R function scLR

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Usage of scLR

A simulated data to compare LR pairs between two conditions: TX1 and TX2. 3 replicates each condition. For each replicate, 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.

3 inputs 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
NB_cell <- function(j) rnbinom(G, size = 0.1, mu = rgamma(G, shape = 2, rate = 2))
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"
##
## TMEM222 15 . 17 . . . 6 27 . .
## RLN2     . .  . . . 4 . 89 . .
## ITGB8    1 .  . . . . .  . . .
## CD96     . .  . . 6 . 2  . . .
## FGF3     1 .  6 . . . .  . 2 .
## GPC5     . .  . . . 4 .  . . .
```

```
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
## 54     ADM2   CALCRL
## 140    APOB    CALCR
## 157   APOC2     LRP2
## 86     AGRP     SDC3
## 81     AGRN     LRP4
## 41  ADCYAP1    PTH1R
## 46  ADCYAP1    VIPR1
## 56     ADM2    GPR84
## 35    ADAM9    ITGB5
## 130   APOA1     LDLR
```

Output:

```
output <- scLR(countmatrix, cellinfo, lrpairs.sample, low.filter = 1,
               parallel.use = FALSE, cpucores = 2) # Do parallel computation if parallel.use = TRUE.
```

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

```
head(output$Rs, 20)
```

```
##    lr.cell.name  lr.gene.name obs.xy.diff null.diff.sd     pvalue stage
## 1       cc1-cc1 ADCYAP1-PTH1R      4.6792       5.9035 0.42000000     1
## 2       cc1-cc1 ADCYAP1-VIPR1      7.7303       5.8353 0.19500000     1
## 3       cc1-cc1    APOA1-LDLR      1.1413       5.9499 0.82000000     1
## 4       cc1-cc2 ADCYAP1-PTH1R      3.9767       5.6762 0.49500000     1
## 5       cc1-cc2 ADCYAP1-VIPR1      7.4522       5.4610 0.18000000     1
## 6       cc1-cc2    APOA1-LDLR     -1.4156       6.0763 0.85000000     1
## 7       cc1-cc3 ADCYAP1-PTH1R     11.7795       5.4812 0.09177253     2
## 8       cc1-cc3 ADCYAP1-VIPR1      6.2115       5.2035 0.28000000     1
## 9       cc1-cc3    APOA1-LDLR      0.1014       5.9871 0.99000000     1
## 10      cc1-cc4 ADCYAP1-PTH1R      2.0802       5.7900 0.69500000     1
## 11      cc1-cc4 ADCYAP1-VIPR1      8.0607       4.5429 0.06500000     1
## 12      cc1-cc4    APOA1-LDLR     -0.8851       5.8746 0.86000000     1
## 13      cc1-cc5 ADCYAP1-PTH1R     11.7131       5.4208 0.07939297     2
## 14      cc1-cc5 ADCYAP1-VIPR1     11.3453       5.8277 0.11134808     2
## 15      cc1-cc5    APOA1-LDLR     -0.3873       5.5185 0.95000000     1
## 16      cc2-cc1 ADCYAP1-PTH1R      1.1508       4.9920 0.83500000     1
## 17      cc2-cc1 ADCYAP1-VIPR1      2.8712       5.7120 0.63000000     1
## 18      cc2-cc1    APOA1-LDLR     -2.6924       5.2710 0.61000000     1
## 19      cc2-cc2 ADCYAP1-PTH1R     -0.8176       6.1312 0.89500000     1
## 20      cc2-cc2 ADCYAP1-VIPR1      2.6599       5.4309 0.61500000     1
##        adj.p Welch.t.stat Welch.t.sd Welch.t.p   adj.t.p
```

```
##  1  0.8250000       3.2131     1.4563  0.041822 0.5185500
##  2  0.6964286       1.6432     4.7044  0.191738 0.7989083
##  3  0.9739583       0.1955     5.8389  0.859995 0.9846586
##  4  0.8250000       2.1816     1.8229  0.100706 0.5809962
##  5  0.6750000       4.4792     1.6637  0.026672 0.5185500
##  6  0.9739583      -0.2992     4.7320  0.787892 0.9687197
##  7  0.6315789       5.9124     1.9923  0.007903 0.4616625
##  8  0.8076923       2.4446     2.5409  0.075114 0.5525932
##  9  0.9900000       0.0212     4.7774  0.984696 0.9924090
## 10 0.8961864       0.5514     3.7727  0.618230 0.8964952
## 11 0.6315789       2.7971     2.8818  0.079583 0.5525932
## 12 0.9739583      -0.1251     7.0724  0.908733 0.9846586
## 13 0.6315789       2.5457     4.6012  0.081047 0.5525932
## 14 0.6315789       4.1001     2.7671  0.038469 0.5185500
## 15 0.9760274      -0.0715     5.4192  0.947113 0.9846586
## 16 0.9739583       0.1910     6.0241  0.858126 0.9846586
## 17 0.8727273       0.6229     4.6091  0.567680 0.8964952
## 18 0.8727273      -0.4352     6.1858  0.686482 0.9125237
## 19 0.9739583      -0.1501     5.4488  0.888397 0.9846586
## 20 0.8727273       0.5609     4.7420  0.608779 0.8964952
```