

Package ‘FTSEM’

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Type Package

Title FT-SEM

Version 4.4.0

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

License GPL-2

Encoding UTF-8

Imports dplyr (>= 1.1.4), OpenMx (>= 2.21.11)

LazyData true

RoxygenNote 7.3.1

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

A robust and powerful GWAS method for family trios

Usage

```
FT_SEM(data_sub = NULL, snp_name = NA)
```

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.

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

A robust and powerful GWAS method for family trios

Usage

```
process_family_data(data, seed = 123)
```

Arguments

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

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