

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

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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 structural equation model based on family trios (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.
snp_name	The names of the SNP loci used for analysis (generally the column names from the 7th to the last column of the data before being processed by the process_family_data method).

process_family_data	<i>The main function for the preliminary processing to obtain the required data frame for FT-SEM</i>
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Description

Filtering the data to obtain the required data frame for FT-SEM

Usage

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

Arguments

data	A data frame about genotype from PLINK 1.9, containing FID, IID, PAT, MAT, SEX, phenotype and genotype (only 1 column)
seed	Random seed for randomly selecting one offspring from a family with multiple offspring

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