Package ‘quickblock’

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Author Fredrik Savje [aut, cre],
Jasjeet Sekhon [aut],
Michael Higgins [aut]
Maintainer Fredrik Savje <fredrik.savje@yale.edu>
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**quickblock-package**

**quickblock: Quick Threshold Blocking**

**Description**

Provides functions for assigning treatments in randomized experiments using near-optimal threshold blocking. The package is made with large data sets in mind and derives blocks more than an order of magnitude quicker than other methods.

**Details**

See `quickblock` for the main blocking function.

See the package’s website for more information: https://github.com/fsavje/quickblock.

Bug reports and suggestions are greatly appreciated. They are best reported here: https://github.com/fsavje/quickblock/issues.

**References**


**assign_treatment**

*Random treatment assignment with blocks*

**Description**

`assign_treatment` randomly assigns treatments to the units in the sample so to best maintain the equal proportions of conditions within each block. The function expects the user to provide a blocking object and treatment conditions.

**Usage**

`assign_treatment(blocking, treatments = c("Treated", "Control"))`

**Arguments**

- `blocking` : `qb_blocking` or `scclust` object with the blocked units.
- `treatments` : character vector with treatment conditions.
Details

When the number of treatment conditions evenly divides the size of a block, the conditions will be repeated that many times within the block. For example, with three conditions, c("T1", "T2", "C"), and a block with six units, two units will be assigned to each condition.

When the number of treatment conditions does not evenly divide the block size, the conditions are repeated up to the closest multiple lower than the block size and the remaining conditions are chosen at random. For example, with the three conditions from above and a block with four units, each condition will be repeated once (since floor(4/3) == 1). One additional condition is needed to assign all units in the block, and that condition is selected at random from c("T1", "T2", "C") with equal probability. In a block with 8 units, each condition will be repeated twice (floor(8/3) == 2). Two additional conditions are now needed, and they are chosen from c("T1", "T2", "C") without replacement.

In all cases, the treatment conditions within a block are shuffled so that all units have the same probability of being assigned to each condition. Units not assigned to blocks will not be assigned treatments (indicated by NA).

Value

Returns a factor with the assigned treatments.

Examples

# Example blocking

# Two treatment conditions
assign_treatment(my_blocking)

# Three treatment conditions
assign_treatment(my_blocking, c("T1", "T2", "C"))

# Four treatment conditions
# (This throws warning because some blocks contain less than four units)
## Not run: assign_treatment(my_blocking, c("T1", "T2", "T3", "C"))
Usage

blocking_estimator(outcomes, blocking, treatments)

Arguments

outcomes numeric vector with observed outcomes.
blocking qb_blocking or scclust object with the block assignments.
treatments factor specifying the units’ treatment assignments.

Details

To produce point estimates, blocking_estimator requires that each block contains at least one unit assigned to each treatment condition. For variance estimation, it requires that each block contains at least two units assigned to each condition. When treatments have been assigned with the assign_treatment function (or an equivalent procedure), the variance estimators are conservative in expectation (see the referenced note below for details). If treatment is assigned with another method, the estimator might not be valid.

The function estimates treatment effects by aggregating block-level effect estimates. It estimates effects within each block by taking the difference in mean outcomes in the block. The sample-level estimate is then derived as the weighted average of the block-level effects using the size of the blocks as weights. In detail, let \( n_b \) be the number of units assigned to block \( b \), and \( n \) be the total number of units in the sample. Let \( Y(t, b) \) be the average outcome for units assigned to treatment \( t \) in block \( b \). The effect of treatment \( t \) versus treatment \( s \) is then estimated as:

\[
\sum \frac{n_b}{n} [Y(t, b) - Y(s, b)],
\]

where the sum is taken over the blocks in the experiment. See the referenced note for more details.

Value

A list with two numeric matrices with estimated treatment effects and their estimated variances is returned. The first matrix (effects) contains estimated treatment effects. Rows in this matrix indicate minuends in the treatment effect contrast and columns indicate subtrahends. For example, in the matrix:

<table>
<thead>
<tr>
<th></th>
<th>a</th>
<th>b</th>
<th>c</th>
</tr>
</thead>
<tbody>
<tr>
<td>a</td>
<td>0.0</td>
<td>4.5</td>
<td>5.5</td>
</tr>
<tr>
<td>b</td>
<td>-4.5</td>
<td>0.0</td>
<td>1.0</td>
</tr>
<tr>
<td>c</td>
<td>-5.5</td>
<td>-1.0</td>
<td>0.0</td>
</tr>
</tbody>
</table>

the estimated treatment effect between conditions \( a \) and \( b \) is 4.5, and the estimated treatment effect between conditions \( c \) and \( b \) is \(-1.0\).

The second matrix (effect_variances) contains estimates of variances of the corresponding effect estimators.
References

Examples

# Example blocking
my_blocking <- qb_blocking(c("A", "A", "B", "C", "B",

# Two treatment conditions
my_treatments <- assign_treatment(my_blocking)
my_outcomes <- rnorm(20)
blocking_estimator(my_outcomes, my_blocking, my_treatments)

# Three treatment conditions
my_treatments <- assign_treatment(my_blocking, c("T1", "T2", "C"))
my_outcomes <- rnorm(20)
blocking_estimator(my_outcomes, my_blocking, my_treatments)

# Four treatment conditions
# (This will throw an error because variances cannot be estimated)
my_treatments <- assign_treatment(my_blocking, c("T1", "T2", "T3", "C"))
my_outcomes <- rnorm(20)
## Not run: blocking_estimator(my_outcomes, my_blocking, my_treatments)

is.qb_blocking

Check qb_blocking object

Description
is.qb_blocking checks whether the provided object is a valid instance of the qb_blocking class.

Usage
is.qb_blocking(x)

Arguments
x object to check.

Details
is.qb_blocking does not check whether the blocking itself is sensible or whether it satisfies some set of constraints. See check_clustering for that functionality.
Value

Returns TRUE if x is a valid `qb_blocking` object, otherwise FALSE.

qb_blocking Constructor for qb_blocking objects

Description

The `qb_blocking` function constructs a `qb_blocking` object from existing block labels. The function does not derive blockings from sets of data points; see `quickblock` for that functionality.

Usage

`qb_blocking(block_labels, unassigned_labels = NULL, ids = NULL)`

Arguments

- `block_labels`: a vector containing each unit’s block label.
- `unassigned_labels`: labels that denote unassigned units. If NULL, NA values in `block_labels` are used to denote unassigned units.
- `ids`: IDs of the units. Should be a vector of the same length as `block_labels` or NULL. If NULL, the IDs are set to 1:length(group_labels).

Details

`qb_blocking` objects are based on integer vectors, and it indexes the blocks starting with zero. The `qb_blocking` class inherits from the `scclust` class.

Value

Returns a `qb_blocking` object with the blocking described by the provided labels.

Examples

```r
# 10 units in 3 blocks
blocking1 <- qb_blocking(c("A", "A", "B", "C", "B",
                         "C", "C", "A", "B", "B"))

# 8 units in 3 blocks, 2 units unassigned
blocking2 <- qb_blocking(c(1, 1, 2, 3, 2,
                          NA, 3, 1, NA, 2))

# Custom labels indicating unassigned units
blocking3 <- qb_blocking(c("A", "A", "B", "C", "NONE",
                          "C", "C", "NONE", "B", "B"),
                          unassigned_labels = "NONE")
```
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# Two different labels indicating unassigned units  
blocking4 <- qb_blocking(c("A", "A", "B", "C", "NONE",  
                        "C", "C", "0", "B", "B"),  
                        unassigned_labels = c("NONE", "0"))  

# Custom unit IDs  
blocking5 <- qb_blocking(c("A", "A", "B", "C", "B",  
                          "C", "C", "A", "B", "B"),  
                          ids = letters[1:10])

quickblock  

Construct threshold blockings

Description

quickblock constructs near-optimal threshold blockings. The function expects the user to provide distances measuring the similarity of units and a required minimum block size. It then constructs a blocking so that units assigned to the same block are as similar as possible while satisfying the minimum block size.

Usage

quickblock(distances, size_constraint = 2L, caliper = NULL,  
break_large_blocks = FALSE, ...)

Arguments

distances  

Object or a numeric vector, matrix or data frame. The parameter describes the similarity of the units to be blocked. It can either be preprocessed distance information using a distances object, or raw covariate data. When called with covariate data, Euclidean distances are calculated unless otherwise specified.

size_constraint  

Integer with the required minimum number of units in each block.

caliper  

Restrict the maximum within-block distance.

break_large_blocks  

Logical indicating whether large blocks should be broken up into smaller blocks.

...  

Additional parameters to be sent either to the distances function when the distances parameter contains covariate data, or to the underlying sc_clustering function.
Details

The caliper parameter constrains the maximum distance between units assigned to the same block. This is implemented by restricting the edge weight in the graph used to construct the blocks (see \texttt{sc\_clustering} for details). As a result, the caliper will affect all blocks and, in general, make it harder for the function to find good matches even for blocks where the caliper is not binding. In particular, a too tight caliper can lead to discarded units that otherwise would be assigned to a block satisfying both the matching constraints and the caliper. For this reason, it is recommended to set the caliper value quite high and only use it to avoid particularly poor blocks. It strongly recommended to use the caliper parameter only when primary\_unassigned\_method = "closest\_seed" in the underlying \texttt{sc\_clustering} function (which is the default behavior).

The main algorithm used to construct the blocking may produce some blocks that are much larger than the minimum size constraint. If break\_large\_blocks is TRUE, all blocks twice as large as size\_constraint will be broken into two or more smaller blocks. Block are broken so to ensure that the new blocks satisfy the size constraint. In general, large blocks are produced when units are highly clustered, so breaking up large blocks will often only lead to small improvements. The blocks are broken using the \texttt{hierarchical\_clustering} function.

quickblock calls \texttt{sc\_clustering} with seed\_method = "inwards\_updating". The seed\_method parameter governs how the seeds are selected in the nearest neighborhood graph that is used to construct the blocks (see \texttt{sc\_clustering} for details). The "inwards\_updating" option generally works well and is safe with most datasets. Using seed\_method = "exclusion\_updating" often leads to better performance (in the sense of blocks with more similar units), but it may increase run time. Discrete data (or more generally when units tend to be at equal distance to many other units) will lead to particularly poor run time with this option. If the dataset has at least one continuous co-variate, "exclusion\_updating" is typically quick. A third option is seed\_method = "lexical", which decreases the run time relative to "inwards\_updating" (sometimes considerably) at the cost of performance. quickblock passes parameters on to \texttt{sc\_clustering}, so to change seed\_method, call quickblock with the parameter specified as usual: quickblock(..., seed\_method = "exclusion\_updating").

Value

Returns a \texttt{qb\_blocking} object with the constructed blocks.

References


See Also

See \texttt{sc\_clustering} for the underlying function used to construct the blocks.

Examples

```r
# Construct example data
my_data <- data.frame(x1 = runif(100),
                      x2 = runif(100))

# Make distances
my_distances <- distances(my_data, dist_variables = c("x1", "x2"))

# Make blocking with at least two units in each block
quickblock(my_distances)

# Require at least three units in each block
quickblock(my_distances, size_constraint = 3)

# Impose caliper
quickblock(my_distances, caliper = 0.2)

# Break large block
quickblock(my_distances, break_large_blocks = TRUE)

# Call `quickblock` directly with covariate data (ie., not pre-calculating distances)
quickblock(my_data[c("x1", "x2")])

# Call `quickblock` directly with covariate data using Mahalanobis distances
quickblock(my_data[c("x1", "x2")], normalize = "mahalanobis")
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