

# Package ‘causalBatch’

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**Type** Package

**Title** Causal Batch Effects

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**Description** Software which provides numerous functionalities for detecting and removing group-level effects from high-dimensional scientific data which, when combined with additional assumptions, allow for causal conclusions, as-described in our manuscripts Bridgeford et al. (2024) <[doi:10.1101/2021.09.03.458920](https://doi.org/10.1101/2021.09.03.458920)> and Bridgeford et al. (2023) <[doi:10.48550/arXiv.2307.13868](https://doi.org/10.48550/arXiv.2307.13868)>. Also provides a number of useful utilities for generating simulations and balancing covariates across multiple groups/batches of data via matching and propensity trimming for more than two groups.

**Depends** R (>= 4.2.0)

**Imports** cdcsis, sva, MatchIt, nnet, dplyr, magrittr, genefilter, BiocParallel, utils

**URL** [https://github.com/neurodata/causal\\_batch](https://github.com/neurodata/causal_batch)

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**VignetteBuilder** knitr

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**License** GPL-3

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cb.align.kway\_match    *K-Way matching*

---

### Description

A function for performing k-way matching using the `matchIt` package. Looks for samples which have corresponding matches across all other treatment levels.

### Usage

```
cb.align.kway_match(
  Ts,
  Xs,
  match.form,
  reference = NULL,
  match.args = list(method = "nearest", exact = NULL, replace = FALSE, caliper = 0.1),
  retain.ratio = 0.05
)
```

### Arguments

<code>Ts</code>	[n] the labels of the samples, with $K < n$ levels, as a factor variable.
<code>Xs</code>	[n, r] the r covariates/confounding variables, for each of the n samples, as a data frame with named columns.
<code>match.form</code>	A formula of columns from Xs, to be passed directly to <code>matchit</code> for subsequent matching. See <code>formula</code> argument from <code>matchit</code> for details.
<code>reference</code>	the name of the reference/control batch, against which to match. Defaults to NULL, which treats the reference batch as the smallest batch.
<code>match.args</code>	A named list arguments for the <code>matchit</code> function, to be used to specify specific matching strategies, where the list names are arguments and the corresponding values the value to be passed to <code>matchit</code> . Defaults to inexact nearest-neighbor caliper (width 0.1) matching without replacement.

`retain.ratio` If the number of samples retained is less than `retain.ratio*n`, throws a warning. Defaults to `0.05`.

### Value

a list, containing the following:

- `Retained.Ids` [m] vector consisting of the sample ids of the n original samples that were retained after matching.
- Reference the reference batch.

### Details

For more details see the help vignette: `vignette("causal_balancing", package = "causalBatch")`

### Author(s)

Eric W. Bridgeford

### References

Eric W. Bridgeford, et al. "A Causal Perspective for Batch Effects: When is no answer better than a wrong answer?" Biorxiv (2024).

Daniel E. Ho, et al. "MatchIt: Nonparametric Preprocessing for Parametric Causal Inference" JSS (2011).

### Examples

```
library(causalBatch)
sim <- cb.sims.sim_linear(a=-1, n=100, err=1/8, unbalancedness=1.5)
cb.align.kway_match(sim$Ts, data.frame(Covar=sim$Xs), "Covar")
```

---

`cb.align.vm_trim`      *Vector Matching*

---

### Description

A function for implementing the vector matching procedure, a pre-processing step for causal conditional distance correlation. Uses propensity scores to strategically include/exclude samples from subsequent inference, based on whether (or not) there are samples with similar propensity scores across all treatment levels (conceptually, a k-way "propensity trimming"). It is imperative that this function is used in conjunction with domain expertise to ensure that the covariates are not colliders, and that the system satisfies the strong ignorability condition to derive causal conclusions.

**Usage**

```
cb.align.vm_trim(
  Ts,
  Xs,
  prop.form = NULL,
  retain.ratio = 0.05,
  ddx = FALSE,
  reference = NULL
)
```

**Arguments**

Ts	[n] the labels of the samples, with $K < n$ levels, as a factor variable.
Xs	[n, r] the r covariates/confounding variables, for each of the n samples.
prop.form	a formula specifying a propensity scoring model. Defaults to NULL, which uses all of the covariates as exposure predictors.
retain.ratio	If the number of samples retained is less than <code>retain.ratio*n</code> , throws a warning. Defaults to 0.05.
ddx	whether to show additional diagnosis messages. Defaults to FALSE. Can help with debugging if unexpected results are obtained.
reference	the name of a reference label, against which to align other labels. Defaults to NULL, which identifies a shared region of covariate overlap across all labels..

**Value**

a [m] vector containing the indices of samples retained after vector matching.

**Details**

For more details see the help vignette: `vignette("causal_balancing", package = "causalBatch")`

**Author(s)**

Eric W. Bridgeford

**References**

Michael J. Lopez, et al. "Estimation of Causal Effects with Multiple Treatments" *Statistical Science* (2017). [ran](#)

**Examples**

```
library(causalBatch)
sim <- cb.sims.sim_linear(a=-1, n=100, err=1/8, unbalancedness=3)
cb.align.vm_trim(sim$Ts, sim$Xs)
```

---

`cb.correct.aipw_cComBat`*Augmented Inverse Probability Weighting Conditional ComBat*

---

## Description

A function for implementing the AIPW conditional ComBat (AIPW cComBat) algorithm. This algorithm allows users to remove batch effects (in each dimension), while adjusting for known confounding variables. It is imperative that this function is used in conjunction with domain expertise (e.g., to ensure that the covariates are not colliders, and that the system could be argued to satisfy the ignorability condition) to derive causal conclusions. See citation for more details as to the conditions under which conclusions derived are causal.

## Usage

```
cb.correct.aipw_cComBat(  
  Ys,  
  Ts,  
  Xs,  
  aipw.form,  
  covar.out.form = NULL,  
  retain.ratio = 0.05  
)
```

## Arguments

<code>Ys</code>	an $[n, d]$ matrix, for the outcome variables with $n$ samples in $d$ dimensions.
<code>Ts</code>	$[n]$ the labels of the samples, with at most two unique batches.
<code>Xs</code>	$[n, r]$ the $r$ covariates/confounding variables, for each of the $n$ samples, as a data frame with named columns.
<code>aipw.form</code>	A covariate model, given as a formula. Applies for the estimation of propensities for the AIPW step.
<code>covar.out.form</code>	A covariate model, given as a formula. Applies for the outcome regression step of the ComBat algorithm. Defaults to <code>NULL</code> , which re-uses <code>aipw.form</code> for the covariate/outcome model.
<code>retain.ratio</code>	If the number of samples retained is less than <code>retain.ratio*n</code> , throws a warning. Defaults to <code>0.05</code> .

## Details

Note: This function is experimental, and has not been tested on real data. It has only been tested with simulated data with binary (0 or 1) exposures.

**Value**

a list, containing the following:

- `Ys.corrected` an  $[m, d]$  matrix, for the  $m$  retained samples in  $d$  dimensions, after correction.
- `Ts`  $[m]$  the labels of the  $m$  retained samples, with  $K < n$  levels.
- `Xs` the  $r$  covariates/confounding variables for each of the  $m$  retained samples.
- `Model` the fit batch effect correction model.
- `Corrected.Ids` the ids to which batch effect correction was applied.

**Details**

For more details see the help vignette: `vignette("causal_ccombat", package = "causalBatch")`

**Author(s)**

Eric W. Bridgeford

**References**

Eric W. Bridgeford, et al. "A Causal Perspective for Batch Effects: When is no answer better than a wrong answer?" *Biorxiv* (2024).

W Evan Johnson, et al. "Adjusting batch effects in microarray expression data using empirical Bayes methods" *Biostatistics* (2007).

**Examples**

```
library(causalBatch)
sim <- cb.sims.sim_linear(a=-1, n=100, err=1/8, unbalancedness=2)
cb.correct.aipw_cComBat(sim$Ys, sim$Ts, data.frame(Covar=sim$Xs), "Covar")
```

---

`cb.correct.apply_aipw_cComBat`

*Fit AIPW ComBat model for batch effect correction*

---

**Description**

This function applies an Augmented Inverse Probability Weighting (AIPW) ComBat model for batch effect correction to new data.

**Usage**

```
cb.correct.apply_aipw_cComBat(Ys, Ts, Xs, Model)
```

**Arguments**

- Ys** an [n, d] matrix, for the outcome variables with n samples in d dimensions.
- Ts** [n] the labels of the samples, with  $K < n$  levels, as a factor variable.
- Xs** [n, r] the r covariates/confounding variables, for each of the n samples, as a data frame with named columns.
- Model** a list containing the following parameters:
- **Prop\_model** Fitted propensity model
  - **Putcome\_models** List of fitted outcome models for each feature and treatment level
  - **Levels** Levels of the treatment factor
  - **Treatment\_effects** Estimated treatment effects
  - **AIPW\_est** AIPW estimator results
  - **covar.out.form** Formula used for the outcome model
- This model is output after fitting with `cb.correct.aipw_cComBat`.

**Details**

Note: This function is experimental, and has not been tested on real data. It has only been tested with simulated data with binary (0 or 1) exposures.

**Value**

an [n, d] matrix, the batch-effect corrected data.

**Examples**

```
library(causalBatch)
sim <- cb.sims.sim_linear(a=-1, n=200, err=1/8, unbalancedness=3)
# fit batch effect correction for first 100 samples
cb.fit <- cb.correct.matching_cComBat(sim$Ys[1:100,,drop=FALSE], sim$Ts[1:100],
                                     data.frame(Covar=sim$Xs[1:100,,drop=FALSE]), "Covar")
# apply to all samples
cor.dat <- cb.correct.apply_cComBat(sim$Ys, sim$Ts, data.frame(Covar=sim$Xs), cb.fit$Model)
```

---

cb.correct.apply\_cComBat

*Adjust for batch effects using an empirical Bayes framework*

---

**Description**

ComBat allows users to adjust for batch effects in datasets where the batch covariate is known, using methodology described in Johnson et al. 2007. It uses either parametric or non-parametric empirical Bayes frameworks for adjusting data for batch effects. Users are returned an expression matrix that has been corrected for batch effects. The input data are assumed to be cleaned and normalized before batch effect removal.

**Usage**

```
cb.correct.apply_cComBat(Ys, Ts, Xs, Model)
```

**Arguments**

**Ys** an  $[n, d]$  matrix, for the outcome variables with  $n$  samples in  $d$  dimensions.

**Ts**  $[n]$  the labels of the samples, with  $K < n$  levels, as a factor variable.

**Xs**  $[n, r]$  the  $r$  covariates/confounding variables, for each of the  $n$  samples, as a data frame with named columns.

**Model** a list containing the following parameters:

- `Var` the pooled variance
- `Grand.mean` the overall mean of the data
- `B.hat` the fit regression coefficients
- `Gamma` additive batch effects
- `Delta` multiplicative batch effects
- `Levels` the order of levels for each batch
- `Covar.Mod` the covariate model for adjustment

This model is output after fitting with `cb.correct.matching_cComBat`.

**Details**

Note: this code is adapted directly from the `ComBat` algorithm featured in the ‘sva’ package.

**Value**

an  $[n, d]$  matrix, the batch-effect corrected data.

**Examples**

```
library(causalBatch)
sim <- cb.sims.sim_linear(a=-1, n=200, err=1/8, unbalancedness=3)
# fit batch effect correction for first 100 samples
cb.fit <- cb.correct.matching_cComBat(sim$Ys[1:100,], drop=FALSE, sim$Ts[1:100],
                                     data.frame(Covar=sim$Xs[1:100,], drop=FALSE), "Covar")
# apply to all samples
cor.dat <- cb.correct.apply_cComBat(sim$Ys, sim$Ts, data.frame(Covar=sim$Xs), cb.fit$Model)
```



---

 cb.correct.matching\_cComBat

*Matching Conditional ComBat*


---

## Description

A function for implementing the matching conditional ComBat (matching cComBat) algorithm. This algorithm allows users to remove batch effects (in each dimension), while adjusting for known confounding variables. It is imperative that this function is used in conjunction with domain expertise (e.g., to ensure that the covariates are not colliders, and that the system could be argued to satisfy the ignorability condition) to derive causal conclusions. See citation for more details as to the conditions under which conclusions derived are causal.

## Usage

```
cb.correct.matching_cComBat(
  Ys,
  Ts,
  Xs,
  match.form,
  covar.out.form = NULL,
  prop.form = NULL,
  reference = NULL,
  match.args = list(method = "nearest", exact = NULL, replace = FALSE, caliper = 0.1),
  retain.ratio = 0.05,
  apply.oos = FALSE
)
```

## Arguments

Ys	an [n, d] matrix, for the outcome variables with n samples in d dimensions.
Ts	[n] the labels of the samples, with $K < n$ levels, as a factor variable.
Xs	[n, r] the r covariates/confounding variables, for each of the n samples, as a data frame with named columns.
match.form	A formula of columns from Xs, to be passed directly to <a href="#">matchit</a> for subsequent matching. See formula argument from <a href="#">matchit</a> for details.
covar.out.form	A covariate model, given as a formula. Applies for the outcome regression step of the ComBat algorithm. Defaults to NULL, which re-uses match.form for the covariate/outcome model.
prop.form	A propensity model, given as a formula. Applies for the estimation of propensities for the propensity trimming step. Defaults to NULL, which re-uses match.form for the covariate/outcome model.
reference	the name of the reference/control batch, against which to match. Defaults to NULL, which treats the reference batch as the smallest batch.

match.args	A named list arguments for the <code>matchit</code> function, to be used to specify specific matching strategies, where the list names are arguments and the corresponding values the value to be passed to <code>matchit</code> . Defaults to inexact nearest-neighbor caliper (width 0.1) matching without replacement.
retain.ratio	If the number of samples retained is less than <code>retain.ratio*n</code> , throws a warning. Defaults to 0.05.
apply.oos	A boolean that indicates whether or not to apply the learned batch effect correction to non-matched samples that are still within a region of covariate support. Defaults to FALSE.

### Value

a list, containing the following:

- `Ys.corrected` an  $[m, d]$  matrix, for the  $m$  retained samples in  $d$  dimensions, after correction.
- `Ts`  $[m]$  the labels of the  $m$  retained samples, with  $K < n$  levels.
- `Xs` the  $r$  covariates/confounding variables for each of the  $m$  retained samples.
- `Model` the fit batch effect correction model. See `ComBat` for details.
- `InSample.Ids` the ids which were used to fit the batch effect correction model.
- `Corrected.Ids` the ids to which batch effect correction was applied. Differs from `InSample.Ids` if `apply.oos` is TRUE.

### Details

For more details see the help vignette: `vignette("causal_ccombat", package = "causalBatch")`

### Author(s)

Eric W. Bridgeford

### References

Eric W. Bridgeford, et al. "A Causal Perspective for Batch Effects: When is no answer better than a wrong answer?" *Biorxiv* (2024).

Daniel E. Ho, et al. "MatchIt: Nonparametric Preprocessing for Parametric Causal Inference" *JSS* (2011).

W Evan Johnson, et al. "Adjusting batch effects in microarray expression data using empirical Bayes methods" *Biostatistics* (2007).

Leek JT, Johnson WE, Parker HS, Fertig EJ, Jaffe AE, Zhang Y, Storey JD, Torres LC (2024). *sva: Surrogate Variable Analysis*. R package version 3.52.0.

### Examples

```
library(causalBatch)
sim <- cb.sims.sim_linear(a=-1, n=100, err=1/8, unbalancedness=2)
cb.correct.matching_cComBat(sim$Ys, sim$Ts, data.frame(Covar=sim$Xs), "Covar")
```

---

 cb.detect.caus\_cdcorr *Causal Conditional Distance Correlation*


---

**Description**

A function for implementing the causal conditional distance correlation (causal cDCorr) algorithm. This algorithm allows users to identify whether a treatment causes changes in an outcome, given assorted covariates/confounding variables. It is imperative that this function is used in conjunction with domain expertise (e.g., to ensure that the covariates are not colliders, and that the system satisfies the strong ignorability condition) to derive causal conclusions. See citation for more details as to the conditions under which conclusions derived are causal.

**Usage**

```
cb.detect.caus_cdcorr(
  Ys,
  Ts,
  Xs,
  prop.form = NULL,
  R = 1000,
  dist.method = "euclidean",
  distance = FALSE,
  seed = 1,
  num.threads = 1,
  retain.ratio = 0.05,
  ddx = FALSE
)
```

**Arguments**

Ys	Either: <ul style="list-style-type: none"> <li>• [n, d] matrix the outcome variables with n samples in d dimensions. In this case, distance should be FALSE.</li> <li>• [n, n] dist object a distance object for the n samples. In this case, distance should be TRUE.</li> </ul>
Ts	[n] the labels of the samples, with K < n levels, as a factor variable.
Xs	[n, r] the r covariates/confounding variables, for each of the n samples.
prop.form	a formula specifying a propensity scoring model. Defaults to NULL, which uses all of the covariates as exposure predictors.
R	the number of repetitions for permutation testing. Defaults to 1000.
dist.method	the method used for computing distance matrices. Defaults to "euclidean". Other options can be identified by seeing the appropriate documentation for the method argument for the <code>dist</code> function.
distance	a boolean for whether (or not) Ys are already distance matrices. Defaults to FALSE, which will use dist.method parameter to compute an [n, n] pairwise distance matrix for Ys.

<code>seed</code>	a random seed to set. Defaults to 1.
<code>num.threads</code>	The number of threads for parallel processing (if desired). Defaults to 1.
<code>retain.ratio</code>	If the number of samples retained is less than <code>retain.ratio*n</code> , throws a warning. Defaults to 0.05.
<code>ddx</code>	whether to show additional diagnosis messages. Defaults to FALSE. Can help with debugging if unexpected results are obtained.

### Value

a list, containing the following:

- `Test` The outcome of the statistical test, from [cdcov.test](#).
- `Retained.Ids` The sample indices retained after vertex matching, which correspond to the samples for which statistical inference is performed.

### Details

For more details see the help vignette: `vignette("causal_cdcorr", package = "causalBatch")`

### Author(s)

Eric W. Bridgeford

### References

Eric W. Bridgeford, et al. "A Causal Perspective for Batch Effects: When is no answer better than a wrong answer?" *Biorxiv* (2024).

Eric W. Bridgeford, et al. "Learning sources of variability from high-dimensional observational studies" *arXiv* (2023).

Xueqin Wang, et al. "Conditional Distance Correlation" *American Statistical Association* (2015).

### Examples

```
library(causalBatch)
sim <- cb.sims.sim_linear(a=-1, n=100, err=1/8, unbalancedness=3)
cb.detect.caus_cdcorr(sim$Ys, sim$Ts, sim$Xs)
```

---

cb.sims.sim\_impulse    *Impulse Simulation*

---

## Description

Impulse Simulation

## Usage

```
cb.sims.sim_impulse(  
  n = 100,  
  pi = 0.5,  
  eff_sz = 1,  
  alpha = 2,  
  unbalancedness = 1,  
  err = 1/2,  
  null = FALSE,  
  a = -0.5,  
  b = 1/2,  
  c = 4,  
  nbreaks = 200  
)
```

## Arguments

n	the number of samples. Defaults to 100.
pi	the balance between the classes, where samples will be from group 1 with probability pi, and group 2 with probability 1 - pi. Defaults to 0.5.
eff_sz	the treatment effect between the different groups. Defaults to 1.
alpha	the alpha for the covariate sampling procedure. Defaults to 2.
unbalancedness	the level of covariate dissimilarity between the covariates for each of the groups. Defaults to 1.
err	the level of noise for the simulation. Defaults to 1/2.
null	whether to generate a null simulation. Defaults to FALSE. Same behavior can be achieved by setting eff_sz = 0.
a	the first parameter for the covariate/outcome relationship. Defaults to -0.5.
b	the second parameter for the covariate/outcome relationship. Defaults to 1/2.
c	the third parameter for the covariate/outcome relationship. Defaults to 1.
nbreaks	the number of breakpoints for computing the expected outcome at a given covariate level for each batch. Defaults to 200.

**Value**

a list, containing the following:

Ys	an [n, 2] matrix, containing the outcomes for each sample. The first dimension contains the "treatment effect".
Ts	an [n, 1] matrix, containing the group/batch labels for each sample.
Xs	an [n, 1] matrix, containing the covariate values for each sample.
Eps	an [n, 1] matrix, containing the error for each sample.
x.bounds	the theoretical bounds for the covariate values.
Ytrue	an [nbreaks*2, 2] matrix, containing the expected outcomes at a covariate level indicated by Xtrue.
Ttrue	an [nbreaks*2, 1] matrix, indicating the group/batch the expected outcomes and covariate breakpoints correspond to.
Xtrue	an [nbreaks*2, 1] matrix, indicating the values of the covariate breakpoints for the theoretical expected outcome in Ytrue.
Effect	The batch effect magnitude.
Overlap	the theoretical degree of overlap between the covariate distributions for each of the two groups/batches.
oracle_fn	A function for fitting outcomes given covariates.

**Details**

A sigmoidal relationship between the covariate and the outcome. The first dimension of the outcome is:

$$Y_i = c \times \phi(X_i, \mu = a, \sigma = b) - \text{eff\_sz} \times T_i + \frac{1}{2}\epsilon_i$$

where  $\phi(x, \mu, \sigma)$  is the probability density function for the normal distribution with mean  $\mu$  and standard deviation  $\sigma$ .

where the batch/group labels are:

$$T_i \stackrel{iid}{\sim} \text{Bern}(\pi)$$

The beta coefficient for the covariate sampling is:

$$\beta = \alpha \times \text{unbalancedness}$$

The covariate values for the first batch are:

$$X_i|T_i = 0 \stackrel{iid}{\sim} 2\text{Beta}(\alpha, \beta) - 1$$

and the covariate values for the second batch are:

$$X_i|T_i = 1 \stackrel{iid}{\sim} 2\text{Beta}(\beta, \alpha) - 1$$

Note that  $X_i|T_i = 0 \stackrel{D}{=} -X_i|T_i = 1$ , or that the covariates are symmetric about the origin in distribution.

Finally, the error terms are:

$$\epsilon_i \stackrel{iid}{\sim} \text{Norm}(0, \text{err}^2)$$

For more details see the help vignette: `vignette("causal_simulations", package = "causalBatch")`

**Author(s)**

Eric W. Bridgeford

**References**

Eric W. Bridgeford, et al. "A Causal Perspective for Batch Effects: When is no answer better than a wrong answer?" Biorxiv (2024).

**Examples**

```
library(causalBatch)
sim = cb.sims.sim_impulse()
```

---

cb.sims.sim\_impulse\_asycov

*Impulse Simulation with Asymmetric Covariates*

---

**Description**

Impulse Simulation with Asymmetric Covariates

**Usage**

```
cb.sims.sim_impulse_asycov(
  n = 100,
  pi = 0.5,
  eff_sz = 1,
  alpha = 2,
  unbalancedness = 1,
  null = FALSE,
  a = -0.5,
  b = 1/2,
  c = 4,
  err = 1/2,
  nbreaks = 200
)
```

**Arguments**

n	the number of samples. Defaults to 100.
pi	the balance between the classes, where samples will be from group 1 with probability pi, and group 2 with probability 1 - pi. Defaults to 0.5.
eff_sz	the treatment effect between the different groups. Defaults to 1.
alpha	the alpha for the covariate sampling procedure. Defaults to 2.

unbalancedness	the level of covariate dissimilarity between the covariates for each of the groups. Defaults to 1.
null	whether to generate a null simulation. Defaults to FALSE. Same behavior can be achieved by setting <code>eff_sz = 0</code> .
a	the first parameter for the covariate/outcome relationship. Defaults to $-0.5$ .
b	the second parameter for the covariate/outcome relationship. Defaults to $1/2$ .
c	the third parameter for the covariate/outcome relationship. Defaults to 1.
err	the level of noise for the simulation. Defaults to $1/2$ .
nbreaks	the number of breakpoints for computing the expected outcome at a given covariate level for each batch. Defaults to 200.

### Value

a list, containing the following:

Ys	an $[n, 2]$ matrix, containing the outcomes for each sample. The first dimension contains the "treatment effect".
Ts	an $[n, 1]$ matrix, containing the group/batch labels for each sample.
Xs	an $[n, 1]$ matrix, containing the covariate values for each sample.
Eps	an $[n, 1]$ matrix, containing the error for each sample.
x.bounds	the theoretical bounds for the covariate values.
Ytrue	an $[nbreaks*2, 2]$ matrix, containing the expected outcomes at a covariate level indicated by Xtrue.
Ttrue	an $[nbreaks*2, 1]$ matrix, indicating the group/batch the expected outcomes and covariate breakpoints correspond to.
Xtrue	an $[nbreaks*2, 1]$ matrix, indicating the values of the covariate breakpoints for the theoretical expected outcome in Ytrue.
Effect	The batch effect magnitude.
Overlap	the theoretical degree of overlap between the covariate distributions for each of the two groups/batches.
oracle_fn	A function for fitting outcomes given covariates.

### Details

A sigmoidal relationship between the covariate and the outcome. The first dimension of the outcome is:

$$Y_i = c \times \phi(X_i, \mu = a, \sigma = b) - \text{eff\_sz} \times T_i + \frac{1}{2}\epsilon_i$$

where  $\phi(x, \mu, \sigma)$  is the probability density function for the normal distribution with mean  $\mu$  and standard deviation  $\sigma$ .

where the batch/group labels are:

$$T_i \stackrel{iid}{\sim} \text{Bern}(\pi)$$



The beta coefficient for the covariate sampling is:

$$\beta = \alpha \times \text{unbalancedness}$$

The covariate values for the first batch are asymmetric, in that for the first batch:

$$X_i|T_i = 0 \stackrel{iid}{\sim} 2Beta(\alpha, \alpha) - 1$$

and the covariate values for the second batch are:

$$X_i|T_i = 1 \stackrel{iid}{\sim} 2Beta(\beta, \alpha) - 1$$

Finally, the error terms are:

$$\epsilon_i \stackrel{iid}{\sim} Norm(0, \text{err}^2)$$

For more details see the help vignette: `vignette("causal_simulations", package = "causalBatch")`

### Author(s)

Eric W. Bridgeford

### References

Eric W. Bridgeford, et al. "A Causal Perspective for Batch Effects: When is no answer better than a wrong answer?" *Biorxiv* (2024).

### Examples

```
library(causalBatch)
sim = cb.sims.sim_impulse_asycov()
```

---

cb.sims.sim\_linear      *Linear Simulation*

---

### Description

Linear Simulation

### Usage

```
cb.sims.sim_linear(
  n = 100,
  pi = 0.5,
  eff_sz = 1,
  alpha = 2,
  unbalancedness = 1,
  err = 1/2,
  null = FALSE,
  a = -2,
  b = -1,
  nbreaks = 200
)
```

**Arguments**

n	the number of samples. Defaults to 100.
pi	the balance between the classes, where samples will be from group 1 with probability pi, and group 2 with probability 1 - pi. Defaults to 0.5.
eff_sz	the treatment effect between the different groups. Defaults to 1.
alpha	the alpha for the covariate sampling procedure. Defaults to 2.
unbalancedness	the level of covariate dissimilarity between the covariates for each of the groups. Defaults to 1.
err	the level of noise for the simulation. Defaults to 1/2.
null	whether to generate a null simulation. Defaults to FALSE. Same behavior can be achieved by setting eff_sz = 0.
a	the first parameter for the covariate/outcome relationship. Defaults to -2.
b	the second parameter for the covariate/outcome relationship. Defaults to -1.
nbreaks	the number of breakpoints for computing the expected outcome at a given covariate level for each batch. Defaults to 200.

**Value**

a list, containing the following:

Ys	an [n, 2] matrix, containing the outcomes for each sample. The first dimension contains the "treatment effect".
Ts	an [n, 1] matrix, containing the group/batch labels for each sample.
Xs	an [n, 1] matrix, containing the covariate values for each sample.
Eps	an [n, 1] matrix, containing the error for each sample.
x.bounds	the theoretical bounds for the covariate values.
Ytrue	an [nbreaks*2, 2] matrix, containing the expected outcomes at a covariate level indicated by Xtrue.
Ttrue	an [nbreaks*2, 1] matrix, indicating the group/batch the expected outcomes and covariate breakpoints correspond to.
Xtrue	an [nbreaks*2, 1] matrix, indicating the values of the covariate breakpoints for the theoretical expected outcome in Ytrue.
Effect	The batch effect magnitude.
Overlap	the theoretical degree of overlap between the covariate distributions for each of the two groups/batches.
oracle_fn	A function for fitting outcomes given covariates.

**Details**

A linear relationship between the covariate and the outcome. The first dimension of the outcome is:

$$Y_i = a \times (X_i + b) - \text{eff\_sz} \times T_i + \frac{1}{2} \epsilon_i$$

where the batch/group labels are:

$$T_i \stackrel{iid}{\sim} \text{Bern}(\pi)$$

The beta coefficient for the covariate sampling is:

$$\beta = \alpha \times \text{unbalancedness}$$

The covariate values for the first batch are:

$$X_i | T_i = 0 \stackrel{iid}{\sim} 2\text{Beta}(\alpha, \beta) - 1$$

and the covariate values for the second batch are:

$$X_i | T_i = 1 \stackrel{iid}{\sim} 2\text{Beta}(\beta, \alpha) - 1$$

Finally, the error terms are:

$$\epsilon_i \stackrel{iid}{\sim} \text{Norm}(0, \text{err}^2)$$

For more details see the help vignette: `vignette("causal_simulations", package = "causalBatch")`

### Author(s)

Eric W. Bridgeford

### References

Eric W. Bridgeford, et al. "A Causal Perspective for Batch Effects: When is no answer better than a wrong answer?" *Biorxiv* (2024).

### Examples

```
library(causalBatch)
sim = cb.sims.sim_linear()
```

---

cb.sims.sim\_sigmoid     *Sigmoidal Simulation*

---

### Description

Sigmoidal Simulation

**Usage**

```
cb.sims.sim_sigmoid(
  n = 100,
  pi = 0.5,
  eff_sz = 1,
  alpha = 2,
  unbalancedness = 1,
  null = FALSE,
  a = -4,
  b = 8,
  err = 1/2,
  nbreaks = 200
)
```

**Arguments**

n	the number of samples. Defaults to 100.
pi	the balance between the classes, where samples will be from group 1 with probability pi, and group 2 with probability 1 - pi. Defaults to 0.5.
eff_sz	the treatment effect between the different groups. Defaults to 1.
alpha	the alpha for the covariate sampling procedure. Defaults to 2.
unbalancedness	the level of covariate dissimilarity between the covariates for each of the groups. Defaults to 1.
null	whether to generate a null simulation. Defaults to FALSE. Same behavior can be achieved by setting eff_sz = 0.
a	the first parameter for the covariate/outcome relationship. Defaults to -4.
b	the second parameter for the covariate/outcome relationship. Defaults to 8.
err	the level of noise for the simulation. Defaults to 1/2.
nbreaks	the number of breakpoints for computing the expected outcome at a given covariate level for each batch. Defaults to 200.

**Value**

a list, containing the following:

Y	an [n, 2] matrix, containing the outcomes for each sample. The first dimension contains the "treatment effect".
Ts	an [n, 1] matrix, containing the group/batch labels for each sample.
Xs	an [n, 1] matrix, containing the covariate values for each sample.
Eps	an [n, 1] matrix, containing the error for each sample.
x.bounds	the theoretical bounds for the covariate values.
Ytrue	an [nbreaks*2, 2] matrix, containing the expected outcomes at a covariate level indicated by Xtrue.
Ttrue	an [nbreaks*2, 1] matrix, indicating the group/batch the expected outcomes and covariate breakpoints correspond to.

Xtrue	an [nbreaks*2, 1] matrix, indicating the values of the covariate breakpoints for the theoretical expected outcome in Ytrue.
Effect	The batch effect magnitude.
Overlap	the theoretical degree of overlap between the covariate distributions for each of the two groups/batches.
oracle_fn	A function for fitting outcomes given covariates.

### Details

A sigmoidal relationship between the covariate and the outcome. The first dimension of the outcome is:

$$Y_i = a \times \text{sigmoid}(b \times X_i) - a - \text{eff\_sz} \times T_i + \frac{1}{2} \epsilon_i$$

where the batch/group labels are:

$$T_i \stackrel{iid}{\sim} \text{Bern}(\pi)$$

The beta coefficient for the covariate sampling is:

$$\beta = \alpha \times \text{unbalancedness}$$

The covariate values for the first batch are:

$$X_i | T_i = 0 \stackrel{iid}{\sim} 2\text{Beta}(\alpha, \beta) - 1$$

and the covariate values for the second batch are:

$$X_i | T_i = 1 \stackrel{iid}{\sim} 2\text{Beta}(\beta, \alpha) - 1$$

Finally, the error terms are:

$$\epsilon_i \stackrel{iid}{\sim} \text{Norm}(0, \text{err}^2)$$

For more details see the help vignette: `vignette("causal_simulations", package = "causalBatch")`

### Author(s)

Eric W. Bridgeford

### References

Eric W. Bridgeford, et al. "A Causal Perspective for Batch Effects: When is no answer better than a wrong answer?" *Biorxiv* (2024).

### Examples

```
library(causalBatch)
sim = cb.sims.sim_sigmoid()
```

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