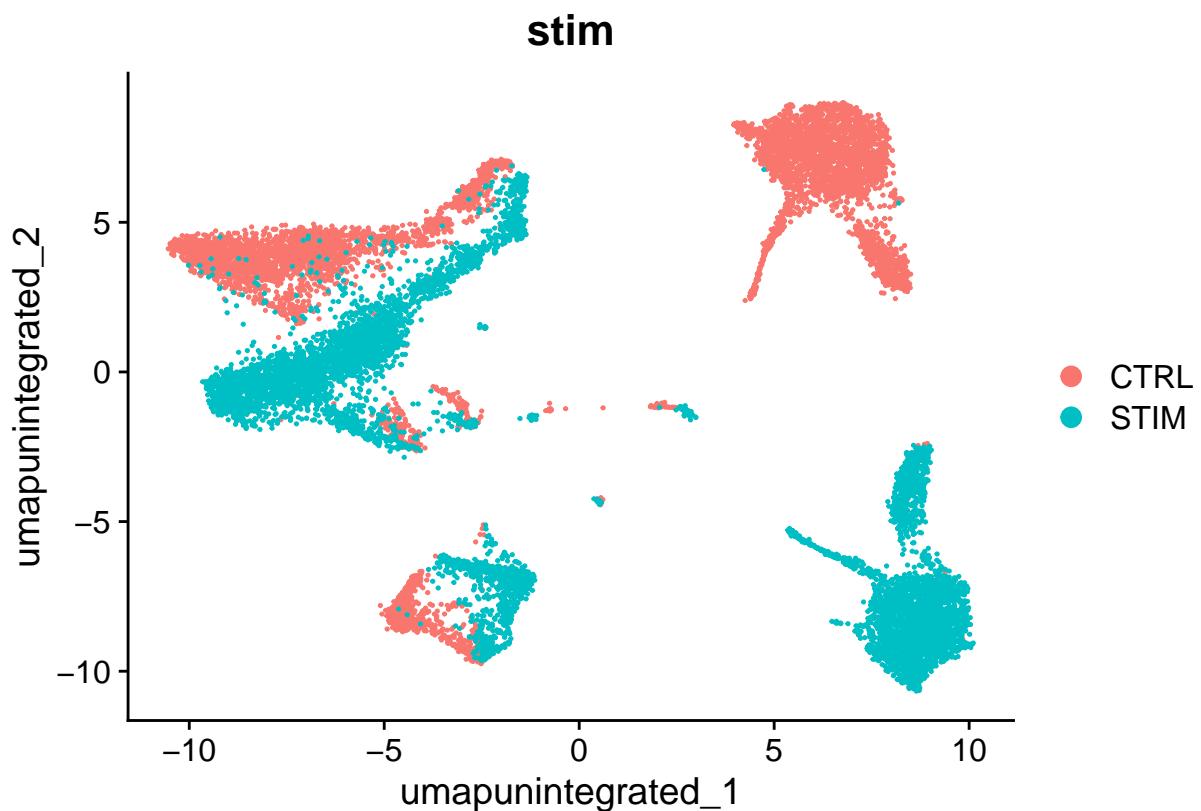


## 02\_seurat\_data\_integration\_tutorial

2025-11-20

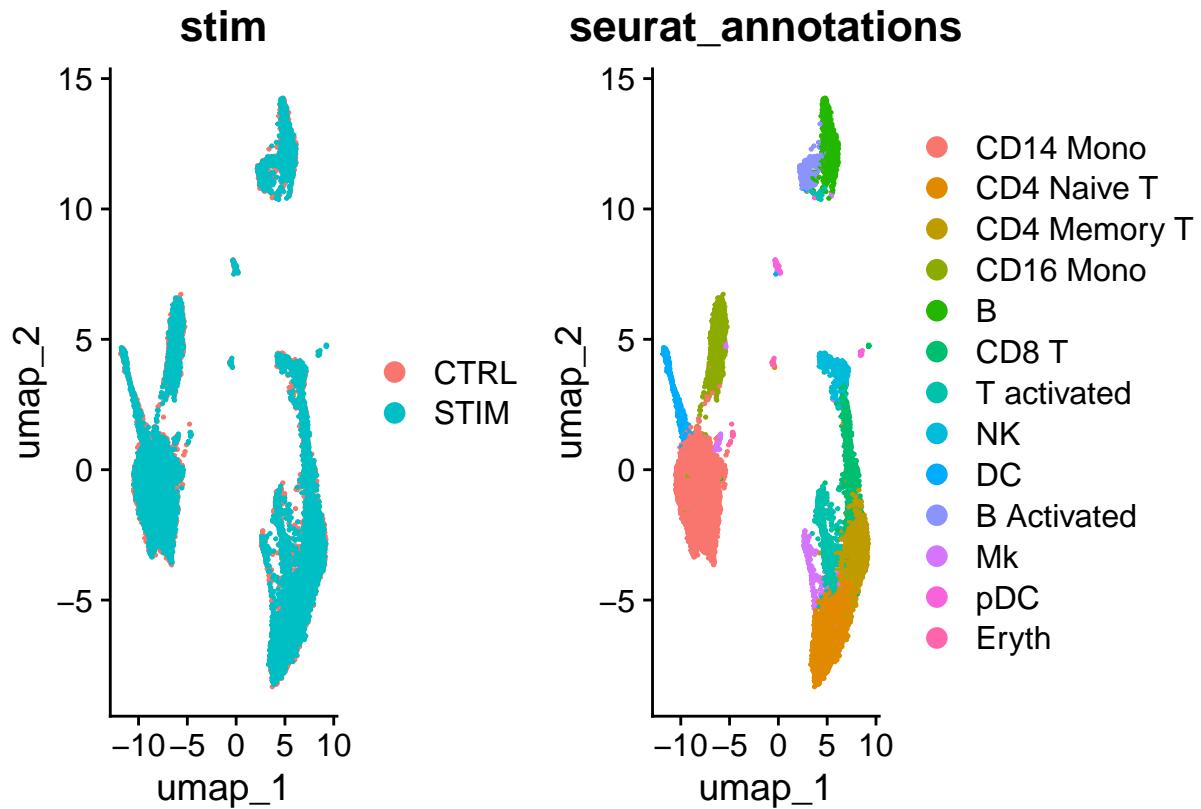
### Perform analysis without integration

```
ifnb <- RunUMAP(ifnb, dims = 1:30, reduction = "pca", reduction.name = "umap.unintegrated")
DimPlot(ifnb, reduction = "umap.unintegrated", group.by = c("stim", "seurat_clusters"))
```

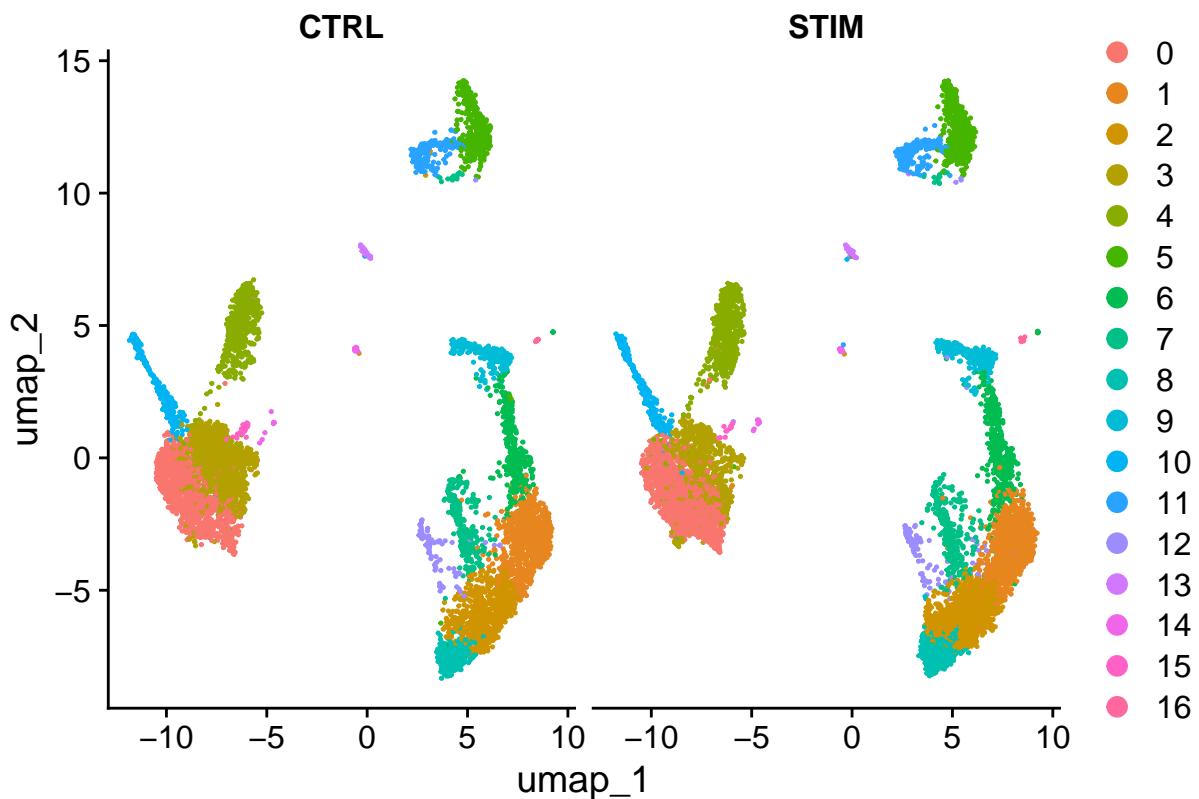


### Perform integration

```
# Visualization
DimPlot(ifnb, reduction = "umap", group.by = c("stim", "seurat_annotations"))
```



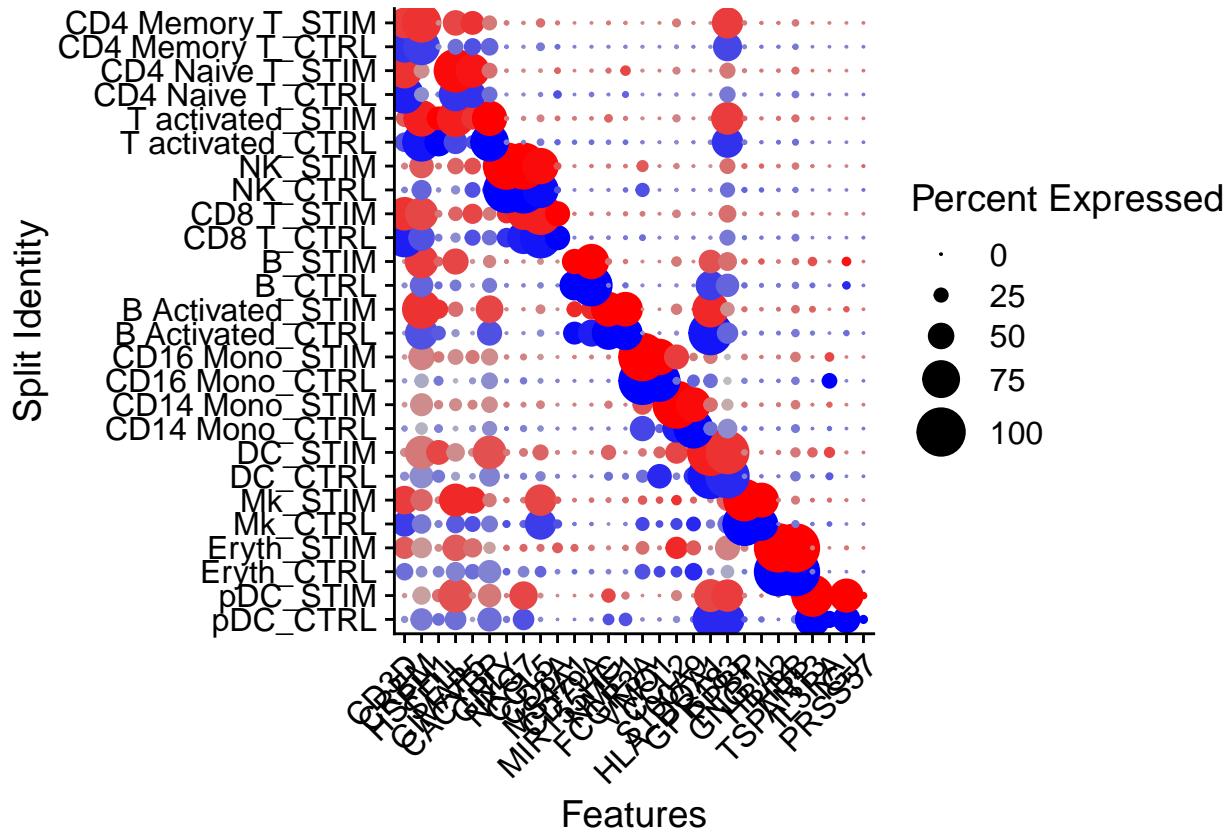
```
DimPlot(ifnb, reduction = "umap", split.by = "stim")
```



## Identify conserved cell type markers

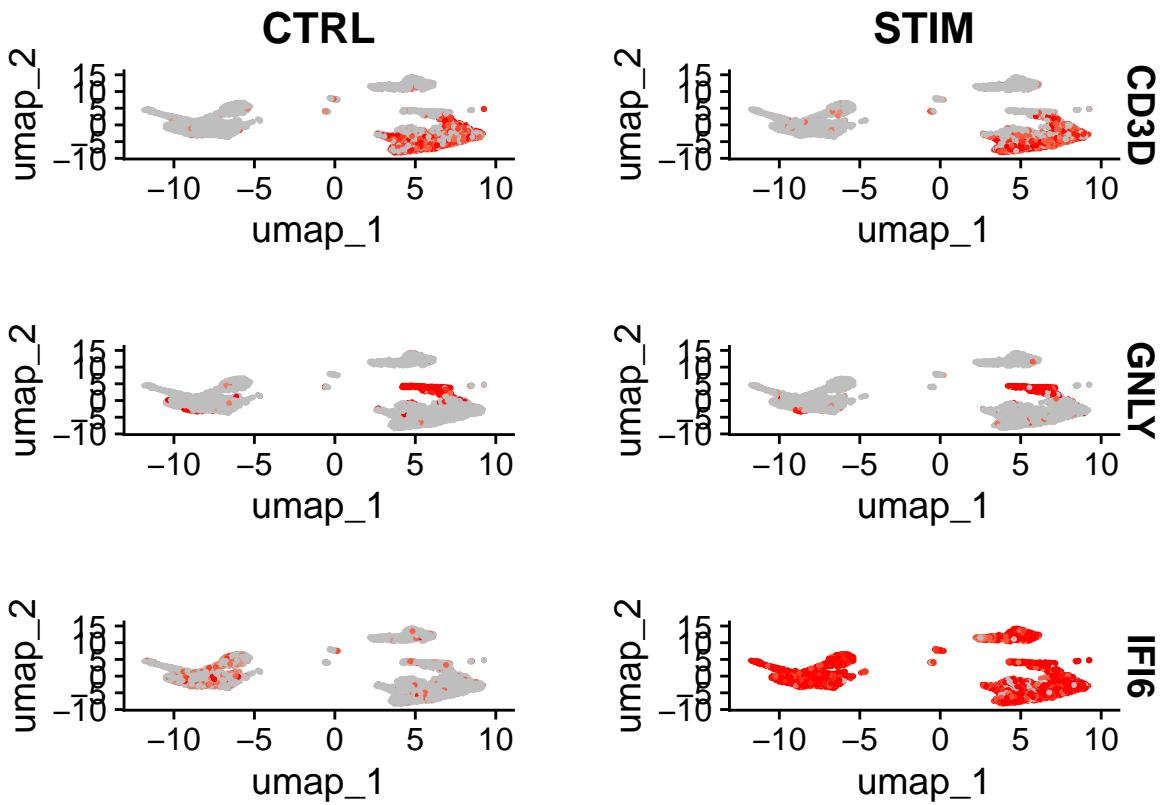
```
# NEEDS TO BE FIXED AND SET ORDER CORRECTLY
Idents(ifnb) <- factor(Idents(ifnb), levels = c("pDC", "Eryth", "Mk", "DC", "CD14 Mono", "CD16 Mono",
    "B Activated", "B", "CD8 T", "NK", "T activated", "CD4 Naive T", "CD4 Memory T"))

markers.to.plot <- c("CD3D", "CREM", "HSPH1", "SELL", "GIMAP5", "CACYPBP", "GNLY", "NKG7", "CCL5",
    "CD8A", "MS4A1", "CD79A", "MIR155HG", "NME1", "FCGR3A", "VM01", "CCL2", "S100A9", "HLA-DQA1",
    "GPR183", "PPBP", "GNG11", "HBA2", "HBB", "TSPAN13", "IL3RA", "IGJ", "PRSS57")
DotPlot(ifnb, features = markers.to.plot, cols = c("blue", "red"), dot.scale = 8, split.by = "stim") +
    RotatedAxis()
```

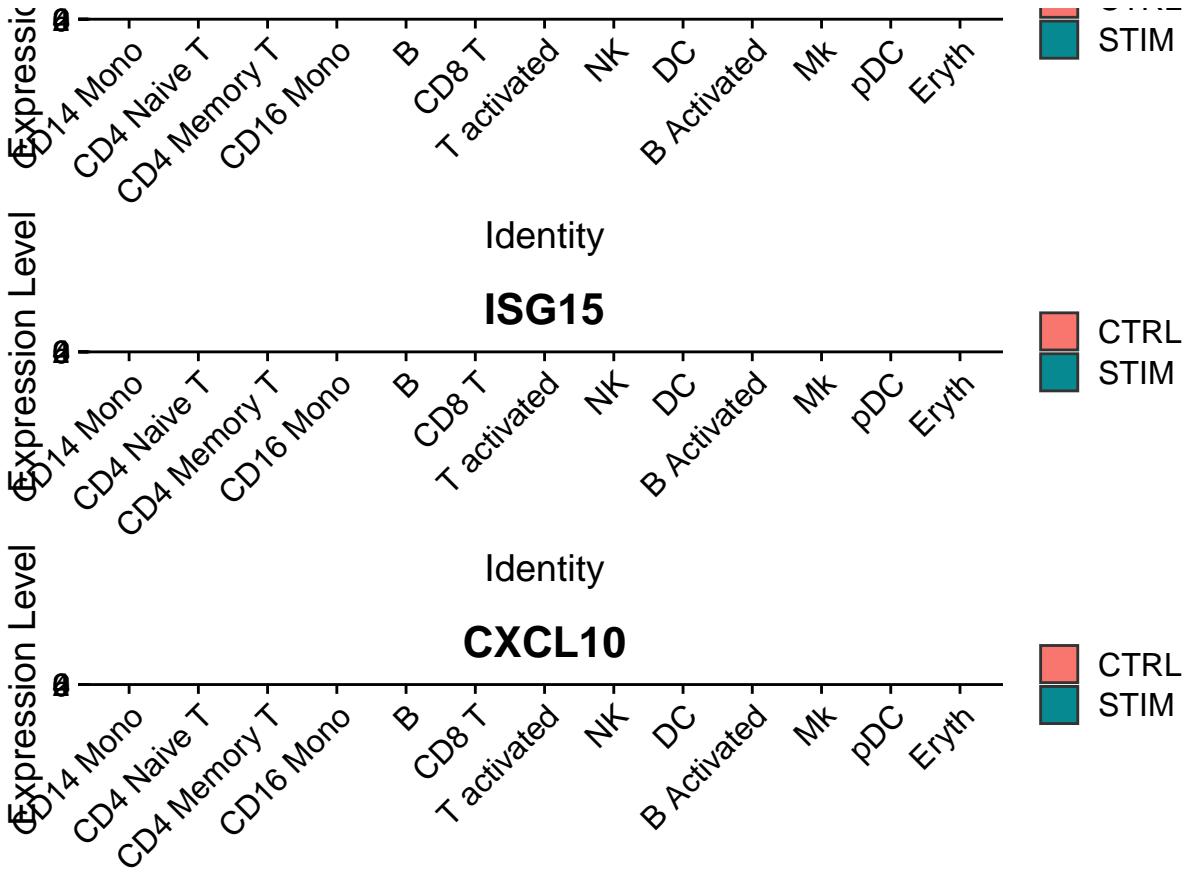


Identify differential expressed genes across conditions

```
FeaturePlot(ifnb, features = c("CD3D", "GNLY", "IFI6"), split.by = "stim", max.cutoff = 3, cols = c("green", "red"), reduction = "umap")
```



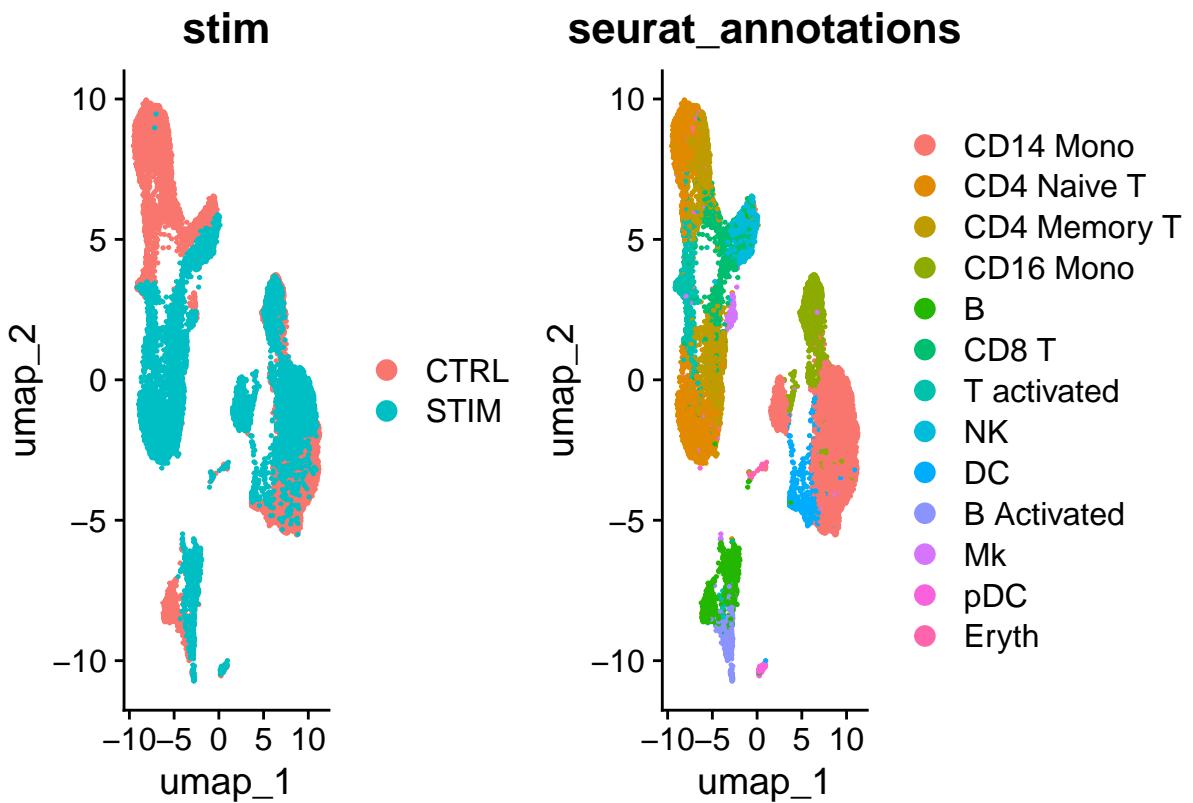
```
plots <- VlnPlot(ifnb, features = c("LYZ", "ISG15", "CXCL10"), split.by = "stim", group.by = "seurat_annotation"
  pt.size = 0, combine = FALSE)
wrap_plots(plots = plots, ncol = 1)
```



Perform integration with STransform-normalized datasets

```
ifnb <- LoadData("ifnb")

# split datasets and process without integration
ifnb[["RNA"]] <- split(ifnb[["RNA"]], f = ifnb$stim)
ifnb <- SCTransform(ifnb)
ifnb <- RunPCA(ifnb)
ifnb <- RunUMAP(ifnb, dims = 1:30)
DimPlot(ifnb, reduction = "umap", group.by = c("stim", "seurat_annotations"))
```



```
ifnb <- RunUMAP(ifnb, dims = 1:30, reduction = "integrated.dr")
DimPlot(ifnb, reduction = "umap", group.by = c("stim", "seurat_annotations"))
```

