Package ‘IBDInfer’

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Type Package

Title Design-Based Causal Inference Method for Incomplete Block Designs

Version 0.1.0

Description This R package implements methods for estimation and inference under Incomplete Block Designs and Balanced Incomplete Block Designs within a design-based finite-population framework. Based on 'Koo and Pashley' (2026) <doi:10.1093/biomet/asag013>, it includes block-level estimators and extends to unit-level effects using 'Horvitz-Thompson' and 'Hájek' estimators. The package also provides asymptotic confidence intervals to support valid statistical inference.

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Encoding UTF-8

RoxygenNote 7.3.2

Imports crossdes, dplyr, tidyr

URL `https://github.com/taehyeonkoo/IBDInfer`

NeedsCompilation no

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`IBDgen` *Generating Incomplete Block Designs*

Description

Generate incomplete block designs.

Usage

```
IBDgen(K, n.trt, t, n.vec = NULL, L = NULL, l = NULL, W = NULL, balanced = T)
```

Arguments

`K`	The number of blocks.
`n.trt`	The number of whole treatments.
`t`	The number of treatments to be assigned to each block.
`n.vec`	The vector of block sizes.
`L`	The vector of the number of blocks having each treatment.
`l`	The matrix of the number of blocks having each pair of treatments.
`W`	The set of treatment subsets used in the design.
`balanced`	Whether the design is balanced or not. If `TRUE`, generate a balanced design.

Value

A list containing the following components:

`W`	The set of treatment subsets used in the design.
`W.uniq`	The unique set of treatment subsets used in the design with proportion in `W`.
`Rk`	The block assignment matrix.
`blk_assign`	The block assignment data frame.

References

Sailer, M. O., & Bornkamp, M. B. (2022). Package ‘crossdes’: Construction of Crossover Designs.

Examples

```
K <- 6
n.trt <- 3
t <- 2
n.vec <- rep(4, K)
IBDgen(K = K, n.trt = n.trt, t = t, n.vec = n.vec)
```

`IBDInfer` *Design-based Inference for Incomplete Block Designs*

Description

Conduct the design-based inference for incomplete block designs.

Usage

```
IBDInfer(y, b, z, g, w = c("Unit", "Block"), alpha = 0.05, data = NULL)
```

Arguments

`y`	Observed outcomes.
`b`	Block identifier (ID).
`z`	Assigned treatments.
`g`	A contrast vector, must sum to zero.
`w`	A weight vector, must sum to one and contain non-negative values.
`alpha`	Confidence level, default set to 0.05.
`data`	A data frame; if provided, y, b, and z should be column names in the data frame.

Value

`IBDInfer` returns an object of class "IBD", which is a list containing the following components: :

`tau.ht`	The Horvitz-Thompson estimator of tau.
`tau.haj`	The Hajek estimator of tau.
`var_tau_ht_bb`	Variance estimator for the Horvitz-Thompson estimator with between-block bias.
`var_tau_ht_wb`	Variance estimator for the Horvitz-Thompson estimator with within-block bias.
`var_tau_haj_bb`	Variance estimator for the Hajek estimator with between-block bias.
`var_tau_haj_wb`	Variance estimator for the Hajek estimator with within-block bias.
`CI_ht_bb`	Confidence interval with the Horvitz-Thompson estimator and variance estimator with between-block bias.
`CI_ht_wb`	Confidence interval with the Horvitz-Thompson estimator and variance estimator with within-block bias.
`CI_haj_bb`	Confidence interval with the Hajek estimator and variance estimator with between-block bias.
`CI_haj_wb`	Confidence interval with the Hajek estimator and variance estimator with within-block bias.
`yht`	The Horvitz-Thompson estimator for each treatment.
`yhaj`	The Hajek estimator for each treatment.

`Sht_bb`	Covariance estimator for the Horvitz-Thompson estimator for each treatment with between-block bias.
`Sht_wb`	Covariance estimator for the Horvitz-Thompson estimator for each treatment with within-block bias.
`Shaj_bb`	Covariance estimator for the Hajek estimator for each treatment with between-block bias.
`Shaj_wb`	Covariance estimator for the Hajek estimator for each treatment with within-block bias.
`alpha`	Confidence level

References

Koo, T., Pashley, N.E. (2024), Design-based Causal Inference for Incomplete Block Designs, *arXiv preprint arXiv:2405.19312*.

Examples

```
K <- 6
n.trt <- 3
t <- 2
n.vec <- rep(4, K)
df <- IBDgen(K = K, n.trt = n.trt, t = t, n.vec = n.vec)$blk_assign
df$y <- rnorm(nrow(df), 0, 1)
IBDInfer <- IBDInfer(y = y, b = blk_id, z = assign, g = c(1, -1, 0), w = "Block", data = df)
```

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