TreeExp basics

Hang Ruan 2017/3/28

TreeExp can be loaded the package in the usual way:

```
library('TreeExp')

## Loading required package: ape

## Loading required package: phytools

## Loading required package: maps

##

## # maps v3.1: updated 'world': all lakes moved to separate new #

## # 'lakes' database. Type '?world' or 'news(package="maps")'. #
```

Input Format:

TreeExp package takes in reads count data and gene information file in certain format:

- 1. Gene information file should be a text file in the shape of a matrix, in which values are separated by tabs. Rows correspond to orthologous genes and columns correspond to species names. And the values in the matrix are in the format of "GeneId:GeneLength".
- 2. Reads count file should also be a text file in the matrix shape, Rows correspond to orthologous genes which should be in one-to-one correspondence with rows in Gene information file, though gene ids are displayed in reads count file. Columns correspond to sample names. Sample names are in format of "TaxaName_SubtaxaName_ReplicatesName".

The example files are included in the TreeExp package, which can be found in extdata folder in the package. One can load them in to take a look:

```
readsCount.table = read.table(system.file('extdata/tetraexp.read.counts.raw.txt',
                                              package='TreeExp'), header = T)
head(readsCount.table[,1:10])
##
     homoSapienGeneId Human_Brain_Female Human_Brain_Male1 Human_Brain_Male2
## 1
      ENSG00000198824
                                     16323
                                                        11147
                                                                           19507
## 2
      ENSG00000118402
                                     31883
                                                        19242
                                                                           32321
## 3
      ENSG00000166167
                                    102711
                                                        80104
                                                                          141338
## 4
      ENSG00000144724
                                     51020
                                                        37861
                                                                           43906
## 5
      ENSG00000183508
                                       988
                                                         1443
                                                                             760
## 6
      ENSG00000008086
                                     27839
                                                        10208
                                                                           20666
     Human_Brain_Male3 Human_Brain_Male4 Human_Brain_Male5
##
## 1
                   4402
                                                          683
                                      6521
## 2
                   9841
                                      1164
                                                         1362
## 3
                  59947
                                     23104
                                                        14613
## 4
                  24645
                                      3968
                                                         5653
## 5
                    456
                                       227
                                                          456
## 6
                  12970
                                      2569
                                                         1940
##
     Human Cerebellum Female Human Cerebellum Male Human Heart Female
## 1
                        20032
                                                43008
                                                                     3381
## 2
                                                57081
                        26732
                                                                      228
```

```
## 3
                       56103
                                            105866
                                                                 17022
## 4
                       26365
                                                                 41876
                                             66177
## 5
                         988
                                              1215
                                                                 16913
## 6
                        4987
                                              11862
                                                                   878
geneInfo.table = read.table(system.file('extdata/tetraexp.length.ortholog.txt',
                                        package='TreeExp'), header = T)
head(geneInfo.table)
##
                    Human
                                       Chimpanzee
                                                                    Bonobo
##
  1 ENSG00000198824:3788 ENSPTRG00000023033:3786 ENSPTRG00000023033:3786
## 2 ENSG00000118402:3042 ENSPTRG00000018370:2962 ENSPTRG00000018370:2962
## 3 ENSG00000166167:6255 ENSPTRG00000002869:6153 ENSPTRG00000002869:6153
## 4 ENSG00000144724:9524 ENSPTRG00000015067:6726 ENSPTRG00000015067:6726
  5 ENSG00000183508:5751 ENSPTRG00000001166:5717 ENSPTRG00000001166:5717
  6 ENSG00000008086:3576 ENSPTRG00000021711:2874 ENSPTRG00000021711:2874
##
                     Gorilla
                                           Orangutan
                                                                      Macaque
##
  1 ENSGGOG00000009918:3808 ENSPPYG00000005537:2442 ENSMMUG00000023599:3781
                              ENSPPYG00000016794:945 ENSMMUG00000020208:2960
  2 ENSGGOGO0000009359:2890
  3 ENSGGOG00000005023:5882 ENSPPYG00000002583:6130 ENSMMUG00000006741:6001
## 4 ENSGGDG00000006858:6049 ENSPPYG00000013752:4933 ENSMMUG00000012487:5949
## 5 ENSGGDG00000004149:5727 ENSPPYG00000000972:1987 ENSMMUG00000004907:3522
  6 ENSGGDG00000010796:3354 ENSPPYG00000020166:3024 ENSMMUG00000005063:3077
##
                       Mouse
                                             Opossum
                                                                     Platypus
## 1 ENSMUSG00000047710:4040 ENSMODG00000003128:2568 ENSOANG00000000610:2487
## 2 ENSMUSG00000032262:2146
                             ENSMODG00000018420:945
                                                      ENSOANGO000001290:909
## 3 ENSMUSG00000025217:2984 ENSMODG00000011788:1888 ENSOANG00000007316:1936
## 4 ENSMUSG00000021745:9375 ENSMDDG00000002722:4448 ENSDANG00000006011:3968
## 5 ENSMUSG00000044468:5640 ENSMODG00000023227:1194 ENSOANG00000003065:1335
  6 ENSMUSG00000031292:3484 ENSMODG00000017140:2589 ENSOANG00000004037:2607
##
                     Chicken
## 1 ENSGALG00000016813:2412
## 2 ENSGALG00000015876:1322
## 3 ENSGALG00000007820:1962
## 4 ENSGALG00000007177:5396
## 5 ENSGALG00000014453:1179
## 6 ENSGALG00000016529:2712
```

Construction:

The construction function TEconstruct loads in the reads count data file as well as a gene information file, and wraps them in a list of taxonExp objects (one taxaExp object).

In the package, we include files transformed from six tissues' expression reads count data of nine tetrapod species. If you want to transform your own data, a transformation Perl script format2treeexp.pl to format raw outputs of *TopHat2* to "*TreeExp* compatible" is available at tools folder in the package. Or you can access the script at https://github.com/hr1912/TreeExp/blob/master/tools/format2treeexp.pl

```
taxa.objects = TEconstruct(readCountsFP = system.file('extdata/tetraexp.read.counts.raw.txt', package='
geneInfoFP = system.file('extdata/tetraexp.length.ortholog.txt', package='TreeExp'),
taxa = "all", subtaxa = c("Brain", "Cerebellum"), normalize = "TPM")
```

The construction process takes **several minutes** on a desktop computer depending on data size and hardware performance. Specify "taxa" and "subtaxa" options in the function when using partial of your data. The construction process will be faster. If you are hesitated to test the *TreeExp*, the package has already bundled

a constructed object and you can load the object through:

data(tetraexp)

You can take a look at what the loaded objects:

```
print(tetraexp.objects, details = TRUE)
```

```
##
##
   59 taxonExp objects
##
## object 1 : Human
## object 2 : Human
                         Cerebellum
## object 3 : Human
                         Heart
## object 4 : Human
                         Kidney
## object 5 : Human
                         Liver
## object 6 : Human
                         Testis
## object 7 : Chimpanzee
                             Brain
## object 8 : Chimpanzee
                             Cerebellum
## object 9 : Chimpanzee
                             Heart
## object 10 : Chimpanzee
                             Kidney
## object 11 : Chimpanzee
                             Liver
## object 12 : Chimpanzee
                             Testis
## object 13 : Bonobo
                         Brain
## object 14 : Bonobo
                         Cerebellum
## object 15 : Bonobo
                         Heart
                         Kidney
## object 16 : Bonobo
## object 17 : Bonobo
                         Liver
## object 18 : Bonobo
                        Testis
## object 19 : Gorilla Brain
## object 20 : Gorilla
                        Cerebellum
## object 21 : Gorilla
                        Heart
## object 22 : Gorilla
                         Kidney
## object 23 : Gorilla
                         Liver
## object 24 : Gorilla
                         Testis
## object 25 : Orangutan
                             Brain
                             Cerebellum
## object 26 : Orangutan
## object 27 : Orangutan
                             Heart
## object 28 : Orangutan
                             Kidney
## object 29 : Orangutan
                             Liver
## object 30 : Macaque
                         Brain
## object 31 : Macaque
                         Cerebellum
## object 32 : Macaque
                         Heart
## object 33 : Macaque
                         Kidney
## object 34 : Macaque
                         Liver
## object 35 : Macaque
                         Testis
## object 36 : Mouse
                         Brain
## object 37 : Mouse
                         Cerebellum
## object 38 : Mouse
                         Heart
## object 39 : Mouse
                         Kidney
## object 40 : Mouse
                         Liver
## object 41 : Mouse
                         Testis
## object 42 : Opossum
                         Brain
## object 43 : Opossum
                         Cerebellum
## object 44 : Opossum
                         Heart
```

```
## object 45 : Opossum
                         Kidney
## object 46 : Opossum
                         Liver
                         Testis
## object 47 : Opossum
## object 48 : Platypus
                             Brain
## object 49 : Platypus
                             Cerebellum
## object 50 : Platypus
                             Heart
## object 51 : Platypus
                             Kidney
## object 52 : Platypus
                             Liver
## object 53 : Platypus
                             Testis
## object 54 : Chicken
                         Brain
## object 55 : Chicken
                         Cerebellum
## object 56 : Chicken
                         Heart
## object 57 : Chicken
                         Kidney
## object 58 : Chicken
                         Liver
## object 59 : Chicken
                         Testis
print(tetraexp.objects[[1]], printlen = 6)
## One taxonExp object
## Taxon name: Human
## Subtaxon name: Brain
## Total gene number: 5636
## Total bio replicates number: 6
## Bio replicates titles:
## [1] "Female" "Male1"
                         "Male2" "Male3" "Male4"
                                                    "Male5"
## Outliers NOT removed
## Normalized expression value calculated
## Normalized method: TPM
## Over-dispersion parameter omega NOT calculated
head(tetraexp.objects[[1]]$normExp.val)
##
                   Human_Brain_Female Human_Brain_Male1 Human_Brain_Male2
## ENSG0000198824
                            28.181700
                                              22.882260
                                                                 32.29216
## ENSG0000118402
                            68.545215
                                              49.186043
                                                                  66.62576
## ENSG0000166167
                           107.390735
                                              99.581296
                                                                141.69295
## ENSG0000144724
                            35.034687
                                              30.911749
                                                                 28.90820
## ENSG0000183508
                             1.123546
                                               1.951074
                                                                  0.82868
## ENSG0000008086
                            50.913540
                                              22.196988
                                                                 36.23894
```