Brief Description:
Description: Simultaneously estimate trait-locus position and its
genetic effect for affected relative pairs using two different
estimation assumptions. Either allow a different trait-locus effect
for each ARP type, or model as a single susceptibility locus. Includes
testing procedures for comparison of the two assumptions.

A further description can be found in DESCRIPTION file within the R
package.

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Installation procedures for arp.gee

We develop the arp.gee library for use in R on a
unix-like system. Intallation procedures in this file are for setting up
a
'local library' for a user. If a large group of users plan to use the
same library, then install on a system-wide 'library' location
designated by a system administrator.

For local installation, execute the following command with the local
"INSTALL LIBRARY DIR PATH" correctly specified.

R CMD INSTALL -l /INSTALL LIBRARY DIR PATH/ arp.gee_x.y.z.tar.gz

Installation instructions for different use may be found on the R project
website (http://www.r-project.org).

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User Documenation:

A user manual is provided in the arp.gee/doc/ directory. Information
on the supplied functions can be found within both the Splus and R
systems by typing help(function), where 'function' is the name of the
procedure of interest (no quotes needed). The code used in the user
manual is located within the arp.gee/demo/ directory. This code can be
used to test the various functions to check the computed output
against the manual. Follow additional instructions in the manual.