

lc1GWAS

Efficient Estimation of Discrete-Time Multivariate Frailty Model
Using Exact Likelihood Function for Grouped Survival Data

2016-11-15

Introduction

- ▶ This document provides an example for using the `lc1GWAS` package to calculate the baseline hazard, effect parameter, and frailty variance for a discrete-time frailty model containing mixed effects by exact likelihood function.
- ▶ The major algorithm in this package is written in C++, which is ported to R by `Rcpp`, to facilitate fast computation.

betaEst

```
beta <- betaEst(fam_size, alpha, dtime,  
               delta, g, var, m, lower = 0, upper = 2)
```

Function arguments:

fam_size: A vector contains the number of sample for each family.

alpha: Baseline hazard vector for each time intervals.

dtime: A vector of observed survival time for each sample.

delta: A event indicator vector: 1 means event and 0 means otherwise.

g: A vector for numerical gene type of each sample.

var: A scalar for frailty variance.

m: A integer for the number of families.

lower: A scalar for the lower bound for the effect parameter estimation.

upper: A scalar for the upper bound for the effect parameter estimation.

Returned Value of betaEst

Function returns:

betaEst: A scalar for the estimated effect size.

varEst

```
var <- varEst(fam_size, alpha, dtime,  
             delta, g, beta, m, lower = 0, upper = 2)
```

Function arguments:

fam_size: A vector contains the number of sample for each family.

alpha: Baseline hazard vector for each time intervals.

dtime: A vector of observed survival time for each sample.

delta: A event indicator vector: 1 means event and 0 means otherwise.

g: A vector for numerical gene type of each sample.

beta: A scalar for effect parameter.

m: A integer for the number of families.

lower: A scalar for the lower bound for the effect parameter estimation.

upper: A scalar for the upper bound for the effect parameter estimation.

Returned Value of varEst

Function returns:

`varEst`: A scalar for the estimated frailty variance.

alphaEst

```
alpha <- alphaEst(fam_size, alpha, dtime,  
                  delta, g, beta, m, lower = 0, upper = 2)
```

Function arguments:

- m**: A integer to indicate which discrete-time baseline hazard.
- dtime**: A vector of observed survival time for each sample.
- delta**: A event indicator vector: 1 means event and 0 means otherwise.
- g**: A vector for numerical gene type of each sample.

Function returns:

- alphaEst**: A scalar for the estimated baseline hazard.

Example

Sample data and parameters:

```
fsize <- rep(3,3)
alphas <- c(0.7500000, 0.6666667, 0.5000000, 0.0000000)
dtimes <- c(1, 3, 3, 2, 1, 1, 2, 3, 1)
deltas <- c(1, 0, 1, 1, 1, 0, 1, 0, 1)
gs <- c(0, 1, 1, 1, 2, 2, 0, 0, 0)
var <- 0.2
m <- 3
beta <- 1
```


Load Package

Load lc1GWAS (after installing its dependent packages):

```
library(lc1GWAS)
```

Example Execution

Example execution

```
res <- betaEst(fsize, alphas, dtimes,  
              deltas, gs, var, m, lower = 0, upper = 2)  
res  
  
## $betaEst  
## [1] 1.13831
```

```
res <- varEst(fsize, alphas, dtimes,  
              deltas, gs, var, beta, lower = 0, upper = 2)  
res  
  
## $varEst  
## [1] 0.0009062077
```

```
res <- alphaEst(1, dtimes, deltas, gs)  
res  
  
## $alphaEst  
## [1] 0.625
```

Session Information

- ▶ R version 3.3.1 (2016-06-21), x86_64-pc-linux-gnu
- ▶ Base packages: base, datasets, grDevices, graphics, methods, stats, utils
- ▶ Other packages: knitr 1.13, lclGWAS 1.0.1
- ▶ 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 3.3.1

```
## [1] "Start Time Tue Nov 15 13:06:02 2016"  
## [1] "End Time Tue Nov 15 13:06:02 2016"
```