

Package ‘FTSEM’

March 5, 2025

Type Package

Title FT-SEM

Version 4.4.0

Author Shun Zhang, Ji-yuan Zhou

Maintainer Shun Zhang <3207042023@i.smu.edu.cn>, Ji-yuan Zhou <zhoujy@smu.edu.cn>

Description A robust and powerful GWAS method for family trios supporting within-family Mendelian randomization analysis

License GPL-2

Encoding UTF-8

LazyData true

RoxygenNote 7.3.1

Contents

FT_SEM_function	1
FT_SEM_process_data function	2
Index	3

FT_SEM_function	<i>The main function for family trios structural equation model (FT-SEM)</i>
-----------------	--

Description

A robust and powerful GWAS method for family trios

Arguments

data_sub A data.frame object for FT-SEM contains six columns: the father’s genotype, the mother’s genotype, the offspring’s genotype, the father’s phenotype, the mother’s phenotype, and the offspring’s phenotype. These columns are named f_snp, m_snp, o_snp, Exposure_f, Exposure_m, and Exposure_o, respectively.

FT_SEM_process_data function

The main function for family trios structural equation model (FT-SEM)

Description

A robust and powerful GWAS method for family trios

Arguments

data	A data.frame about genotype from plink1.9, containing FID,IID,PAT,MAT,SEX, phenotype and genotype (only 1 column)
seed	random seed for select offspring from a family with multiple offsprings

Index

FT_SEM_function, [1](#)
FT_SEM_process_data function, [2](#)