

# Package ‘discord’

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**Type** Package

**Title** Functions for Discordant Kinship Modeling

**Version** 1.1.0

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**Description** Functions for discordant kinship modeling (and other sibling-based quasi-experimental designs). Currently, the package contains data restructuring functions and functions for generating biometrically informed data for kin pairs.

**URL** <https://github.com/R-Computing-Lab/discord>

**License** GPL-3

**LazyData** TRUE

**RoxygenNote** 7.1.1.9000

**Encoding** UTF-8

**Depends** R (>= 2.10)

**Imports** stats

**Suggests** testthat

**NeedsCompilation** no

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discord-package      *Functions for Discordant Kinship Modeling.*

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## Description

Utilities and functions for discordant kinship modeling (and other sibling-based quasi-experimental designs). Currently, the package contains data restructuring functions and functions for generating biometrically informed data for kin pairs.

## Note

The release version is available through [CRAN](#) by running `install.packages('discord')`. The most recent development version is available through [GitHub](#) by running `devtools::install_github(repo = 'R-Computing-Lab/discord')` (make sure [devtools](#) is already installed). If you're having trouble with the package, please install the development version. If this doesn't solve your problem, please create a [new issue](#), or email Mason.

## Author(s)

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## References

test

## Examples

```
library(discord) #Load the package into the current R session.

## Not run:
# Install/update discord with the release version from CRAN.
install.packages('discord')

# Install/update discord with the development version from GitHub
#install.packages('devtools') #Uncomment if `devtools` isn't installed already.
devtools::install_github('R-Computing-Lab/discord')

## End(Not run)
```

---

check\_discord\_errors    *Check for common errors in the discord regression function*

---

**Description**

Check for common errors in specifying id, sex, and race columns for discord regressions.

**Usage**

```
check_discord_errors(data, id, sex, race, pair_identifiers)
```

**Arguments**

data	The data to perform a discord regression on.
id	A unique kinship pair identifier.
sex	A character string for the sex column name.
race	A character string for the race column name.
pair_identifiers	A character vector of length two that contains the variable identifier for each kinship pair.

**Value**

An error message if one of the conditions are met.

---

check\_sibling\_order    *Check which sibling has more of the outcome*

---

**Description**

This function adds a column order by comparing which familial member has more of the outcome. This is done per pair (i.e. row).

**Usage**

```
check_sibling_order(data, outcome, pair_identifiers, row)
```

**Arguments**

data	The data set with kinship pairs.
outcome	A character string containing the outcome variable of interest.
pair_identifiers	A character vector of length two that contains the variable identifier for each kinship pair.
row	The row number of the data frame

**Value**

A character string signifying which familial member (1, 2, or neither) has more of the outcome.

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 discord\_data

*Restructure Data to Determine Kinship Differences*


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**Description**

Restructure Data to Determine Kinship Differences

**Usage**

```
discord_data(
  data,
  outcome,
  predictors,
  id = "extended_id",
  sex = "sex",
  race = "race",
  pair_identifiers,
  demographics = "both"
)
```

**Arguments**

data	A data frame.
outcome	A character string containing the outcome variable of interest.
predictors	A character vector containing the column names for predicting the outcome.
id	A unique kinship pair identifier.
sex	A character string for the sex column name.
race	A character string for the race column name.
pair_identifiers	A character vector of length two that contains the variable identifier for each kinship p
demographics	Indicator variable for if the data has the sex and race demographics. If both are present (default, and recommended), value should be "both". Other options include "sex", "race", or "none".

**Value**

A data frame that contains analyzable, paired data for performing kinship regressions.

## Examples

```
discord_data(data = sample_data,  
outcome = "height",  
predictors = "weight",  
pair_identifiers = c("_s1", "_s2"),  
sex = NULL,  
race = NULL,  
demographics = "none")
```

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discord_regression	<i>Perform a Linear Regression within the Discordant Kinship Framework</i>
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---

## Description

Perform a Linear Regression within the Discordant Kinship Framework

## Usage

```
discord_regression(  
  data,  
  outcome,  
  predictors,  
  id = "extended_id",  
  sex = "sex",  
  race = "race",  
  pair_identifiers = c("_s1", "_s2")  
)
```

## Arguments

data	A data frame.
outcome	A character string containing the outcome variable of interest.
predictors	A character vector containing the column names for predicting the outcome.
id	A unique kinship pair identifier.
sex	A character string for the sex column name.
race	A character string for the race column name.
pair_identifiers	A character vector of length two that contains the variable identifier for each kinship pair.

## Value

Resulting 'lm' object from performing the discordant regression.

**Examples**

```
discord_regression(data = sample_data,
  outcome = "height",
  predictors = "weight",
  pair_identifiers = c("_s1", "_s2"),
  sex = NULL,
  race = NULL)
```

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 kinsim

---

*Simulate Biometrically informed Multivariate Data*


---

**Description**

Generate paired multivariate data, given ACE parameters.

**Usage**

```
kinsim(
  r_all = c(1, 0.5),
  npg_all = 500,
  npergroup_all = rep(npg_all, length(r_all)),
  mu_all = 0,
  variables = 2,
  mu_list = rep(mu_all, variables),
  reliability_list = NULL,
  r_vector = NULL,
  ace_all = c(1, 1, 1),
  ace_list = matrix(rep(ace_all, variables), byrow = TRUE, nrow = variables),
  cov_a = 0,
  cov_c = 0,
  cov_e = 0,
  ...
)
```

**Arguments**

<code>r_all</code>	Levels of relatedness; default is MZ and DZ twins <code>c(1,.5)</code> .
<code>npg_all</code>	Sample size per group; default is 500.
<code>npergroup_all</code>	Vector of sample sizes by group; default repeats <code>npg_all</code> for all groups
<code>mu_all</code>	Mean for each generated variable; default is 0.
<code>variables</code>	Number of variables to generate; default is 2. Currently, limited to max of two variables.
<code>mu_list</code>	List of means by variable; default repeats <code>mu_all</code> for all variables

reliability_list	Vector of Reliabilities for each generated variable; default is to repeat reliability_all for each variable
r_vector	Alternative, give vector of r coefficients for entire sample.
ace_all	Vector of variance components for each generated variable; default is c(1,1,1).
ace_list	Matrix of ACE variance components by variable, where each row is its own variable; default is to repeat ace_all for each variable.
cov_a	Shared variance for additive genetics (a); default is 0.
cov_c	Shared variance for shared-environment (c); default is 0.
cov_e	shared variance for non-shared-environment (e); default is 0.
...	Optional pass on additional inputs.

**Value**

Returns data.frame with the following:

Ai_1	genetic component for variable i for kin1
Ai_2	genetic component for variable i for kin2
Ci_1	shared-environmental component for variable i for kin1
Ci_2	shared-environmental component for variable i for kin2
Ei_1	non-shared-environmental component for variable i for kin1
Ei_2	non-shared-environmental component for variable i for kin2
yi_1	generated variable i for kin1
yi_2	generated variable i for kin2
r	level of relatedness for the kin pair
id	id

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kinsim\_internal      *Simulate Biometrically informed Univariate Data*

---

**Description**

Generate paired univariate data, given ACE parameters.

**Usage**

```
kinsim_internal(
  r = c(1, 0.5),
  npg = 100,
  npergroup = rep(npg, length(r)),
  mu = 0,
  ace = c(1, 1, 1),
  r_vector = NULL,
  ...
)
```

**Arguments**

r	Levels of relatedness; default is MZ and DZ twins c(1,.5)
npg	Sample size per group; default is 100.
npergroup	List of sample sizes by group; default repeats npg for all groups.
mu	Mean for generated variable; default is 0.
ace	Vector of variance components, ordered by c(a, c, e); default is c(1,1,1).
r_vector	Alternative, give vector of relatedness coefficients for entire sample.
...	Optional pass on additional inputs.

**Value**

Returns data.frame with the following:

id	id
A1	genetic component for kin1
A2	genetic component for kin2
C1	shared-environmental component for kin1
C2	shared-environmental component for kin2
E1	non-shared-environmental component for kin1
E2	non-shared-environmental component for kin2
y1	generated variable for kin1 with mean of mu
y2	generated variable for kin2 with mean of mu
r	level of relatedness for the kin pair

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sample\_data

*Sample Data from NLSY*

---

**Description**

A data frame output from the NlsyLinks package that contains data for kinship pairs' height and weight.

**Usage**

```
sample_data
```

**Format**

A data frame.

Kinship pairs and their relatedness, height, and weight information.

**Source**

NLSY/R Lab



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