

jtGWAS

Efficient Jonckheere-Terpstra Test Statistics

2016-06-15

# Outline

Introduction

Example

Session Information

# Introduction

- ▶ This document provides an example for using the `jtGWAS` package to calculate the Jonckheere-Terpstra test statistics for large data sets (multiple markers and genome-wide SNPs) commonly encountered in GWAS.
- ▶ 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 OpenMP supported parallelization
  - 2 Customized output of top  $m$  significant SNPs for each marker
  - 3  $O(N \times \log(N))$  computational complexity (where  $N$  is the number of the samples)

# jtGWAS

```
res <- jtGWAS(X, G, outTopN=15, numThreads=1, standardized=TRUE)
```

Function arguments:

- X**: Matrix of marker levels, with sample IDs as row names and marker IDs as column names.
- G**: Matrix of genotypes, with sample IDs as row names and SNP IDs as column names.
- outTopN**: Number of top statistics to return (i.e., the largest  $n$  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.

# Returned Values

Function returns:

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

# Simulate Data

## 1 Define the number of markers, patients, and SNPs:

```
num_patient <- 100  
num_marker  <- 4  
num_SNP     <- 50
```

## 2 Create two matrices containing marker levels and genotype information.

- X\_pat\_mak contains the patients' marker levels.
- G\_pat\_SNP contains the patients' genotypes.

```
set.seed(12345);  
X_pat_mak <- matrix(rnorm(num_patient*num_marker),  
                    num_patient,  
                    num_marker)  
G_pat_SNP <- matrix(rbinom(num_patient*num_SNP,2,0.5),  
                    num_patient,  
                    num_SNP)  
colnames(X_pat_mak) <- colnames(X_pat_mak, do.NULL = FALSE, prefix = "Mrk:" )  
colnames(G_pat_SNP) <- colnames(G_pat_SNP, do.NULL = FALSE, prefix = "SNP:" )
```

# Load Package

Load jtGWAS (after installing its dependent packages):

```
library(jtGWAS)
```

# Example Execution

```
JTStat <- jtGWAS(X_pat_mak, G_pat_SNP, outTopN=10)
summary(JTStat, marker2Print=1:4, SNP2Print=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|
## -----
##          SNP:35 1.7e-02|          SNP:35 2.0e-02|          SNP:20 1.9e-02|          SNP:46 1.2e-02|
##          SNP:17 1.7e-02|          SNP:7 5.7e-02|          SNP:49 3.5e-02|          SNP:34 1.7e-02|
##          SNP:27 7.0e-02|          SNP:46 9.1e-02|          SNP:26 3.8e-02|          SNP:47 3.7e-02|
##          SNP:28 7.0e-02|          SNP:40 9.4e-02|          SNP:47 5.6e-02|          SNP:23 4.5e-02|
##          SNP:14 8.8e-02|          SNP:29 1.5e-01|          SNP:30 9.7e-02|          SNP:16 5.1e-02|
```

## Example Execution: Statistics in the Summary

```
summary(JTStat, marker2Print=1:4, SNP2Print=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*|
## -----
##      SNP:35  -2.390|      SNP:35  -2.331|      SNP:20   2.350|      SNP:46   2.505|
##      SNP:17  -2.388|      SNP:7   1.905|      SNP:49  -2.106|      SNP:34   2.396|
##      SNP:27  -1.813|      SNP:46   1.693|      SNP:26  -2.072|      SNP:47  -2.089|
##      SNP:28   1.813|      SNP:40   1.676|      SNP:47   1.914|      SNP:23   2.000|
##      SNP:14   1.706|      SNP:29   1.432|      SNP:30  -1.662|      SNP:16   1.955|
```

## Example Execution: Sorting in the Summary

```
JTAll <- jtGWAS(X_pat_mak, G_pat_SNP, outTopN=NA)
summary(JTAll, marker2Print=1:4, SNP2Print=1:3)
summary(JTAll, marker2Print=1:4, outTopN=3)
```

```
##
##      Johckheere-Terpstra Test
##      P-values Based on Standardized Statistics
##
##      Mrk:1      Mrk:2      Mrk:3      Mrk:4
## SNP:1 0.2931953 0.7711424 0.5877522 0.1610595
## SNP:2 0.9120503 0.6085816 0.8017917 0.3169385
## SNP:3 0.5081104 0.3280014 0.5546797 0.2823776
##
##
##      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|
## -----
##      SNP:35 1.7e-02|      SNP:35 2.0e-02|      SNP:20 1.9e-02|      SNP:46 1.2e-02|
##      SNP:17 1.7e-02|      SNP:7 5.7e-02|      SNP:49 3.5e-02|      SNP:34 1.7e-02|
##      SNP:27 7.0e-02|      SNP:46 9.1e-02|      SNP:26 3.8e-02|      SNP:47 3.7e-02|
```

## References

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

# Session Information

- ▶ R version 3.3.0 (2016-05-03), x86\_64-pc-linux-gnu
- ▶ Base packages: base, datasets, grDevices, graphics, methods, stats, utils
- ▶ Other packages: jtGWAS 1.3, 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 3.3.0

```
## [1] "Start Time Wed Jun 15 10:44:00 2016"  
## [1] "End Time Wed Jun 15 10:44:00 2016"
```