R function scLR

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Usage of scLR

A simulated data to compare the products of the expressions of LR pairs between two conditions: TX1 and TX2. 3 samples for each condition. For each sample, there are 1000 genes and 100 cells (5 cell types, 20 cells each). 10 ligand-receptor gene pairs across 5 cell types are compared between TX1 and TX2.

Three inputs are required: countmatrix (gene names required), cellinfo, lrpairs.sample

```
library(scLR)
set.seed(2021)
G <- 1000; n <- 600 # To create a simulated data consisting of 1000 genes and 600 cells
# Data are generated from NB distribution
mu1 <- rgamma(G, shape = 2, rate = 2)
NB_cell <- function(j) rnbinom(G, size = 0.1, mu = mu1)
countmatrix <- as(sapply(1:n, NB_cell), "sparseMatrix")
# 1000 gene names are taken from lrpairs0 [LR pairs which are commonly compared (built in scLR)]
genenames <- unique(unlist(lrpairs0))
rownames(countmatrix) <- genenames[sample(1:length(genenames),1000)]

# Information for all cells
cellinfo <- data.frame(sampleID = factor(paste0("s", rep(1:6, each=100))),
                       condition = factor(paste0("tx", rep(1:2, each=300))),
                       cellcluster = factor(paste0("cc", rep(rep(1:5, each=20), 6))) )

# Names of 10 ligand-receptor pairs which will be compared
lrpairs.sample <- data.frame(lrpairs0[sample(1:200, 10),])
```

Formats of 3 inputs:

```
countmatrix[1:6, 1:10] # format of countmatrix, gene expressions (the first 6 genes and 10 cells)
```

```
## 6 x 10 sparse Matrix of class "dgCMatrix"
##
## NID1    15 . . . . 2 . . 1 .
## IAPP     . . . 2 . . . . . .
## MRGPRX1  1 . 1 4 . . . . . .
## GPR182   . 3 . . . . . . . 3
## CD58     1 1 . . . . . 7 4 5
## SLC45A3  . 1 . . . . . 1 1 .
```

```
head(cellinfo, 10) # format of cellinfo, categories of cells (the first 10 cells)
```

```
##    sampleID condition cellcluster
## 1        s1       tx1         cc1
## 2        s1       tx1         cc1
```

```
## 3        s1       tx1         cc1
## 4        s1       tx1         cc1
## 5        s1       tx1         cc1
## 6        s1       tx1         cc1
## 7        s1       tx1         cc1
## 8        s1       tx1         cc1
## 9        s1       tx1         cc1
## 10       s1       tx1         cc1
```

```
head(lrpairs.sample, 10) # format of lrpairs.sample, LR gene pairs to compare.
```

```
##     ligand receptor
## 200   ASIP     MC1R
## 94    AHSG     INSR
## 126   APLN   ADRA2A
## 56    ADM2    GPR84
## 173   APOE    VLDLR
## 23  ADAM23    ITGA5
## 33   ADAM9    ITGAV
## 123  ANXA1     FPR3
## 80    AGRN     LRP2
## 129   APLN   MTNR1A
```

Output:

```
output <- scLR(countmatrix, cellinfo, lrpairs.sample, low.filter = 1,
               parallel.use = FALSE) # Do parallel computation if parallel.use = TRUE.
```

```
## converting counts to integer mode
```

```
head(output$Rs[,1:11], 10)
```

```
##    lr.cell.name lr.gene.name obs.xy.diff null.diff.sd pvalue stage     adj.p
## 1       cc1-cc1    AHSG-INSR     -5.2920       4.9649  0.270     1 0.9157303
## 2       cc1-cc1   ADM2-GPR84     -2.4461       6.1604  0.670     1 0.9157303
## 3       cc1-cc1   APOE-VLDLR      6.8263       5.6427  0.235     1 0.9157303
## 4       cc1-cc1    AGRN-LRP2      1.2687       4.4613  0.805     1 0.9157303
## 5       cc1-cc2    AHSG-INSR     -3.6669       5.2848  0.510     1 0.9157303
## 6       cc1-cc2   ADM2-GPR84      2.2378       6.2299  0.660     1 0.9157303
## 7       cc1-cc2   APOE-VLDLR     -3.6713       4.9467  0.440     1 0.9157303
## 8       cc1-cc2    AGRN-LRP2      4.3512       5.3004  0.385     1 0.9157303
## 9       cc1-cc3    AHSG-INSR     -2.1883       5.1682  0.705     1 0.9157303
## 10      cc1-cc3   ADM2-GPR84      1.8088       5.7703  0.735     1 0.9157303
##    Welch.t.stat Welch.t.sd Welch.t.p Welch.t.adj.p
## 1       -0.9930     5.3294  0.391501     0.9267978
## 2       -0.4570     5.3522  0.677112     0.9267978
## 3        1.3982     4.8821  0.269773     0.9267978
## 4        0.3150     4.0270  0.768918     0.9267978
## 5       -1.8562     1.9755  0.145036     0.9267978
## 6        0.4669     4.7929  0.684686     0.9267978
## 7       -0.5773     6.3589  0.597654     0.9267978
## 8        0.7012     6.2055  0.527396     0.9267978
## 9       -0.2922     7.4899  0.784703     0.9267978
## 10       0.2549     7.0966  0.819315     0.9267978
```

Assume sample s2 does NOT have cell type cc3

```
idx.remove <- which(cellinfo$sampleID=="s2" & cellinfo$cellcluster=="cc3")
cellinfo1 <- cellinfo[-idx.remove,]; cellinfo1 <- droplevels(cellinfo1)
countmatrix1 <- countmatrix[,-idx.remove]
```

Output:

```
output <- scLR(countmatrix1, cellinfo1, lrpairs.sample, low.filter = 1, parallel.use = FALSE)
```

```
## converting counts to integer mode
```

```
head(output$Rs[,1:11], 10)
```

```
##    lr.cell.name lr.gene.name obs.xy.diff null.diff.sd pvalue stage     adj.p
## 1       cc1-cc1    AHSG-INSR     -5.2976       4.9795  0.285     1 0.9204545
## 2       cc1-cc1   ADM2-GPR84     -2.4810       6.1112  0.665     1 0.9204545
## 3       cc1-cc1   APOE-VLDLR      6.8325       5.7182  0.240     1 0.9204545
## 4       cc1-cc1    AGRN-LRP2      1.2488       4.4714  0.800     1 0.9204545
## 5       cc1-cc2    AHSG-INSR     -3.6596       5.2271  0.495     1 0.9204545
## 6       cc1-cc2   ADM2-GPR84      2.2899       6.2776  0.665     1 0.9204545
## 7       cc1-cc2   APOE-VLDLR     -3.6278       4.9547  0.445     1 0.9204545
## 8       cc1-cc2    AGRN-LRP2      4.3865       5.2123  0.355     1 0.9204545
## 9       cc1-cc3    AHSG-INSR      2.2369       5.9937  0.730     1 0.9204545
## 10      cc1-cc3   ADM2-GPR84      1.7947       6.4812  0.755     1 0.9204545
##    Welch.t.stat Welch.t.sd Welch.t.p Welch.t.adj.p
## 1       -0.9850     5.3780  0.395984     0.9310549
## 2       -0.4588     5.4070  0.675716     0.9310549
## 3        1.3734     4.9750  0.277129     0.9310549
## 4        0.3065     4.0749  0.774943     0.9310549
## 5       -1.8344     1.9950  0.148310     0.8892294
## 6        0.4733     4.8376  0.680849     0.9310549
## 7       -0.5688     6.3784  0.602728     0.9310549
## 8        0.7033     6.2369  0.525957     0.9310549
## 9        0.3007     7.4385  0.785657     0.9310549
## 10       0.2341     7.6670  0.830869     0.9310549
```