Integration

Ricardo Martins-Ferreira

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Integration pipeline

```
libs <- c("Seurat", "tidyverse")
suppressMessages(
   suppressWarnings(sapply(libs, require, character.only = TRUE))
)

## Seurat tidyverse
## TRUE TRUE</pre>
```

Integration of the sixteen Seurat objects consisting of the immune cells from each of the original dataset.

Upload input seurat objects

Integration with SCTransform

Dimensionality reduction and clustering

```
# Perform linear dimensiona reduction
Seurat <- RunPCA(Seurat, verbose = FALSE)</pre>
```

```
#Dimensionality reduction and clustering
DefaultAssay(Seurat) <- "integrated"</pre>
Seurat <- RunUMAP(Seurat, reduction = "pca", dims = 1:50, verbose = FALSE)
Seurat <- FindNeighbors(Seurat, reduction = "pca",dims = 1:50)</pre>
Seurat <- FindClusters(Seurat,resolution =0.25)</pre>
## Modularity Optimizer version 1.3.0 by Ludo Waltman and Nees Jan van Eck
## Number of nodes: 64438
## Number of edges: 4031078
## Running Louvain algorithm...
## Maximum modularity in 10 random starts: 0.9240
## Number of communities: 18
## Elapsed time: 28 seconds
\#Visualization
\verb|color2| <-c("#E6AB02", "#FC8D62", "#7570B3", "#38470B", "#E5D8BD", "#874C62", "#874C
                                      "#937666", "#666666" ,"#FA7070" ,"#B3E2CD", "#344D67","#B3CDE3",
                                      "#D9D9D9" ,"#BC80BD", "#DE6E4B" ,"#430D27")
DimPlot(Seurat, reduction = "umap",
                           cols = color2,
                           repel = TRUE, pt.size = 0.01, label = F)
```

