

Package: ACEsimFit (via r-universe)

September 18, 2026

Title ACE Kin Pair Data Simulations and Model Fitting

Version 0.0.0.9

Description A few functions aim to provide a statistic tool for three purposes. First, simulate kin pairs data based on the assumption that every trait is affected by genetic effects (A), common environmental effects (C) and unique environmental effects (E). Second, use kin pairs data to fit an ACE model and get model fit output. Third, calculate power of A estimate given a specific condition. For the mechanisms of power calculation, we suggest to check Visscher(2004)<[doi:10.1375/twin.7.5.505](https://doi.org/10.1375/twin.7.5.505)>.

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Encoding UTF-8

RoxygenNote 7.1.2

Imports OpenMx (>= 2.19.6), stats (>= 3.5.0)

Suggests knitr, testthat (>= 3.0.0), rmarkdown

Config/testthat/edition 3

VignetteBuilder knitr

NeedsCompilation no

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Config/pak/sysreqs cmake make

Repository <https://xuanyu-lyu.r-universe.dev>

Date/Publication 2022-10-12 07:34:04 UTC

RemoteUrl <https://github.com/cran/ACEsimFit>

RemoteRef HEAD

RemoteSha 86f0f85eca348ac2b1cb9f7ecdc416ea767df357

Contents

fit_uniACE	2
kinsim_double	3
kinsim_single	4
Power_LS	5
Sim_Fit	6
Index	8

fit_uniACE	<i>fit_uniACE</i>
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Description

Use OpenMx to quickly fit a univariate ACE model

Usage

```
fit_uniACE(  
  data_1,  
  data_2,  
  GroupRel = c(1, 0.5),  
  GroupR_c = c(1, 1),  
  lbound = FALSE  
)
```

Arguments

data_1	A n by 2 data.frame consisting of the group1 kin pairs
data_2	A n by 2 data.frame consisting of the group2 kin pairs
GroupRel	A numeric vector specifying two genetic relatedness values of two groups of kin pairs
GroupR_c	A numeric vector specifying two common environment correlation coefficients of two groups of kin pairs
lbound	A logical value indicating if a lower boundary of .0001 will be imposed to the estimated A, C and E components

Value

Returns a list with the following:

df_nested	A data.frame displaying the nested comparison model between ACE, AE, CE, E models
fitACE	A list of all model fit information generated from OpenMx

kinsim_double

*kinsim_double***Description**

The function to generate two groups of univariate kin pair(e.g., both MZ and DZ twins) data using a multivariate norm approach, given the ACE components.

Two approaches can be selected: a) simulate two groups of kin pairs using the genetic relatedness directly b) simulate two groups of kin pairs by combining MZ twins and DZ twins to achieve the required genetic relatedness ($.5 < R < 1$).

Usage

```
kinsim_double(
  GroupNames = c("KinPair1", "KinPair2"),
  GroupSizes = c(100, 100),
  GroupRel = c(1, 0.5),
  GroupR_c = c(1, 1),
  mu = c(0, 0),
  ace1 = c(1, 1, 1),
  ace2 = c(1, 1, 1),
  ifComb = FALSE
)
```

Arguments

GroupNames	A character vector specifying two names of the simulated kin pairs
GroupSizes	A numeric vector specifying two group sizes indicating the amount of kin pairs in respective group.
GroupRel	A numeric vector specifying two genetic relatedness values of the simulated kin pairs
GroupR_c	A numeric vector specifying two common environment correlation coefficients of the simulated kin pairs
mu	A numeric vector specifying two mean values for the generated variable of the kin pairs
ace1	A numeric vector specifying three variance components under an ACE (additive genetics, common environment, unique environment) structure for group1
ace2	A numeric vector specifying three variance components under an ACE (additive genetics, common environment, unique environment) structure for group2
ifComb	A logical value specifying the approach to achieve the required genetic relatedness value. TRUE = using combination approach. FALSE = using direct approach. (See function description for a detailed explanation of two approaches.)

Value

Returns data.frame with the following:

GroupName	group name of the kin pairs
R	level of relatedness for the kin pair
r_c	level of common environment correlation of the kin pairs
id	id
A1	Additive genetic component for kin1 of the kin pairs
A2	Additive genetic component for kin2 of the kin pairs
C1	shared-environmental component for kin1 of the kin pairs
C2	shared-environmental component for kin2 of the kin pairs
E1	non-shared-environmental component for kin1 of the kin pairs
E2	non-shared-environmental component for kin2 of the kin pairs
y1	generated variable i for kin1
y2	generated variable i for kin2

kinsim_single

kinsim_single

Description

The function to generate one group of univariate kin pair (e.g., only DZ twins) data using a multi-variate norm approach, given the ACE components.

Usage

```
kinsim_single(
  name = "KinPair1",
  Rel = 1,
  r_c = 1,
  n = 100,
  mu = 0,
  ace = c(1, 1, 1)
)
```

Arguments

name	Assigned name for the simulated group of kin pairs
Rel	Genetic relatedness of the simulated kin pairs
r_c	Assumed common environment correlation
n	The number of generated kin pairs.(n PAIRS of data; The total number of participants is 2n)
mu	The mean for generated variable
ace	Vector of variance components under an ACE (additive genetics, common environment, unique environment) structure

Value

Returns data.frame with the following:

GroupName	group name of the kin pairs
R	level of genetic relatedness for the kin pairs
r_c	level of common environment correlation of the kin pairs
id	id
A1	Additive genetic component for kin1 of the kin pairs
A2	Additive genetic component for kin2 of the kin pairs
C1	shared-environmental component for kin1 of the kin pairs
C2	shared-environmental component for kin2 of the kin pairs
E1	non-shared-environmental component for kin1 of the kin pairs
E2	non-shared-environmental component for kin2 of the kin pairs
y1	generated variable i for kin1
y2	generated variable i for kin2

Power_LS

Power_LS

Description

The function is designed for calculating the power of heritability estimation from ACE models given the parameter settings. Or calculate one of the parameter settings (N,R,h2,c2) given the rest of known parameters. This power calculator is made based on the Least Squares theory and follows the mathematical derivation proposed by Visscher(2004).

Usage

```
Power_LS(N1, N2, power, p_N1 = NULL, h2, c2, R1 = 1, R2 = 0.5, alpha = 0.05)
```

Arguments

N1	The number of kin pairs for group1 (amount of PAIRS)
N2	The number of kin pairs for group2
power	The power of heritability estimation. Specified if you want to return the required sample sizes.
p_N1	The proportion of kin group1 over the . Required to be specified if the user wants to calculate the N1 and N2 simultaneously.
h2	The assumed standard heritability value of the target trait. $0 < h2 < 1$
c2	The assumed standard common environmental effects on the target trait. $0 < c2 < 2$
R1	The genetic relatedness of kin pair group1
R2	The genetic relatedness of kin pair group2
alpha	The type-one error rate for heritability estimation.

Value

A numeric vector of power when N1 and N2 are both specified.

A numeric vector of N1 (or N2) when N2 (or N1) is specified. A numeric vector of N1 and N2 when RatioN is specified.

Sim_Fit

Sim_Fit

Description

A function to simulate a set of kin pair data and fit them with ACE models. Can be helpful with checking model performance for a given parameter setting.

Usage

```
Sim_Fit(
  GroupNames = c("KinPair1", "KinPair2"),
  GroupSizes = c(100, 100),
  nIter = 100,
  SSeed = 62,
  GroupRel = c(1, 0.5),
  GroupR_c = c(1, 1),
  mu = c(0, 0),
  ace1 = c(1, 1, 1),
  ace2 = c(1, 1, 1),
  ifComb = FALSE,
  lbound = FALSE,
  saveRaw = FALSE
)
```

Arguments

GroupNames	A character vector specifying two names of the simulated kin pairs
GroupSizes	A numeric vector specifying two group sizes indicating the amount of kin pairs in respective group.
nIter	A numeric value specifying the number of iteration you want to run given the parameters assigned (i.e. the number of model fitting results you want to get)
SSeed	An integer specifying the starting seed of the random number. This parameter will make sure the simulated results are replicable across time
GroupRel	A numeric vector specifying two genetic relatedness values of the simulated kin pairs
GroupR_c	A numeric vector specifying two common environment correlation coefficients of the simulated kin pairs
mu	A numeric vector specifying two mean values for the generated variable of the kin pairs

ace1	A numeric vector specifying three variance components under an ACE (additive genetics, common environment, unique environment) structure for group1
ace2	A numeric vector specifying three variance components under an ACE (additive genetics, common environment, unique environment) structure for group2
ifComb	A logical value specifying the approach to achieve the required genetic relatedness value. TRUE = using combination approach. FALSE = using direct approach. (See function description for a detailed explanation of two approaches.)
lbound	A logical value indicating if a lower boundary of .0001 will be imposed to the estimated A, C and E components
saveRaw	A logical value specifying if the raw simulated data should be saved in the output list

Value

Returns a two-level list. Level-one is the number of iterations. Level-two is the model fitting results and raw data (if saveRaw = TRUE) of the simulated data from the respective iteration. Level-two includes:

Results	A list including 1) A data.frame displaying the nested comparison model between ACE, AE, CE, E models and 2) A list of all model fit information generated from OpenMx
Data	A data.frame consists of the simulated raw data

Index

`fit_uniACE`, [2](#)

`kinsim_double`, [3](#)

`kinsim_single`, [4](#)

`Power_LS`, [5](#)

`Sim_Fit`, [6](#)