Testing unmatched feature integration using simulated data

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This guide will demonstrate the usage of bindSC to intergrate two datasets with unmatched features from simulation dataset.

Stage 1: Load data

For convenience, we have prepared the pre-processed data which are ready to use. User can refer to `sim.R` for the details of running the pre-processing workflow (It will take 10 mins).

```
library(bindSC)

dim(sim$X)
```

```
## [1] 400 300
```

```
dim(sim$Y)
```

```
## [1] 400 300
```

```
dim(sim$Z0)
```

```
## [1] 400 300
```

Usage of BiCCA

```
?BiCCA
```

In this example, dataset `X` is the same with `Y`. The inital transiton matrix `Z0` is generated by permutating rows of `X` with 10% probablity the same with `X`. Seurat and Liger use (`X`, `Z0`) as input and BiCCA uses (`X`, `Z0`, `Y`) as input.

The option `tolereance` is usually set from 0.01 to 0.05 to reduce unnecessary iteration when data size is large. Here I set it to 0.0001 for small sample size.

```
out <- BiCCA(X=sim$X, Z0=sim$Z0, Y=sim$Y,
       num.X = 5, num.Y = 5,
       num.iteration = 100,
       temp.path = "./tp",
       tolerance = 0.0001,
       save = FALSE,
       bigMemory = TRUE,
       block.size = 1000,
       ncore = 1)
```

```
## 2020-07-08 13:59:36  Started!
```

```
## 2020-07-08 13:59:36  Dimension Check: X[400x300] Y[400x300] Z0[400x300]
```

```
##
```

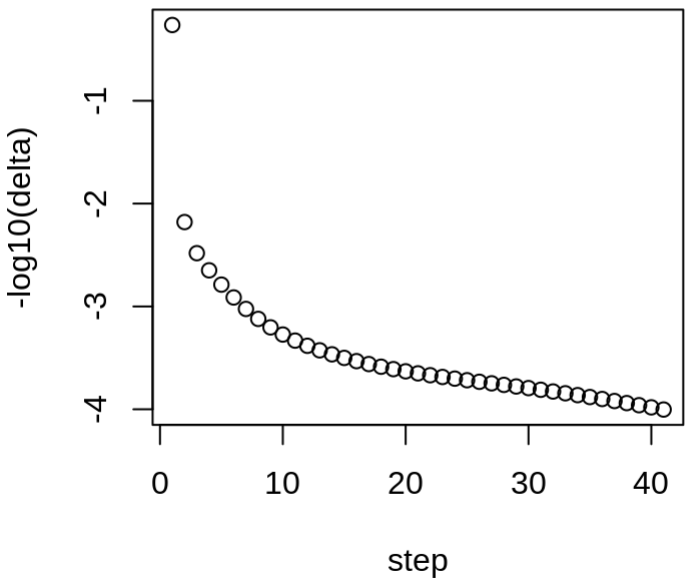
```
## 2020-07-08 14:00:05  Done! The decomposition is converged.
```

```
summary(out)
```

```
##       Length Class  Mode
## u       1500 -none- numeric
## r       1500 -none- numeric
## s       2000 -none- numeric
## v       2000 -none- numeric
## Z     120000 -none- numeric
## delta     41 -none- numeric
```

Show the iteration index `delta` (The iteration will stop in the second step if we set it to be 0.05)

```
plot(log10(out$delta), xlab="step", ylab="-log10(delta)")
```



Stage 2: Comparsion among bindSC, Seurat, and Liger methods

Three metrics are used to measure method performance since we have the cell correspondence as the gold standard. **For convenience, we have prepared the results for Seurat and Liger which are ready to use.**

- `Silhoutte coefficient` : High value means cell-type architectures is well preserved
- `Alignment score` : High value means uniformity of mixing for two datasets in the latent space
- `Anchor accuracy` : High value means cell correspondence can be found in cell's neighbor given fixed neighbor size

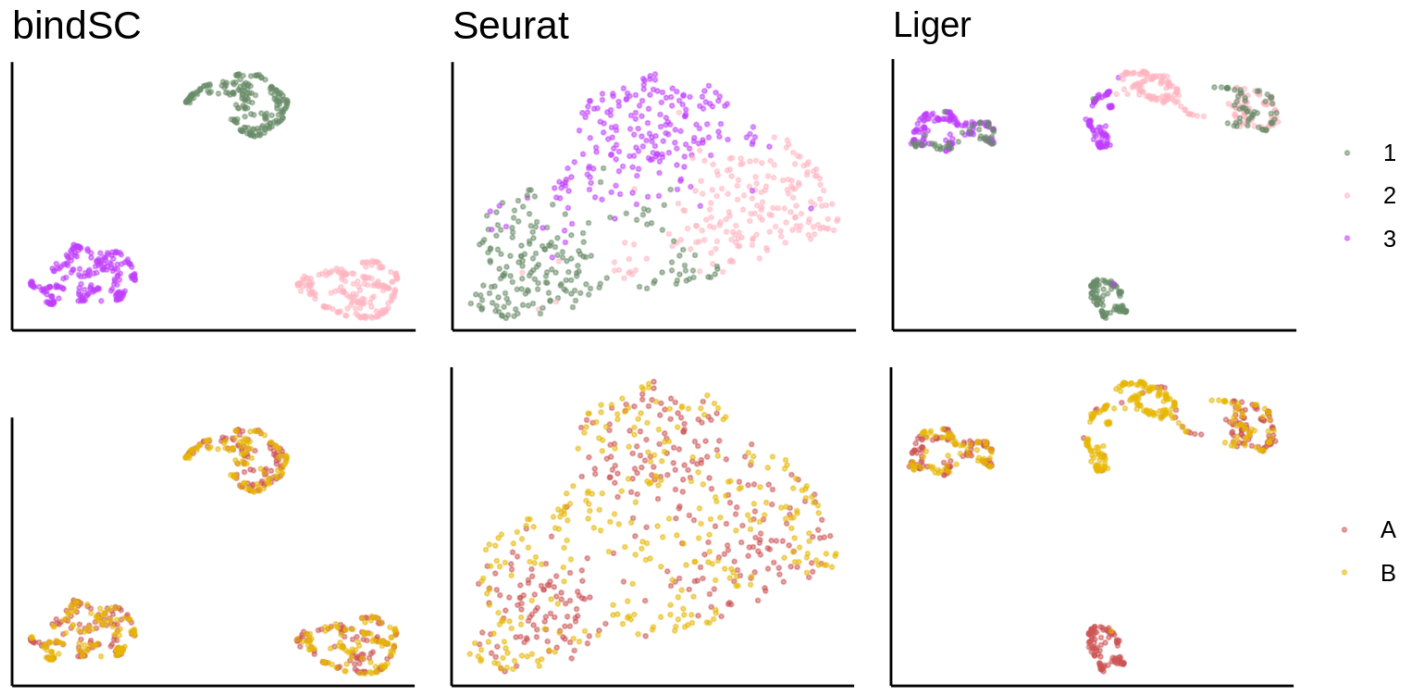
```
source("../A549/eval_plot.r")
```

```
## Loading required package: ggplot2
```

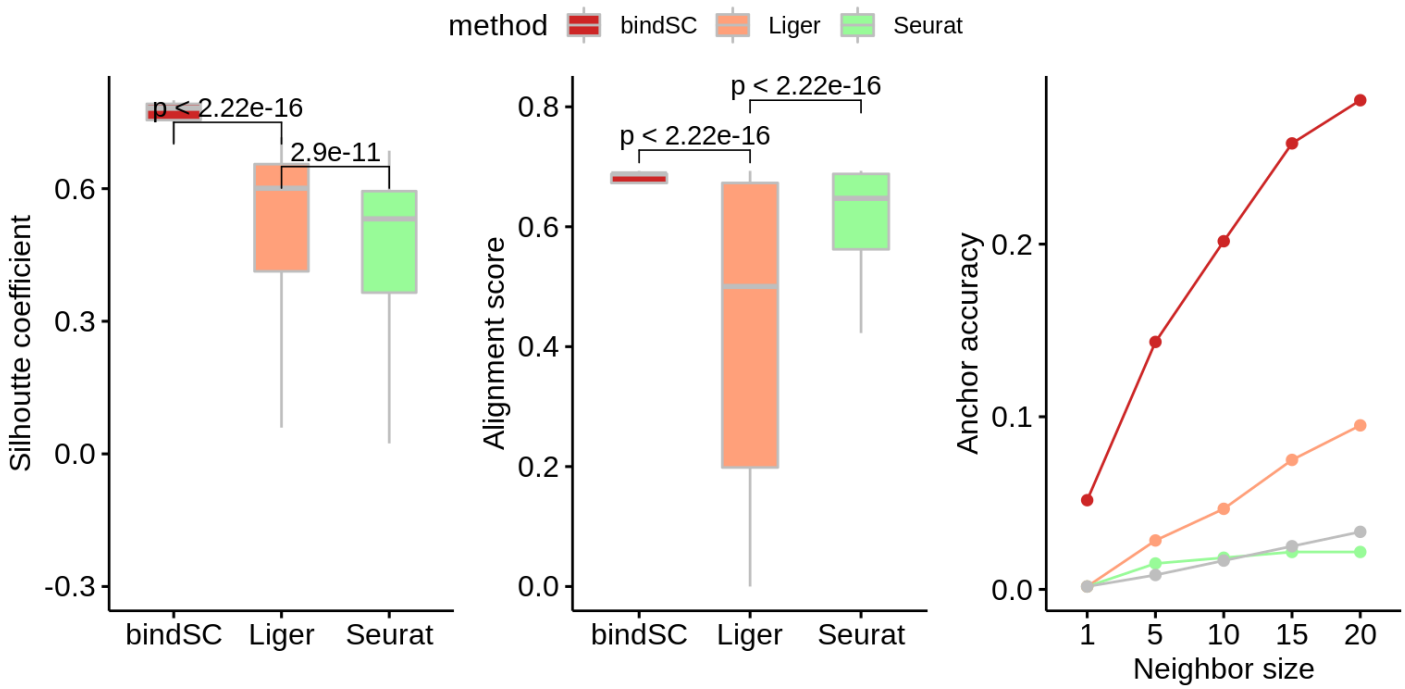
```
## Loading required package: magrittr
```

```
cell_type <- c(sim$X_meta$Group, sim$Y_meta$Group)
data_type <- c(rep("A", dim(out$u)[1]), rep("B",dim(out$r)[1]))
result <- umap_plot(out, cell_type, data_type)
eval <-  method_compare(result$plt_dt, "Sim")
```

```
eval$coembeding
```


bindSC
Seurat
Liger
1
2
3
A
B

```
eval$eval
```


method
bindSC
Liger
Seurat
p < 2.22e-16
2.9e-11
Silhoutte coefficient
0.6
0.3
0.0
-0.3
bindSC
Liger
Seurat
p < 2.22e-16
p < 2.22e-16
Alignment score
0.8
0.6
0.4
0.2
0.0
bindSC
Liger
Seurat
Anchor accuracy
0.2
0.1
0.0
1
5
10
15
20
Neighbor size