset

- ▶ 3 DLBCL (malignant)
- ▶ 3 Follicular Lymphoma (malignant)
- ▶ 2 transformed lymphoma (malignant)
- ▶ 3 reactive lymph nodes (non-malignant)
- ▶ unsupervised clustering
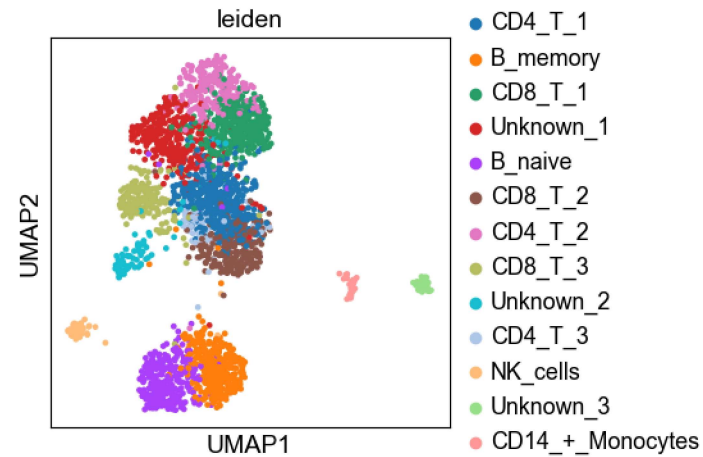
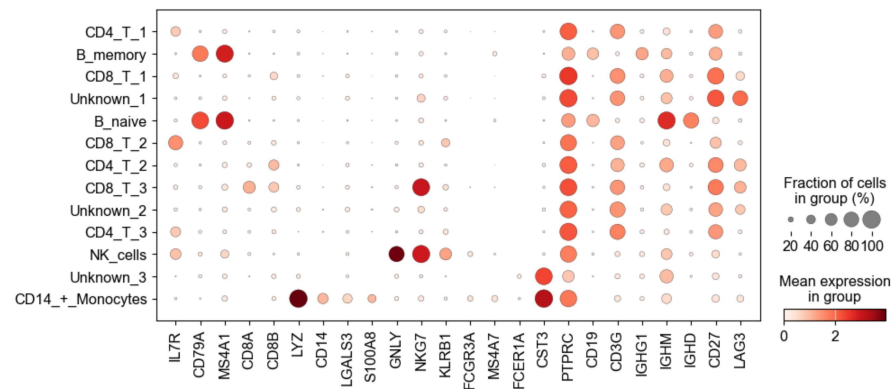# UMAP with leidenalg cluster with one sample

Figure 3: rLN1

Figure 4: Genes expression per clusters in rLN1

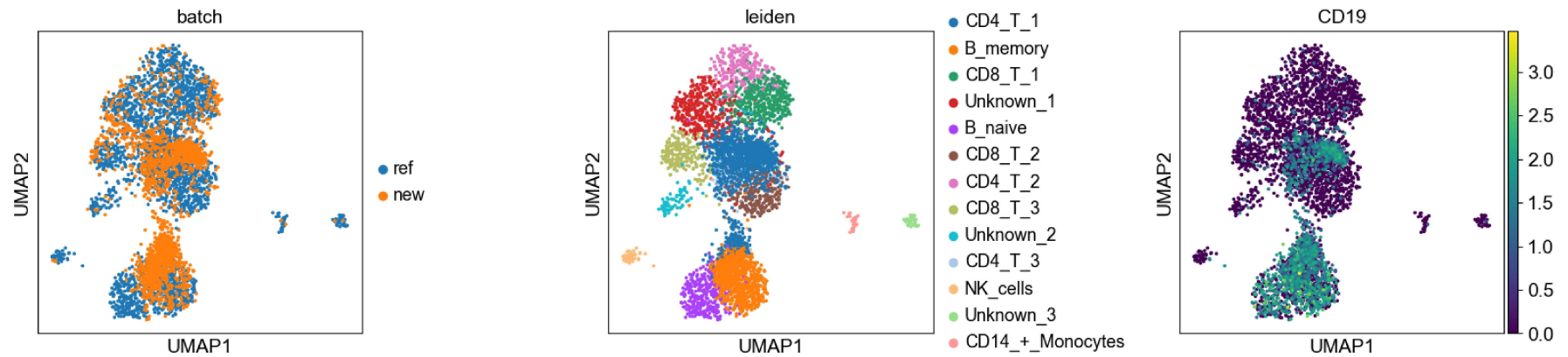# UMAP and leidenalg clustering does not prevent batch effect

Figure 5: rLN1 +rLN2

Future work to correct batch effect

- Try different clustering methods
- Apply a deep learning method
- Use already developped model : SCALEX