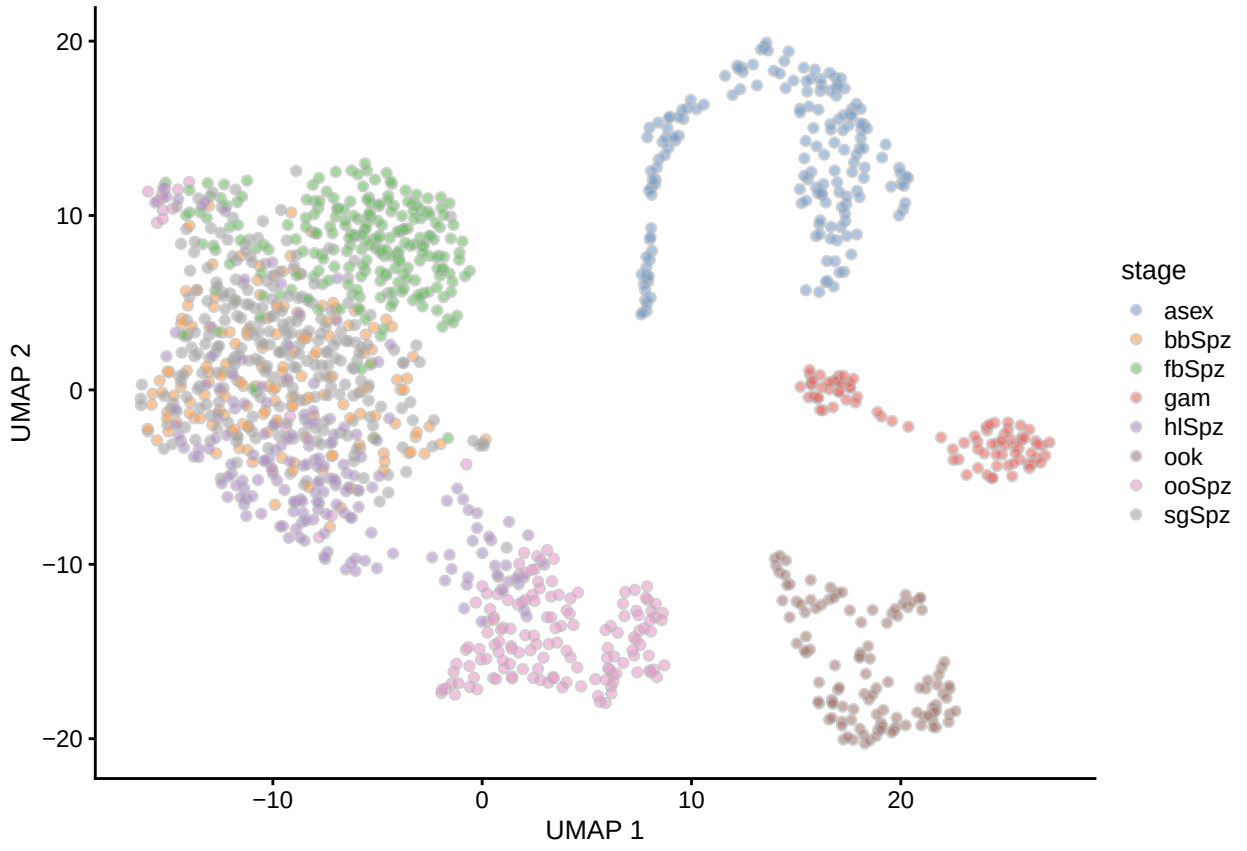
R Notebook

```
setwd("/Users/vh3/Documents/PfMCA/ANALYSIS_2/")
library(scater)
library(viridis)
library(RColorBrewer)
library(dplyr)
```

```
mca.qc2 <- readRDS("pfmca.withelifeasex.subook_20200626.rds")
```

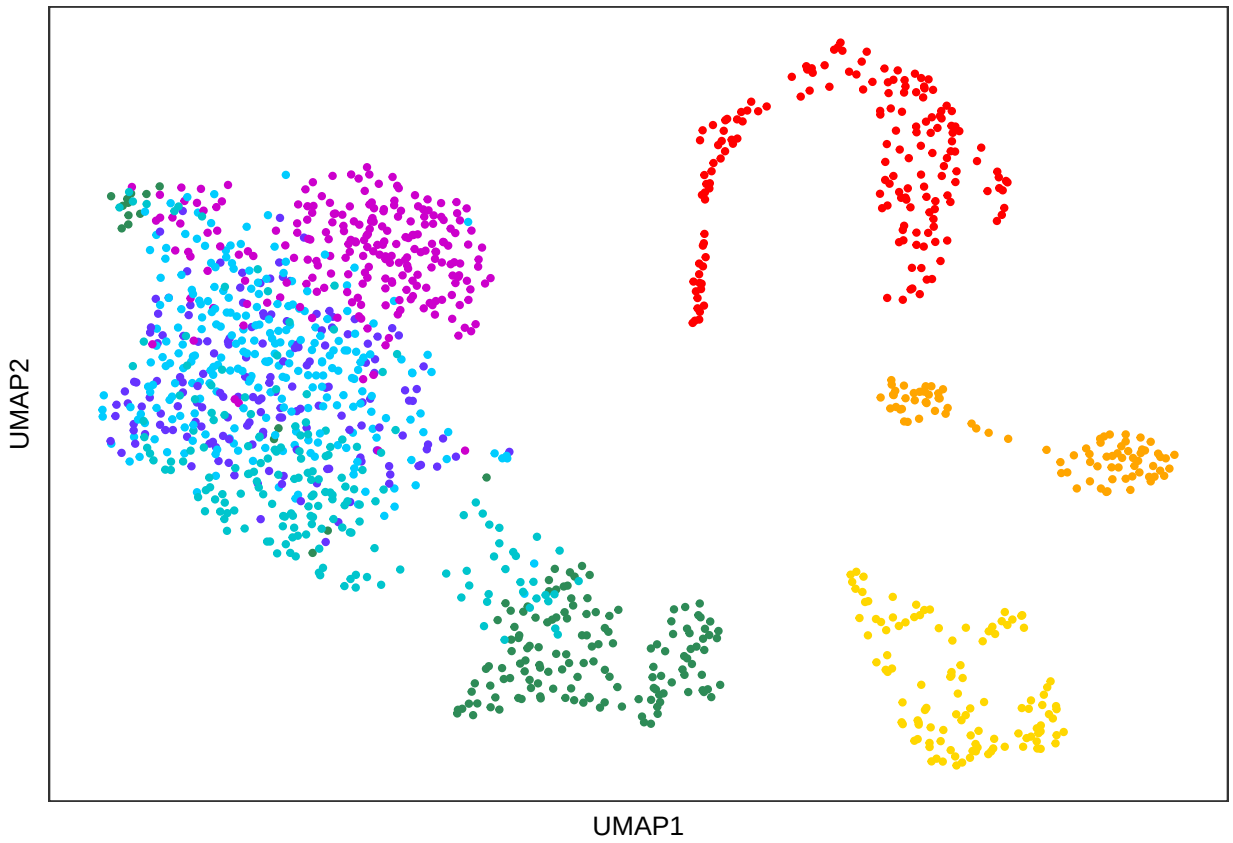
```
set.seed(666)
mca.qc2 <- runUMAP(mca.qc2, n_neighbors = 5, min_dist = 1, spread = 3)
p <- plotUMAP(mca.qc2, colour_by = "stage")
p
```



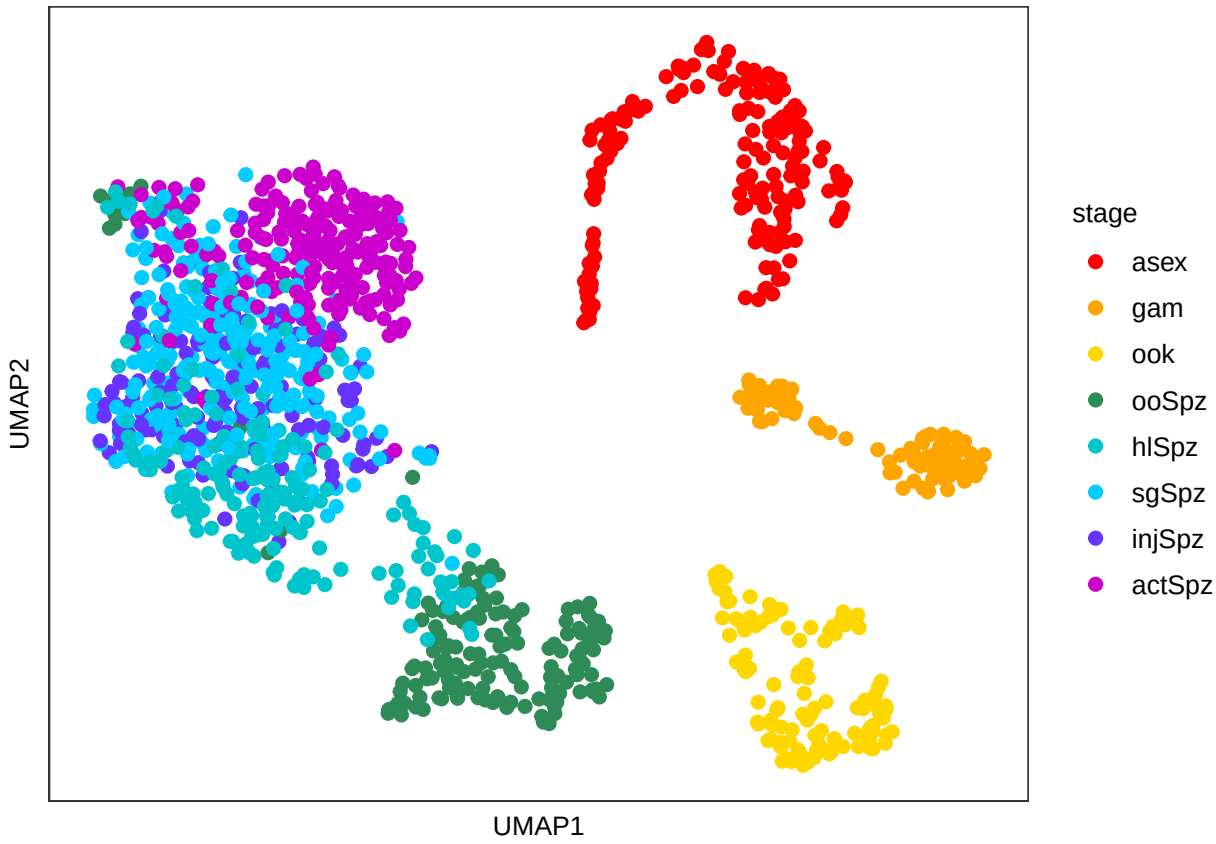

```
all2 <- p$data
colnames(all2) <- c("UMAP1", "UMAP2", "stage")
colors = c(asex = "red", gam = "orange", ook = "gold", ooSpz = "seagreen", hlSpz = "turquoise3",
    sgSpz = "#00CCFF", bbSpz = "#6633FF", fbSpz = "#CC00CC")

ggplot(all2, aes(UMAP1, UMAP2)) + geom_point(aes(colour = stage), size=0.8) + theme_bw() +
    scale_colour_manual(values = colors, breaks = c("asex", "gam", "ook", "ooSpz",
```

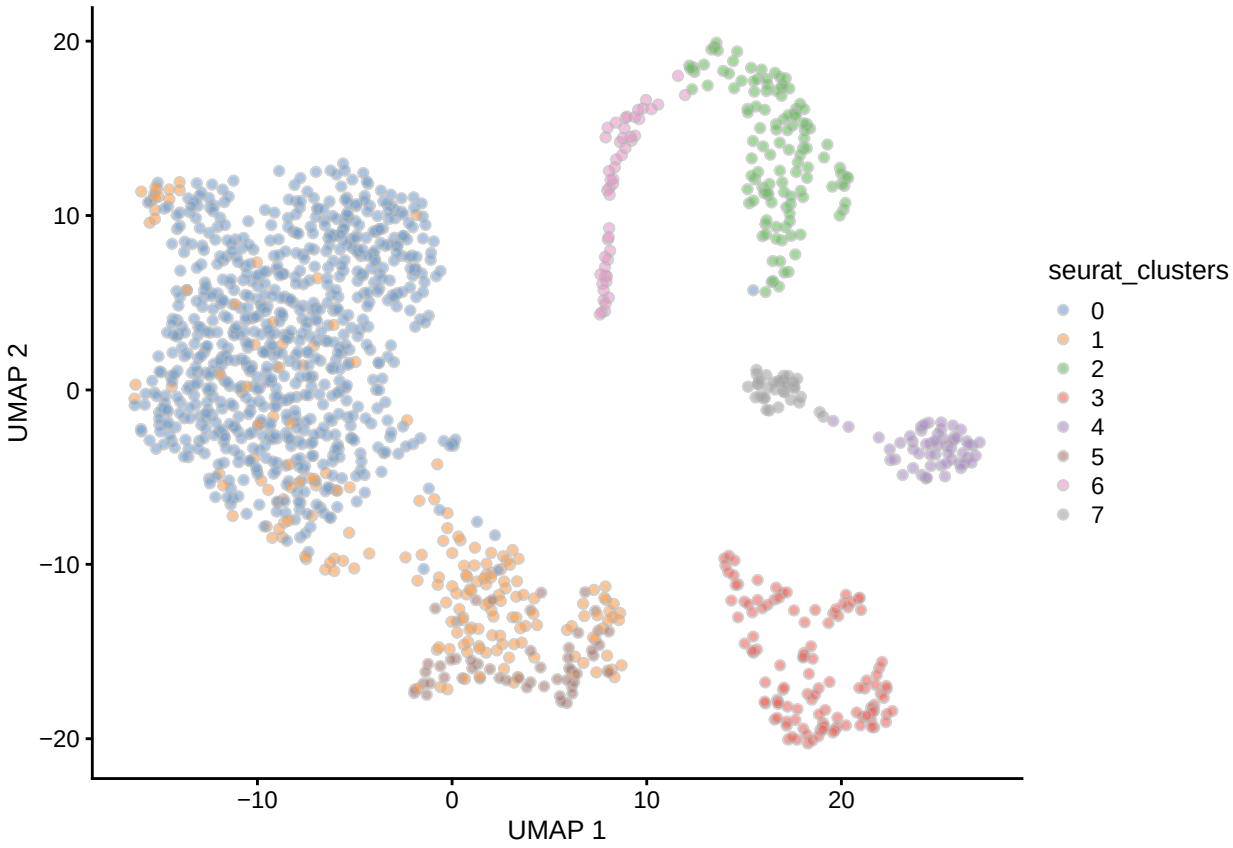
```
        "hlSpz", "sgSpz", "bbSpz", "fbSpz"), labels = c("asex", "gam", "ook", "ooSpz",
        "hlSpz", "sgSpz", "injSpz", "actSpz")) + theme(axis.text = element_blank(),
    axis.ticks = element_blank(), panel.grid.major = element_blank(), panel.grid.minor = element_blank()
    axis.title = element_text(size = 10), legend.position = "none")
```




```
ggplot(all2, aes(UMAP1, UMAP2)) + geom_point(aes(colour = stage), size=2) + theme_bw() +
    scale_colour_manual(values = colors, breaks = c("asex", "gam", "ook", "ooSpz",
        "hlSpz", "sgSpz", "bbSpz", "fbSpz"), labels = c("asex", "gam", "ook", "ooSpz",
        "hlSpz", "sgSpz", "injSpz", "actSpz")) + theme(axis.text = element_blank(),
    axis.ticks = element_blank(), panel.grid.major = element_blank(), panel.grid.minor = element_blank()
    axis.title = element_text(size = 10), legend.text = element_text(size = 10),
    legend.title = element_text(size = 10))
```

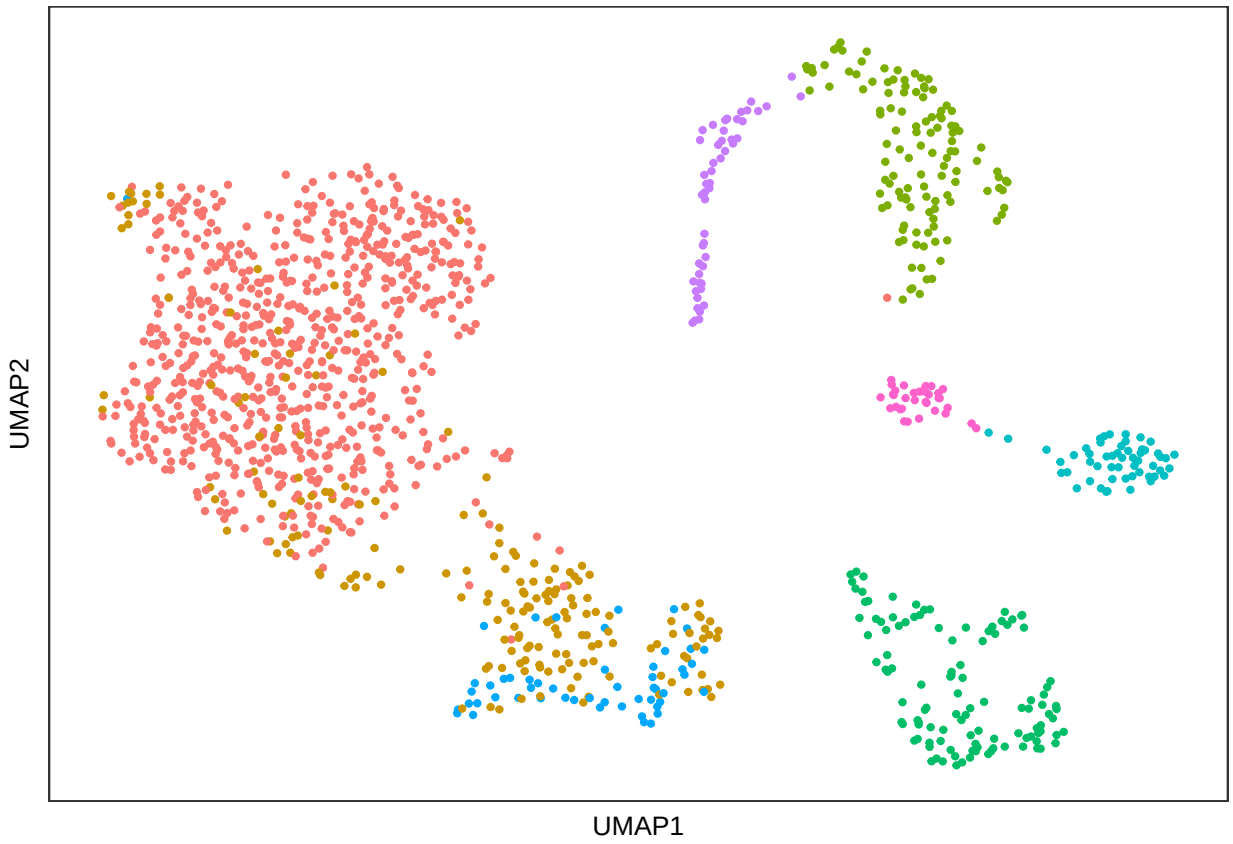



```
p <- plotUMAP(mca.qc2, colour_by = "seurat_clusters")
p
```

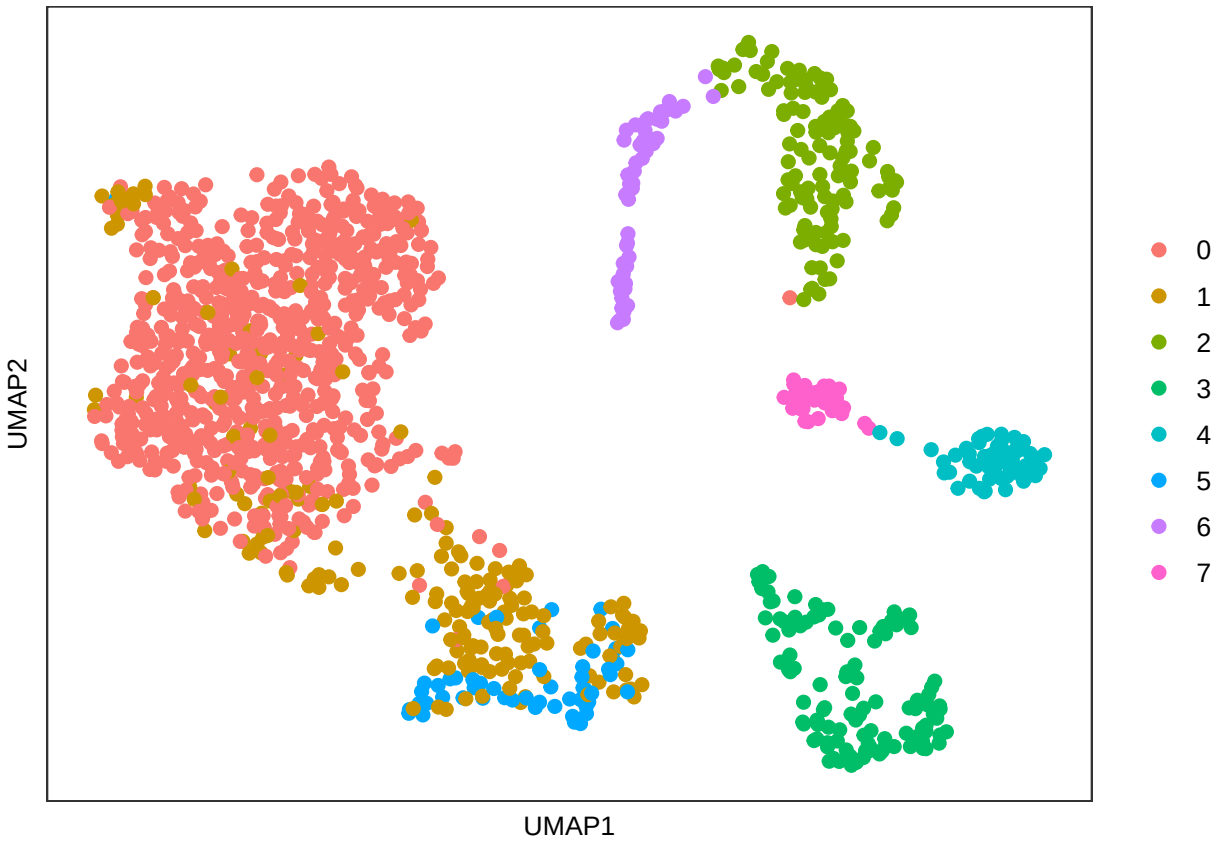



```
all2 <- p$data
colnames(all2) <- c("UMAP1", "UMAP2", "cluster")

ggplot(all2, aes(UMAP1, UMAP2)) + geom_point(aes(colour = as.factor(cluster)),
    size = 0.8) + theme_bw() + theme(axis.text = element_blank(), axis.ticks = element_blank(),
    panel.grid.major = element_blank(), panel.grid.minor = element_blank(), axis.title = element_text(si
    legend.position="none")
```




```
ggplot(all2, aes(UMAP1, UMAP2)) + geom_point(aes(colour = as.factor(cluster)),
    size = 2) + theme_bw() + theme(axis.text = element_blank(), axis.ticks = element_blank(),
    panel.grid.major = element_blank(), panel.grid.minor = element_blank(), axis.title = element_text(s
    legend.text = element_text(size = 10), legend.title = element_blank())
```


UMAP2
UMAP1
0
1
2
3
4
5
6
7