A

UMI count Matrix

```
##           CCTAAGCTCCGCAAGG AGCATCACCATAGAAC GCGTCACTCCGTGACG
## Gene_0001               57                45                98
## Gene_0002               38                 0                 7
## Gene_0003                0                48                 0
## Gene_0004                0                 0                 0
## Gene_0005                0                 0                 0
```

Cell-level metadata

```
##                  clusters cell_type     UMAP_1     UMAP_2
## CCTAAGCTCCGCAAGG        1         T -1.2718440  0.1879957
## AGCATCACCATAGAAC        1       Mac -0.8520433  0.2962663
## GCGTCACTCCGTGACG        2       Mac  1.2252609  0.6999774
## GTCGAATAAACAACTG        2         B  1.4901552 -0.8958026
## TGCATAACAGTCGAGT        2         B -1.3291095 -0.8355533
```

B

SingleCellExperiment

```r
mdata <- as.data.frame(colData(sce))
umap <- reducedDim(sce, "UMAP")
colnames(umap) <- c("UMAP_1", "UMAP_2")
mdata <- cbind(mdata, umap)
write.csv(mdata, file = "cell-level-mdata.csv")
```

Seurat

```r
mdata <- cbind(seurat_object@meta.data, Embeddings(seurat_object, "umap"))
write.csv(mdata, file = "cell-level-mdata.csv")
```

Scanpy

```python
import scanpy
import pandas
adata = scanpy.datasets.pbmc3k_processed()
mdata = adata.obs
umap = adata.obsm.to_df()[['X_umap1', "X_umap2"]]
pandas.concat([mdata, umap]).to_csv('cell-level-metadata.csv')
```

C