

fastJT

Efficient Jonckheere-Terpstra Test Statistics for Robust Machine
Learning and Genome-Wide Association Studies

2017-02-06

Outline

Introduction

Examples

Session Information

Introduction

- ▶ This document provides an example for using the `fastJT` package to calculate the Jonckheere-Terpstra test statistics for large data sets (multiple dependent and independent variables) commonly encountered in machine learning or GWAS. The functionality is also included to perform k-fold cross validation or feature sets.
- ▶ The calculation of the standardized test statistic employs the null variance equation as defined by Hollander and Wolfe (1999, eq. 6.19) to account for ties in the data.
- ▶ The major algorithm in this package is written in C++, which is ported to R by Rcpp, to facilitate fast computation.
- ▶ Features of this package include:
 - 1 $O(N \times \log(N))$ computational complexity (where N is the number of the samples)
 - 2 OpenMP supported parallelization
 - 3 Customized output of top m significant independent variables for each dependent variable

fastJT

```
res <- fastJT(Y, X, outTopN=15, numThreads=1, standardized=TRUE)
```

Function arguments:

Y: Matrix of continuous values, representing dependent variables, with sample IDs as row names and variable names as column names.

X: A matrix of integer values, representing independent variables, with sample IDs as row names and feature IDs as column names.

outTopN: Number of top statistics to return (i.e., the largest standardized statistics). The default value is 15. If outTopN is set to NA, all results will be returned.

numThreads: Number of threads to use for parallel computation. The default value is 1 (sequential computation).

standardized: A boolean to specify whether to return standardized statistics or non-standardized statistics. The default value is TRUE, returning standardized statistics.

Users may wish to consider the `dplyr::recode()` function for converting non-numeric group indices into ordinal values for argument X.

Returned Values

Function returns:

- J:** A matrix of standardized/non-standardized Jonckheere-Terpstra test statistics, depending on option `standardized`, with column names from input `Y`. If `outTopN` is not `NA`, results are sorted within each column.
- XIDs:** If `outTopN` is not `NA`, this is a matrix of column names from `X` associated with top standardized Jonckheere-Terpstra test statistics from `J`. Otherwise this is an unsorted vector of column names from input `X`.

fastJT.select

```
res <- fastJT.select(Y, X, cvMesh=NULL, kFold=10L,  
                    selCrit=NULL, outTopN=15L, numThreads=1L)
```

Function arguments:

- Y:** Matrix of continuous values, representing dependent variables, with sample IDs as row names and variable names as column names.
- X:** Matrix of integer values, representing independent variables, with sample IDs as row names and feature IDs as column names.
- cvMesh:** A user-defined function to specify how to separate the data into training and testing parts. The inputs of this function are a vector of the sample IDs and **kFold**, an integer representing the number of folds for cross validation. The output of this function is a list of **kFold** vectors of sample IDs forming the testing subset for each fold. The default value is **NULL**, and if no function is specified, the data are partitioned sequentially into **kFold** equal sized subsets. Optional.

fastJT.select

Function arguments continued:

kFold: An integer to indicate the number of folds. Optional. The default value is 10.

selCrit: A user-defined function to specify the criteria for selecting the top features. The inputs of this function include J, the matrix of statistics resulting from fastJT, and P, the matrix of p-values from pvalues(J). The output is a data frame containing the selected feature IDs for each trait of interest. Optional. The default value is NULL, and if no function is specified, the features the largest standardized Jonckheere-Terpstra test statistics are selected.

outTopN: An integer to indicate the number of top hits to be returned when selCrit=NULL. Unused if selCrit!=NULL. Optional. The default value is 15.

numThreads: A integer to indicate the number of threads to be used in the computation. Optional. The default value is 1 (sequential computation).

The function withholds one subset while the remaining kFold-1 subsets are used to test the features. The process is repeated kFold times, with each of the subsets withheld exactly once as the validation data.

Returned Values

Function returns: Three lists of length `kFold`:

- `J`: A list of matrices of standardized Jonckheere-Terpstra test statistics, one for each cross validation.
- `Pval`: A list of matrices of p-values, one for each cross validation.
- `XIDs`: A list of matrices of the selected feature IDs, one for each cross validation.

Simulate Data

- 1 Define the number of markers, samples, and features:

```
num_sample    <- 100  
num_marker    <- 4  
num_feature   <- 50
```

- 2 Create two matrices containing marker levels and feature information.
 - a. Data contains the samples' marker levels.
 - b. Feature contains the samples' feature values.

```
set.seed(12345);  
Data      <- matrix(rnorm(num_sample*num_marker),  
                    num_sample, num_marker)  
Feature <- matrix(rbinom(num_sample*num_feature,2,0.5),  
                  num_sample, num_feature)  
colnames(Data)      <- paste0("Mrk:",1:num_marker)  
colnames(Feature) <- paste0("Ftr:",1:num_feature)
```

Load Package

Load fastJT (after installing its dependent packages):

```
library(fastJT)
```

Example Execution

```
JTStat <- fastJT(Y=Data, X=Feature, outTopN=10)
summary(JTStat, Y2Print=1:4, X2Print=1:5)
```

```
##
##
##          Johckheere-Terpstra Test for Large Matrices
##          P-values for Top Standardized Statistics
## =====
##
##          Mrk:1|          Mrk:2|          Mrk:3|          Mrk:4|
## -----
##          SNPID P-value|          SNPID P-value|          SNPID P-value|          SNPID P-value|
## -----
##          Ftr:35 1.7e-02|          Ftr:35 2.0e-02|          Ftr:20 1.9e-02|          Ftr:46 1.2e-02|
##          Ftr:17 1.7e-02|          Ftr:7  5.7e-02|          Ftr:49 3.5e-02|          Ftr:34 1.7e-02|
##          Ftr:27 7.0e-02|          Ftr:46 9.1e-02|          Ftr:26 3.8e-02|          Ftr:47 3.7e-02|
##          Ftr:28 7.0e-02|          Ftr:40 9.4e-02|          Ftr:47 5.6e-02|          Ftr:23 4.5e-02|
##          Ftr:14 8.8e-02|          Ftr:29 1.5e-01|          Ftr:30 9.7e-02|          Ftr:16 5.1e-02|
```

Example Execution: Statistics in the Summary

```
summary(JTStat, Y2Print=1:4, X2Print=1:5, printP=FALSE)
```

```
##
##
##              Johckheere-Terpstra Test for Large Matrices
##              Top Standardized Statistics
## =====
##
##              Mrk:1|              Mrk:2|              Mrk:3|              Mrk:4|
## -----
##              SNP ID      J*|      SNP ID      J*|      SNP ID      J*|      SNP ID      J*|
## -----
##      Ftr:35  -2.390|      Ftr:35  -2.331|      Ftr:20   2.350|      Ftr:46   2.505|
##      Ftr:17  -2.388|              Ftr:7   1.905|      Ftr:49  -2.106|      Ftr:34   2.396|
##      Ftr:27  -1.813|      Ftr:46   1.693|      Ftr:26  -2.072|      Ftr:47  -2.089|
##      Ftr:28   1.813|      Ftr:40   1.676|      Ftr:47   1.914|      Ftr:23   2.000|
##      Ftr:14   1.706|      Ftr:29   1.432|      Ftr:30  -1.662|      Ftr:16   1.955|
```

Example Execution: Sorting in the Summary

```
JTA11 <- fastJT(Y=Data, X=Feature, outTopN=NA)
summary(JTA11, Y2Print=1:4, outTopN=3)
```

```
##
##
##              Johckheere-Terpstra Test for Large Matrices
##              P-values for Top Standardized Statistics
## =====
##
##              Mrk:1|              Mrk:2|              Mrk:3|              Mrk:4|
## -----
##              SNPID P-value|              SNPID P-value|              SNPID P-value|              SNPID P-value|
## -----
##              Ftr:35 1.7e-02|              Ftr:35 2.0e-02|              Ftr:20 1.9e-02|              Ftr:46 1.2e-02|
##              Ftr:17 1.7e-02|              Ftr:7 5.7e-02|              Ftr:49 3.5e-02|              Ftr:34 1.7e-02|
##              Ftr:27 7.0e-02|              Ftr:46 9.1e-02|              Ftr:26 3.8e-02|              Ftr:47 3.7e-02|
```

Example Execution: fastJT.select

```
fastJT.select(Y=Data, X=Feature, cvMesh=NULL, kFold=5,  
selCrit=NULL, outTopN=5, numThreads=1)
```

```
## $J  
## $J[[1]]  
##           Mrk:1      Mrk:2      Mrk:3      Mrk:4  
## [1,] -2.449202 -2.401972  2.402878  2.491444  
## [2,] -2.356094  1.863353  2.159547  2.333146  
## [3,] -1.798716  1.662280 -2.066804 -2.185883  
## [4,]  1.796900  1.662069 -1.902853  2.004838  
## [5,]  1.754959  1.399926 -1.893419  1.955443  
##  
## $J[[2]]  
##           Mrk:1      Mrk:2      Mrk:3      Mrk:4  
## [1,] -2.449202 -2.401972  2.402878  2.491444  
## [2,] -2.356094  1.863353  2.159547  2.333146  
## [3,] -1.798716  1.662280 -2.066804 -2.185883  
## [4,]  1.796900  1.662069 -1.902853  2.004838  
## [5,]  1.754959  1.399926 -1.893419  1.955443  
##  
## $J[[3]]  
##           Mrk:1      Mrk:2      Mrk:3      Mrk:4  
## [1,] -2.449202 -2.401972  2.402878  2.491444  
## [2,] -2.356094  1.863353  2.159547  2.333146  
## [3,] -1.798716  1.662280 -2.066804 -2.185883  
## [4,]  1.796900  1.662069 -1.902853  2.004838  
## [5,]  1.754959  1.399926 -1.893419  1.955443  
##  
## $J[[4]]  
##           Mrk:1      Mrk:2      Mrk:3      Mrk:4  
## [1,] -2.449202 -2.401972  2.402878  2.491444  
## [2,] -2.356094  1.863353  2.159547  2.333146  
## [3,] -1.798716  1.662280 -2.066804 -2.185883  
## [4,]  1.796900  1.662069 -1.902853  2.004838  
## [5,]  1.754959  1.399926 -1.893419  1.955443  
##  
## $J[[5]]
```

Example User-Defined cvMesh Function

```
Mesh <- function(rownamesData, kFold){  
  numSamples <- length(rownamesData)  
  res <- NULL  
  subSampleSize <- floor(numSamples/kFold)  
  for (i in 1:kFold){  
    start <- (i-1)*subSampleSize + 1  
    if(i < kFold)  
      end <- i*subSampleSize  
    else  
      end <- numSamples  
    if(i == 1)  
      res <- list(c(start:end))  
    else  
      res[[i]] <- c(start:end)  
  }  
  res  
}
```

Example User-Defined selCrit Function

```
whichpart <- function(x, n=30) {  
  nx <- length(x)  
  p <- nx-n  
  xp <- sort(x, partial=p)[p]  
  which(x > xp)  
}  
  
selectCrit <- function(J, P){  
  pcut <- 0.95  
  hit <- NULL  
  for(i in 1:ncol(P)){  
    if(i == 1)  
      hit <- list(rownames(P)[whichpart(P[,i], 4)])  
    else  
      hit[[i]] = rownames(P)[whichpart(P[,i], 4)]  
  }  
  res <- do.call(cbind, hit)  
  colnames(res) <- colnames(P)  
  res  
}
```


Example Execution with User-Defined Functions

```
fastJT.select(Data, Feature, cvMesh=Mesh, kFold=5,  
              selCrit=selectCrit, outTopN=5, numThreads=1)
```

```
## $J  
## $J[[1]]  
##  
##      Mrk:1      Mrk:2      Mrk:3      Mrk:4  
## Ftr:1  1.044871948  0.30810327 -0.52243597 -1.41325629  
## Ftr:2  0.064765493 -0.57607202  0.48744556  0.91694304  
## Ftr:3  0.708932518 -0.93211498  0.38072302 -0.99775688  
## Ftr:4  0.177698249 -0.10530267  1.24388774  0.13820975  
## Ftr:5 -0.135648047  0.29164330 -1.58029974  1.23439722  
## Ftr:6  0.626045363  0.20007635 -1.20691219 -0.61313721  
## Ftr:7 -1.007934807  1.86335316  0.53712315  1.32623001  
## Ftr:8  0.382152784 -1.08715878 -1.30459054  0.17789871  
## Ftr:9 -0.627298931 -1.04772268  0.28695589  1.08776304  
## Ftr:10 -0.552417489 -1.03827865  0.62562945 -0.54576186  
## Ftr:11  0.718808299  0.69218577  0.79867589 -0.06655632  
## Ftr:12  0.214931358 -0.73882654 -1.25600512 -1.24928852  
## Ftr:13 -0.637403711 -1.34635274 -0.27317302 -0.61138723  
## Ftr:14  1.754958762 -0.17582763 -0.27535270  0.53411788  
## Ftr:15 -0.987651750  0.20792668  0.01299542 -1.13709905  
## Ftr:16  1.487980337  0.09875976  0.72423822  1.95544319  
## Ftr:17 -2.356093867 -0.36605978  0.00000000 -1.92347776  
## Ftr:18  0.846622444  1.31915590  0.22970376  0.01312593  
## Ftr:19  0.006991013  0.34955065  0.78998447 -1.37023855  
## Ftr:20 -0.055126760 -0.45074233  2.40287819  0.49614084  
## Ftr:21 -0.201986904  0.05212565 -0.19547120 -0.81446332  
## Ftr:22 -0.242183804 -0.22254728  0.88364361 -0.96873521  
## Ftr:23 -0.359172943  0.58773754  0.34611211  2.00483806  
## Ftr:24  0.661565280 -0.17050652 -1.35041160  1.05032014  
## Ftr:25  0.892047636  0.20079301  1.25413339 -0.41146109  
## Ftr:26  0.275352698 -0.93221817 -2.06680399  0.82605809  
## Ftr:27 -1.798716484 -0.26774787 -0.46684245  0.51489976  
## Ftr:28  1.796899533  1.09120808  0.31364065  1.17615242  
## Ftr:29  0.364631969  1.39992631  0.20184984 -0.71624137  
## Ftr:30  0.451127576  0.81993260 -1.89341866  1.28752469  
## Ftr:31 -0.868212309 -0.42431429  0.41125846  0.15014198
```

References

Hollander, M. and Wolfe, D. A., *Nonparametric Statistical Methods*. New York, Wiley, 2nd edition, 1999.

Session Information

- ▶ R version 3.3.2 (2016-10-31), x86_64-pc-linux-gnu
- ▶ Base packages: base, datasets, grDevices, graphics, methods, stats, utils
- ▶ Other packages: fastJT 1.0.1, knitr 1.13
- ▶ Loaded via a namespace (and not attached): Rcpp 0.12.4, evaluate 0.8, formatR 1.2.1, highr 0.5.1, magrittr 1.5, stringi 1.0-1, stringr 1.0.0, tools 3.3.2

```
## [1] "Start Time Mon Feb 6 12:04:55 2017"  
## [1] "End Time Mon Feb 6 12:04:55 2017"
```