Association Analysis of Complex Diseases Using Triads, Parent-child Dyads and Singleton Monads

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1 Overview

This document describes a R package to implement the models for association analysis of complex diseases using triads, parent-child dyads, and singleton monads. The document contains two parts: Joint_Association_Analysis_web.zip and Count_Triad_Dyad_Monad.zip. The first one can analyze combined data of triads, dyads, and monads, supposed you have their counts. The second part, Count_Triad_Dyad_Monad.zip, contains sas and R codes to count the number of triads, dyads, and monads written by Mr. Deangelis.

Section 2 briefly describes the installation of the program of Joint_Association_Analysis_web.zip. Section 3 explains how to run the program using one example. Section 4 provides sas and R codes to count the number of triads, dyads, and monads.

The theoretical basis for this program is given in our research paper in **Reference**. Please refer to the reference if you use the program in any published work. In case of suggestions and questions and/or problems, you can contact us via e-mail (fanr@mail.nih.gov).

2 Download and Installation

The package is written in R. First, download the package "FT_Add.R", "FT_Dom.R", "FT_Mult.R", "FT_Rec.R", and "FT_Unr.R" from Joint_Association_Analysis_web.zip. Then, put the "Example.R", "dyad.csv", "monad.csv", and "triad.csv" in one directory.

3 How to Run the Program

Open the "example.R" file on an R Console in a PC window. Change the paths leading to the directory of the package "FT_Add.R", "FT_Dom.R", "FT_Mult.R", "FT_Rec.R", and "FT_Unr.R", and the directory of the data files of "dyad.csv", "monad.csv", and "triad.csv" on your computer. Then, you may run the program.

4 Count Number of Triads, Dyads, and Monads

In Count_Triad_Dyad_Monad.zip, sas and R codes are provided to count the number of triads, dyads, and monads. The codes use simped.csv as an example, which contains

- 1. 200 triad families: Famid is between 1.1 and 200.1;
- 2. 12 dyad families with missing dad: Famid is between 201.1 and 212.1;
- 3. 13 dyad families with missing mom: Famid is between 213.1 and 225.1;
- 4. 25 monads: Famid is between 226.1 and 250.1;

To run the R codes, you need to install two libraries library(sqldf) and library(reshape). Then, upload the R codes "count_triad_dyad_monad.R". It should run after you modify the paths such as

C:/NICHD/Research/software/Fan/Joint_association_analysis/Count_Triad_Dyad_Monad/

The sas codes "count_triad_dyad_monad.sas" generate the same results as the R codes. Hence, you don't have to use the sas codes. To run the sas codes, double click on "sas.bat - Shortcut". Then, upload the sas codes "count_triad_dyad_monad.sas", and it should run.

5 References

 Fan RZ, Lee A, Liu AY, Troendle J, and Mills JL (2013) Association analysis of complex diseases using triads, parent-child dyads and singleton monads. *BMC Genetics* 14:78. DOI: 10.1186/10.1186/1471-2156-14-78. URL: http://www.biomedcentral.com/1471-2156/14/78.