

ExprX-vignette

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1 Introduction

ExprX is an R package to streamline interspecies differential expression analysis. Taking TPM or FPKM/RPKM files for samples from different species as input, it provides functions to handle all the necessary steps, including data loading, ortholog matching, normalization, differential analysis and visualization.

ExprX is freely available at: <https://github.com/mingansun/ExprX>.

2 How to install ExprX

ExprX can be installed using the **install_git** function from devtools package. However, it depends on several other R packages, which should be installed first.

To install ExprX and its dependencies:

```
# install several dependent packages from Bioconductor using BiocManager
install.packages("BiocManager")
BiocManager::install(c("biomaRt", "edgeR", "RankProd"))

# install ExprX from GitHub using devtools
install.packages("devtools")
devtools::install_git("https://github.com/mingansun/ExprX")
```

To load the ExprX package:

```
library(ExprX)
#> Welcome to use ExprX!
```

For more details about how to install and use **ExprX**, please refer to the website:
<https://github.com/mingansun/ExprX>

3 Apply ExprX for interspecies differential expression analysis

Using RNA-Seq data for human and mouse brain, this vignette demonstrates how to detect differentially expressed genes between species using ExprX. All the involved steps are described below.

3.1 Generate ExprX object by integrating interspecies expression data

By parsing the meta table (as a data frame or CSV file) which contains information about expression data files (usually contain TPM, FPKM or RPKM values) for different species, the function **make_ExprX_dataset** can read these data files to create an object which contains the expression levels of the replicates of different species. The created ExprX object can also contain additional data such as orthologue pairs, normalized expression etc, and will be used by most of the subsequent analysis.

To use **make_ExprX_dataset** to read CSV file with meta data for expression data files and compared species (ie. human and mouse) to create an ExprX object:

```
# meta table file
hs2mm.meta_file <- paste0(path.package("ExprX"), "/extdata/brain_metatable.csv")

# make ExprX object from meta table
hs2mm.data <- make_ExprX_dataset(
  hs2mm.meta_file,
  data_dir = paste0(path.package("ExprX"), "/extdata")
)

#> x is detected as a file name. Read to a data frame:
#> Species  FullName  AbbrName  IdColumn  ExprColumn  ExprType  RepIndex  File
#> human    Homo Sapiens  hsapiens   1    6    tpm 1    human_brain_1.genes.results
#> human    Homo Sapiens  hsapiens   1    6    tpm 2    human_brain_2.genes.results
#> human    Homo Sapiens  hsapiens   1    6    tpm 3    human_brain_3.genes.results
#> mouse    mmusculus  mmusculus  1    6    tpm 1    mouse_brain_1.genes.results
#> mouse    mmusculus  mmusculus  1    6    tpm 2    mouse_brain_2.genes.results
#> mouse    mmusculus  mmusculus  1    6    tpm 3    mouse_brain_3.genes.results
#>
#> Read gene IDs for each species ...
#> human: 1042 genes.
#> mouse: 1037 genes.
#>
#> Loading expression data for each species ...
#> human: 1042 genes from 3 files.
#> mouse: 1037 genes from 3 files.
```

3.2 Determine the 1-to-1 orthologs among compared species

The 1-to-1 orthologs among species are constructed based on the homolog annotations from ENSEMBL database. Thus, only species available in in ENSEMBL database (about 200 as checked on 2020-4-7) can be used for analysis.

To use the **list_species** function to get the information (eg. species name, abbreviation) for all the species supported by ExprX:

```
sp.lst <- list_species()
head(sp.lst)
#>      Dataset      Species      Version
#> 1  acalliptera Eastern happy  fAstCal1.2
#> 2  acarolinensis Anole Lizard  AnoCar2.0
#> 3  acchrysaetos Golden eagle  bAquChr1.2
#> 4  acitrinellus Midas cichlid  Midas_v5
#> 5  amelanoleuca Panda          ailMel1
#> 6  amexicanus Mexican tetra Astyanax_mexicanus-2.0
```

Match and save 1-to-1 orthologs among species

The **ortholog_match** function invokes **biomaRt** package to retrieve homolog annotation from ENSEMBL database, then matches 1-to-1 orthologs by reciprocal comparison. This step usually takes a few minutes - depending on the network speed). To speed up, the obtained ortholog data can be stored on hard disk with **saveRDS** for later use.

```
# Match 1:1 orthologs between human and mouse
hs2mm.orth <- ortholog_match("human", "mouse")

# Save the ortholog results on hard disk for later use
saveRDS(hs2mm.orth, "hs2mm.orth.rds")
```

Load previously saved ortholog matching results from hard disk

Below shows how to use **readRDS** to load ortholog matching result that is previously saved on hard disk. Alternatively, the ortholog matching result can be generated with **ortholog_match** as demonstrated above.

The ortholog matching result includes information for each involved species, such as GeneID, GeneName, Chrom, GeneType and so on.

```
# Load ortholog result with readRDS
hs2mm.orth <- readRDS(paste0(path.package("ExprX"), "/data/hs2mm.orth.rds"))

# View the structure of hs2mm.orth
str(hs2mm.orth)
#> List of 2
#> $ human:'data.frame': 16536 obs. of 4 variables:
#> ..$ GeneID : chr [1:16536] "ENSG00000198695" "ENSG00000198712" "ENSG00000198727"
"ENSG00000198763" ...
#> ..$ GeneName: chr [1:16536] "MT-ND6" "MT-CO2" "MT-CYB" "MT-ND2" ...
#> ..$ Chrom : chr [1:16536] "MT" "MT" "MT" "MT" ...
#> ..$ GeneType: chr [1:16536] "protein_coding" "protein_coding" "protein_coding" "protein_coding"
...
#> $ mouse:'data.frame': 16536 obs. of 4 variables:
#> ..$ GeneID : chr [1:16536] "ENSMUSG00000064368" "ENSMUSG00000064354" "ENSMUSG00000064370"
"ENSMUSG00000064345" ...
#> ..$ GeneName: chr [1:16536] "mt-Nd6" "mt-Co2" "mt-Cytb" "mt-Nd2" ...
#> ..$ Chrom : chr [1:16536] "MT" "MT" "MT" "MT" ...
#> ..$ GeneType: chr [1:16536] "protein_coding" "protein_coding" "protein_coding" "protein_coding"
...
#> - attr(*, "Species")= chr [1:2] "human" "mouse"
#> - attr(*, "SpeciesAbbr")= chr [1:2] "hsapiens" "mmusculus"
#> - attr(*, "SpeciesFull")= chr [1:2] "Homo Sapiens" "mmusculus"
```

To summarize the ortholog results by genotype (eg. protein_coding, miRNA, lncRNA etc):

```
hs2mm.orth.genotype <- summarize_ortholog_gene(hs2mm.orth, group = "genotype")
head(hs2mm.orth.genotype)
#>           human mouse
#> IG_C_gene      3      3
#> IG_V_gene      2      2
```

```
#> TR_C_gene      1      1
#> TR_V_gene     16     16
#> LncRNA          1      0
#> miRNA          218    218
```

To summarize the ortholog matching results by chromosome:

```
hs2mm.orth.chrom <- summarize_ortholog_gene(hs2mm.orth, group = "chrom")
head(hs2mm.orth.chrom)
#>   human mouse
#> 1   1727 1050
#> 10   636  779
#> 11  1048 1342
#> 12   889  565
#> 13   286  546
#> 14   572  588
```

Filter 1-to-1 orthologs to exclude specific groups of genes

In many cases, specific groups of genes (eg. pseudogenes or genes from sex chromosomes) are undesirable for gene expression comparison. The function **ortholog_filter** enables the filtering of ortholog pairs based on gene type, chromosome, or provided gene list, as demonstrated below.

```
# Filter orthologs by excluding genes from chromosomes X, Y and MT, and only keep
# protein_coding genes
hs2mm.orth.flt <- ortholog_filter(
  hs2mm.orth,
  genotype_include = "protein_coding",
  chrom_exclude = c("X", "Y", "MT")
)
#> Check data for human
#> genotype_include matches: 15849
#> chrom_exclude matches: 595
#>
#> Check data for mouse
#> genotype_include matches: 15855
#> chrom_exclude matches: 590
#>
#> Original gene number: 16536
#> Filtered gene number: 15275
```

To check the number of 1:1 orthologs before and after filtering:

```
# Before filtering
dim(hs2mm.orth[[1]])
#> [1] 16536      4

# After filtering
dim(hs2mm.orth.flt[[1]])
#> [1] 15275      4
```

3.3 Integrate the 1-to-1 ortholog matching result to ExprX object

Take the original ExprX object generated with **make_ExprX_dataset** and the ortholog matching data generated using **ortholog_match** as input, the function **ortholog_expression_merge** integrates together the expression data for all 1:1 orthologs among compared species. The integrated data will be appended to the original ExprX object and returned as an updated object. To be noted, for orthologs that don't have matched expression data, they will be excluded from the returned data.

```
# Merge data
hs2mm.data <- ortholog_expression_merge(
  expr_data = hs2mm.data, orth_data = hs2mm.orth.flt
)
#> Number of ortholog pairs absent from expr_data
#> human: 14233
#> mouse: 14238
#>
#> Original ortholog number: 15275
#> Discarded ortholog number: 14375
#> Resulted ortholog number: 900
```

3.4 Integrate the normalized expression data for 1-to-1 orthologs to ExprX object

Normalization of the expression data for 1:1 orthologs among species can be performed by using the **ortholog_expression_normalize** function. Different normalization approaches are supported, including TMM, TMMwsp, RLE, upperquartile and quantile. The normalized data matrix will be appended to the original ExprX object and returned as the updated ExprX object.

To normalize the expression data of 1:1 orthologs among samples using the TMM approach:

```
# Load required package
library(edgeR)
#> Loading required package: limma

# Perform data normalization
hs2mm.data <- ortholog_expression_normalize(
  expr_data = hs2mm.data, method = "TMM"
)
```

3.5 Perform interspecies differential expression analysis

Differential expression analysis of 1:1 orthologs between species can be performed using the **ortholog_expression_compare** function. Expression data of 1:1 orthologs after normalization are used for differential expression analysis. Statistics such as average expression level, log2foldChange and p-values are calculated and returned as a dataframe.

Below shows how to perform interspecies differential analysis for 1:1 orthologs using RankProd approach. To be noted, the demo dataset is only for less than 1000 genes, thus only a couple of genes are called as differentially expressed. If use full dataset, the number of called differential genes can be as many as several hundreds.

```

# Load required package
library(RankProd)
#> Loading required package: Rmpfr
#> Loading required package: gmp
#>
#> Attaching package: 'gmp'
#> The following objects are masked from 'package:base':
#>
#>      %*%, apply, crossprod, matrix, tcrossprod
#> C code of R package 'Rmpfr': GMP using 64 bits per limb
#>
#> Attaching package: 'Rmpfr'
#> The following object is masked from 'package:gmp':
#>
#>      outer
#> The following objects are masked from 'package:stats':
#>
#>      dbinom, dgamma, dnorm, dpois, pnorm
#> The following objects are masked from 'package:base':
#>
#>      cbind, pmax, pmin, rbind

# Perform differential analysis and then sort by p-value
hs2mm.deg <- ortholog_expression_compare(
  hs2mm.data, method = "RankProd", p_adjust = "fdr"
)
#> Rank Product analysis for unpaired case
#>
#>
#> done
hs2mm.deg <- hs2mm.deg[order(hs2mm.deg$P_value),]

# Check what the differential analysis result looks like
head(hs2mm.deg)
#>      GeneID_human      GeneID_mouse GeneName_human GeneName_mouse
#> 233 ENSG00000131095 ENSMUSG00000020932      GFAP      Gfap
#> 256 ENSG00000197971 ENSMUSG00000041607      MBP      Mbp
#> 316 ENSG00000120885 ENSMUSG00000022037      CLU      CLu
#> 858 ENSG00000167996 ENSMUSG00000024661      FTH1      Fth1
#> 396 ENSG00000136161 ENSMUSG00000022106      RCBTB2      Rcbtb2
#> 674 ENSG00000120094 ENSMUSG00000018973      HOXB1      Hoxb1
#>      Expression_human Expression_mouse Expression_average Log2foldChange
#> 233      98707.9359      1.947577      49354.9418      15.299531
#> 256      207093.3485      91.182026      103592.2653      11.141358
#> 316      137866.0153      345.075280      69105.5453      8.640056
#> 858      99991.8187      3601.512987      51796.6659      4.794942
#> 396      244.2676      34316.340494      17280.3041      -7.131360
#> 674      0.0000      276.888419      138.4442      -9.115764
#>      P_value
#> 233 0.009575705
#> 256 0.009575705
#> 316 0.016379287
#> 858 0.037521803

```

```
#> 396 0.047574220
#> 674 0.047574220
```

To determine differential genes (based on cutoff of p-value and log2foldChange) which can be saved for downstream analysis:

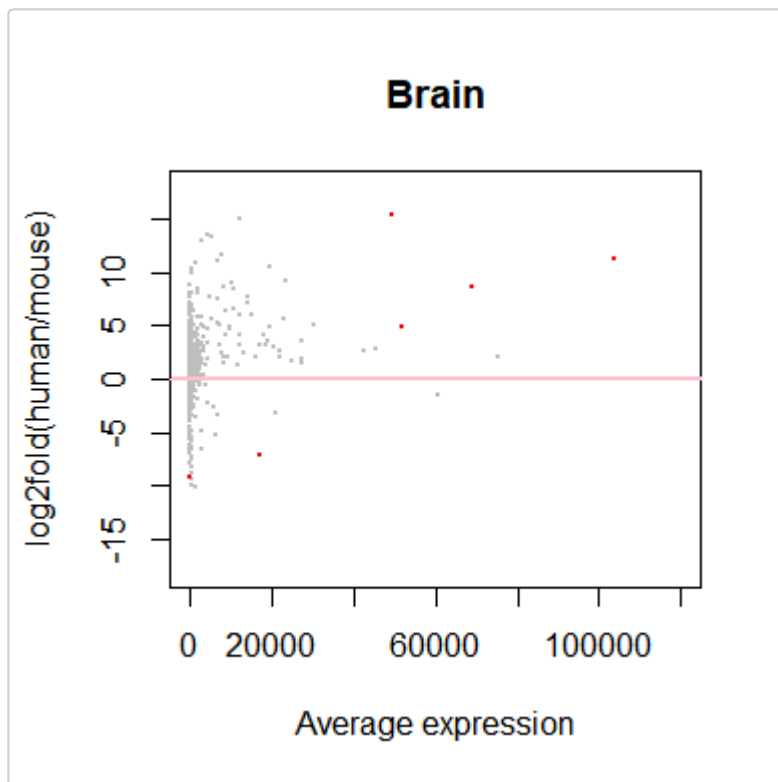
```
# Determine significant differential genes (human>mouse) based on p-values and log2foldChange
hs2mm.hsHigh <- subset(hs2mm.deg, subset = log2foldChange > 1 & P_value < 0.05)
head(hs2mm.hsHigh)
#>      GeneID_human      GeneID_mouse GeneName_human GeneName_mouse
#> 233 ENSG00000131095 ENSMUSG00000020932      GFAP      Gfap
#> 256 ENSG00000197971 ENSMUSG00000041607      MBP      Mbp
#> 316 ENSG00000120885 ENSMUSG00000022037      CLU      Clu
#> 858 ENSG00000167996 ENSMUSG00000024661      FTH1      Fth1
#>      Expression_human Expression_mouse Expression_average Log2foldChange
#> 233          98707.94          1.947577          49354.94          15.299531
#> 256          207093.35          91.182026          103592.27          11.141358
#> 316          137866.02          345.075280          69105.55          8.640056
#> 858          99991.82          3601.512987          51796.67          4.794942
#>      P_value
#> 233 0.009575705
#> 256 0.009575705
#> 316 0.016379287
#> 858 0.037521803
```

```
# Determine significant differential genes (human<mouse) based on p-values and log2foldChange
hs2mm.mmHigh <- subset(hs2mm.deg, subset = log2foldChange < -1 & P_value < 0.05)
head(hs2mm.mmHigh)
#>      GeneID_human      GeneID_mouse GeneName_human GeneName_mouse
#> 396 ENSG00000136161 ENSMUSG00000022106      RCBTB2      Rcbtb2
#> 674 ENSG00000120094 ENSMUSG00000018973      HOXB1      Hoxb1
#>      Expression_human Expression_mouse Expression_average Log2foldChange
#> 396          244.2676          34316.3405          17280.3041          -7.131360
#> 674           0.0000          276.8884          138.4442          -9.115764
#>      P_value
#> 396 0.04757422
#> 674 0.04757422
```

3.6 Visualize differential expression analysis result

The differential expression can be visualized as MA-plot or Volcano-plot, with differential genes highlighted by color. Below shows how to use the **ortholog_expression_plot** function to generate MA-plot and Volcano-plot, respectively.

```
# Generate MA-plot
ortholog_expression_plot(
  hs2mm.deg, "MA",
  main = "Brain", xlim = c(0,120000), ylim = c(-18,18)
)
```



```
# Generate Volcano-plot
ortholog_expression_plot(
  hs2mm.deg, "volcano",
  main = "Brain", xlim = c(-18,18), ylim = c(0, 3)
)
```

