Author Contributions Checklist Form

Data

Abstract

The dataset BCCT is a clinical data from a 3-year NIH-sponsored randomized Bovine Collagen Trial for Scleroderma patients conducted at 12 centers in the USA which contains 297 samples.

The dataset ACTG175 was a randomized clinical trial to compare monotherapy with zidovudine or didanosine with combination therapy with zidovudine and didanosine or zidovudine and zalcitabine in adults infected with the human immunodeficiency virus type I whose CD4 T cell counts were between 200 and 500 per cubic millimeter.

Availability

- The dataset BCCT is available if required

- The dataset ACTG175 is a public dataset in R package **speff2trial**.

Description

- The dataset BCCT is a .csv file named "mrss.csv", in the file path: MCPL_Rcode/realdata/BCTG/mrss.csv .

- The dataset ACTG175 is an R data.frame which can be load from R package **speff2trial**.

Code

Abstract

The code file MCPL_Rcode include the simulation and real data.

- Simulation file includes the R code for the single change plane and multiple change plane cases

- Realdata file includes the R code for two datasets BCCT and ACTG175.

Description

All codes are written in software R, and available if required. The code will be deposited in the github `https://github.com/liygCR/MCPL` if the manuscript is accepted.

Instructions for Use

Reproducibility

In the simulation part, all tables and figures in example $1 - 4$ can be reproduced by sourcing R code in simulation file.

- Example 1: Table $1 - 3$ can be reproduced by "single_changeplane.R".

- Example 2: Table 4, 6 and 7 can be reproduced by "multiple_changeplane.R".

- Example 3: no change plane results in Table 4 can be reproduced by "no_changeplane.R".

- Example 4: Table 5, 8 and 9 can be reproduced by "unbalance_multiple_changeplane.R".

- Figure 1, 2 and 3 can be reproduced by NMI.fun in "fig1.R", "fig2.R" and "fig3.R" respectively.

We explain the detailed implementation with the "multiple_changeplane.R" of Example 2.

1. Source R function multiplecpfun.R by source("multiplecpfun.R") which is the main function.

2. Generate the data by function dg.fun() for different design matrix.

3. Do the 500 replications by function sim.res().

4. The main estimation function is iter.fun(), and the input "ini.theta" is a guesstimate of θ.

In the real data part, Table $11-14$ can be reproduced by R function "BCCT.R" and "ACTG175.R". We explain the detailed implementation with the example BCCT dataset.

1. Source R function BCCT_fun.R by source("BCCT_fun.R") which is the main function.

2. Obtain the estimator by R function iter.fun() and the input "ini.theta" is a guesstimate of θ.