

Package ‘discord’

November 10, 2020

Type Package

Title Functions for Discordant Kinship Modeling

Version 1.0.0

Date 2020-11-09

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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 dplyr, purrr, magrittr, rlang, janitor, stats, broom,

Suggests NlsyLinks, testthat, knitr, rmarkdown

NeedsCompilation no

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Repository CRAN

Date/Publication 2020-11-10 22:50:02 UTC

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discord-package *Functions for Discordant Kinship Modeling.*

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.

 discord_data

Restructure Data to Determine Kinship Differences

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

Examples

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

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

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

A tidy dataframe containing the model metrics via the [tidy](#) function.

Examples

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

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 |

 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 |

sample_data

Sample Data from NLSY

Description

A data frame output from [CreatePairLinksSingleEntered](#) 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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