

Package ‘randomizr’

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Title Easy to Use Tools for Common Forms of Random Assignment

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Description Generates random assignments for common experimental designs: simple, complete, blocked, and clustered.

Depends R (>= 2.10.0)

License GPL-3

LazyData true

Suggests knitr, dplyr, blockTools, testthat

VignetteBuilder knitr

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Author Alexander Coppock [aut, cre]

Maintainer Alexander Coppock <ac3242@columbia.edu>

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block_and_cluster_ra *Blocked and Clustered Random Assignment.*

Description

If clusters are nested within blocks, blocked and clustered random assignment is possible. For example, imagine that villages are nested within regions.

Usage

```
block_and_cluster_ra(clust_var, block_var, num_arms = NULL, block_m = NULL,
  prob_each = NULL, condition_names = NULL)
```

Arguments

clust_var	A vector of length N that indicates which cluster each unit belongs to.
block_var	A vector of length N that indicates which block each unit belongs to.
num_arms	The total number of treatment arms. If unspecified, will be determined from the number of columns of block_m, the length of prob_each, or the length of condition_names.
block_m	A matrix of arm sizes with blocks in the rows and treatment conditions in the columns. The rows should respect the alphabetical ordering of the blocks as determined by sort(unique(block_var)). The columns should be in the order of condition_names, if specified.
prob_each	A vector whose length is equal to the number of treatment assignments. When specified, prob_each assigns the same (within rounding) proportion of each block to each treatment condition, using complete random assignment. prob_each must sum to 1.
condition_names	A character vector giving the names of the treatment conditions. If unspecified, the treatment conditions. will be named T1, T2, T3, etc.

Value

A random assignment

Examples

```
clust_var <- rep(letters, times=1:26)
block_var <- rep(NA, length(clust_var))
block_var[clust_var %in% letters[1:5]] <- "block_1"
block_var[clust_var %in% letters[6:10]] <- "block_2"
block_var[clust_var %in% letters[11:15]] <- "block_3"
block_var[clust_var %in% letters[16:20]] <- "block_4"
block_var[clust_var %in% letters[21:26]] <- "block_5"

table(block_var, clust_var)

Z <- block_and_cluster_ra(clust_var = clust_var, block_var = block_var)

table(Z, clust_var)
```

```

table(Z, block_var)

Z <- block_and_cluster_ra(clust_var = clust_var, block_var = block_var, num_arms = 3)

table(Z, clust_var)
table(Z, block_var)

Z <- block_and_cluster_ra(clust_var = clust_var, block_var = block_var, prob_each = c(.2, .5, .3))

block_m <- rbind(c(2, 3),
                 c(1, 4),
                 c(3, 2),
                 c(2, 3),
                 c(5, 1))

Z <- block_and_cluster_ra(clust_var = clust_var, block_var = block_var, block_m = block_m)

table(Z, clust_var)
table(Z, block_var)

```

block_and_cluster_ra_probabilities

Probabilities of assignment: Blocked and Clustered Random Assignment

Description

Probabilities of assignment: Blocked and Clustered Random Assignment

Usage

```

block_and_cluster_ra_probabilities(clust_var, block_var, num_arms = NULL,
                                   block_m = NULL, prob_each = NULL, condition_names = NULL)

```

Arguments

clust_var	A vector of length N that indicates which cluster each unit belongs to.
block_var	A vector of length N that indicates which block each unit belongs to.
num_arms	The total number of treatment arms. If unspecified, will be determined from the number of columns of block_m or the length of condition_names.
block_m	A matrix of arm sizes whose number of rows is equal to the number of blocks and whose number of columns is equal to the number of treatment arms. The rows should respect the alphabetical ordering of the blocks as determined by sort(unique(block_var)). The columns should be in the order of condition_names, if specified.
prob_each	A vector whose length is equal to the number of treatment assignments. When specified, prob_each assigns the same (within rounding) proportion of each block to each treatment condition, using complete random assignment. prob_each must sum to 1.
condition_names	A character vector giving the names of the treatment conditions. If unspecified, the treatment conditions. will be named T1, T2, T3, etc.

Value

A matrix of probabilities of assignment.

block_ra	<i>Block Random Assignment</i>
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Description

This function assigns a fixed number of units within each block to treatment.

Usage

```
block_ra(block_var, num_arms = NULL, block_m = NULL, prob_each = NULL,
         condition_names = NULL)
```

Arguments

block_var	A vector of length N indicating which block each unit belongs to.
num_arms	The total number of treatment arms. If unspecified, will be determined from the number of columns of block_m, the length of prob_each, or the length of condition_names.
block_m	A matrix of arm sizes with blocks in the rows and treatment conditions in the columns. The rows should respect the alphabetical ordering of the blocks as determined by sort(unique(block_var)). The columns should be in the order of condition_names, if specified.
prob_each	A numeric vector whose length is equal to the number of treatment conditions. When specified, prob_each assigns the same (within rounding) proportion of each block to each treatment condition, using complete random assignment. prob_each must sum to 1.
condition_names	A character vector giving the names of the treatment conditions. If unspecified, the treatment conditions. will be named T1, T2, T3, etc.

Examples

```
block_var <- rep(c("A", "B", "C"), times=c(50, 100, 200))
Z <- block_ra(block_var=block_var)
table(block_var, Z)

block_m <- rbind(c(25, 25),
                 c(50, 50),
                 c(100, 100))

Z <- block_ra(block_var=block_var, block_m=block_m)
table(block_var, Z)

block_m <- rbind(c(10, 40),
                 c(30, 70),
                 c(50, 150))

Z <- block_ra(block_var=block_var, block_m=block_m,
```

```

      condition_names=c("control", "treatment"))
table(block_var, Z)

# Multi-arm Designs
Z <- block_ra(block_var=block_var, num_arms=3)
table(block_var, Z)

block_m <- rbind(c(10, 20, 20),
                 c(30, 50, 20),
                 c(50, 75, 75))
Z <- block_ra(block_var=block_var, block_m=block_m )
table(block_var, Z)

Z <- block_ra(block_var=block_var, block_m=block_m,
              condition_names=c("control", "placebo", "treatment"))
table(block_var, Z)

Z <- block_ra(block_var=block_var, prob_each=c(.1, .1, .8))
table(block_var, Z)

```

block_ra_probabilities

Probabilities of assignment: Block Random Assignment

Description

Probabilities of assignment: Block Random Assignment

Usage

```

block_ra_probabilities(block_var, num_arms = NULL, block_m = NULL,
  prob_each = NULL, condition_names = NULL)

```

Arguments

block_var	A vector of length N indicating which block each unit belongs to.
num_arms	The total number of treatment arms. If unspecified, will be determined from the number of columns of block_m or the length of condition_names.
block_m	A matrix of arm sizes whose number of rows is equal to the number of blocks and whose number of columns is equal to the number of treatment arms. The rows should respect the alphabetical ordering of the blocks as determined by sort(unique(block_var)). The columns should be in the order of condition_names, if specified.
prob_each	A vector whose length is equal to the number of treatment conditions. When specified, prob_each assigns the same (within rounding) proportion of each block to each treatment condition, using complete random assignment. prob_each must sum to 1.
condition_names	A character vector giving the names of the treatment conditions. If unspecified, the treatment conditions. will be named T1, T2, T3, etc.

Value

A matrix of probabilities of assignment.

cluster_ra

Cluster Random Assignment

Description

This function conducts complete random assignment by cluster. Clusters are collections of units that are assigned to a treatment together.

Usage

```
cluster_ra(clust_var, m = NULL, num_arms = NULL, m_each = NULL,
  prob_each = NULL, condition_names = NULL)
```

Arguments

clust_var	A vector of length N that indicates which cluster each unit belongs to.
m	The total number clusters to be treated. Should only be specified for a two group design in which exactly m of N clusters is assigned to treatment. If not specified, half of the clusters will be assigned to treatment. Is NULL by default.
num_arms	The total number of treatment arms. If unspecified, will be determined from the length of m_each or condition_names.
m_each	A numeric vector giving the number of clusters to be assigned to each treatment group. Must sum to the total number of clusters. If unspecified, equally sized (rounded) groups will be assumed.
prob_each	A numeric vector giving the probability of assignment to each treatment arm. Must sum to 1. Please note that due to rounding, these probabilities are approximate. For finer control, please use m_each.
condition_names	A character vector giving the names of the treatment groups. If unspecified, the treatment groups will be names T1, T2, T3, etc.

Examples

```
# Two Group Designs
clust_var <- rep(letters, times=1:26)

Z <- cluster_ra(clust_var=clust_var)
table(Z, clust_var)

Z <- cluster_ra(clust_var=clust_var, m=13)
table(Z, clust_var)

Z <- cluster_ra(clust_var=clust_var, m_each = c(10, 16),
  condition_names = c("control", "treatment"))
table(Z, clust_var)

# Multi-arm Designs
Z <- cluster_ra(clust_var=clust_var, num_arms=3)
```

```

table(Z, clust_var)

Z <- cluster_ra(clust_var=clust_var, m_each=c(7, 7, 12))
table(Z, clust_var)

Z <- cluster_ra(clust_var=clust_var, m_each=c(7, 7, 12),
               condition_names=c("control", "placebo", "treatment"))
table(Z, clust_var)

Z <- cluster_ra(clust_var=clust_var,
               condition_names=c("control", "placebo", "treatment"))
table(Z, clust_var)

```

cluster_ra_probabilities

Probabilities of assignment: Cluster Random Assignment

Description

Probabilities of assignment: Cluster Random Assignment

Usage

```
cluster_ra_probabilities(clust_var, m = NULL, num_arms = NULL,
                        m_each = NULL, prob_each = NULL, condition_names = NULL)
```

Arguments

clust_var	A vector of length N that indicates which cluster each unit belongs to.
m	The total number clusters to be treated. Should only be specified for a two group design in which exactly m of N clusters is assigned to treatment. If not specified, half of the clusters will be assigned to treatment. Is NULL by default.
num_arms	The total number of treatment arms. If unspecified, will be determined from the length of m_each or condition_names.
m_each	A numeric vector giving the number of clusters to be assigned to each treatment group. Must sum to the total number of clusters. If unspecified, equally sized (rounded) groups will be assumed.
prob_each	A numeric vector giving the probability of assignment to each treatment arm. Must sum to 1. Please note that due to rounding, these probabilities are approximate. For finer control, please use m_each.
condition_names	A character vector giving the names of the treatment groups. If unspecified, the treatment groups will be names T1, T2, T3, etc.

Value

A matrix of probabilities of assignment.

complete_ra

*Complete Random Assignment***Description**

This function conducts complete random assignment, a procedure in which a pre-specified number of units is assigned to each treatment condition. This function can accomodate any number of treatment arms.

Usage

```
complete_ra(N, m = NULL, prob = NULL, num_arms = NULL, m_each = NULL,
  prob_each = NULL, condition_names = NULL)
```

Arguments

N	the total number of units in the experimental sample (required).
m	If specified, a two-group design is assumed. m is the total number of units to be assigned to treatment. Should only be specified for a two group design in which exactly m of N units are assigned to treatment. If not specified (and no other arguments are specified), half of the sample (N/2) will be assigned to treatment (if N is odd, m will be set to either floor(N/2) or ceiling(N/2) with equal probability. m is NULL by default.
prob	If specified, a two-group design is assumed. prob is the probability of assignment to treatment. Within rounding, N*prob subjects will be assigned to treatment.
num_arms	The total number of treatment arms. If unspecified, num_arms will be determined from the length of m_each or condition_names.
m_each	A numeric vector giving the size of each treatment group. Must sum to N. If unspecified, equally sized (rounded) groups will be assumed.
prob_each	A numeric giving the probability of assignment to each treatment arm. Must sum to 1. Please note that due to rounding, these probabilities are approximate. For finer control, please use m_each.
condition_names	A character vector giving the names of the treatment groups. If unspecified, the treatment groups will be names T1, T2, T3, etc. An exception is a two-group design in which N only or N and m are specified, in which the condition names are 0 and 1.

Value

A vector of length N that indicates the treatment condition of each unit.

Examples

```
# Two Group Designs

Z <- complete_ra(N=100)
table(Z)
```



```

Z <- complete_ra(N=100, m=50)
table(Z)

Z <- complete_ra(N=100, m_each = c(30, 70),
                  condition_names = c("control", "treatment"))
table(Z)

# Multi-arm Designs
Z <- complete_ra(N=100, num_arms=3)
table(Z)

Z <- complete_ra(N=100, m_each=c(30, 30, 40))
table(Z)

Z <- complete_ra(N=100, m_each=c(30, 30, 40),
                  condition_names=c("control", "placebo", "treatment"))
table(Z)

Z <- complete_ra(N=100, condition_names=c("control", "placebo", "treatment"))
table(Z)

```

complete_ra_probabilities

Probabilities of assignment: Complete Random Assignment

Description

Probabilities of assignment: Complete Random Assignment

Usage

```
complete_ra_probabilities(N, m = NULL, prob = NULL, num_arms = NULL,
                          m_each = NULL, prob_each = NULL, condition_names = NULL)
```

Arguments

N	the total number of units in the experimental sample (required).
m	If specified, a two-group design is assumed. m is the total number of units to be assigned to treatment. Should only be specified for a two group design in which exactly m of N units are assigned to treatment. If not specified, half of the sample (N/2) will be assigned to treatment (if N is odd, m will be set to either floor(N/2) or ceiling(N/2) with equal probability. m is NULL by default.
prob	If specified, a two-group design is assumed. prob is the probability of assignment to treatment. Within rounding, N*prob subjects will be assigned to treatment.
num_arms	The total number of treatment arms. If unspecified, num_arms will be determined from the length of m_each or condition_names.
m_each	A numeric vector giving the size of each treatment group. Must sum to N. If unspecified, equally sized (rounded) groups will be assumed.

prob_each	A numeric giving the probability of assignment to each treatment arm. Must sum to 1. Please note that due to rounding, these probabilities are approximate. For finer control, please use m_each.
condition_names	A character vector giving the names of the treatment groups. If unspecified, the treatment groups will be names T1, T2, T3, etc. An exception is a two-group design in which N only or N and m are specified, in which the condition names are 0 and 1.

Value

A matrix of probabilities of assignment.

condition_probs	<i>Calculate Probability of Observed Condition</i>
-----------------	--

Description

This function calculates the probability that each experimental unit is in the experimental condition that it is in.. You specify designs exactly as you do in 'simple_ra()', 'complete_ra()', 'block_ra()' or 'cluster_ra()', adding only the 'design' argument. Especially when units have different probabilities of assignment, this function can be useful for calculating inverse probability weights.

Usage

```
condition_probs(Z, N = NULL, prob = NULL, prob_each = NULL, m = NULL,
  m_each = NULL, block_var = NULL, block_m = NULL, clust_var = NULL,
  num_arms = NULL, condition_names = NULL, design, return_design = FALSE)
```

Arguments

Z	a random assignment generated by 'randomizr'. Use the identical parameters when generating the assignment and calculating the probabilities.
N	the total number of units in the experimental sample
prob	if specified, a two-group design is assumed. prob is the probability of assignment to treatment.
prob_each	a numeric giving the probability of assignment to each treatment arm. Must sum to 1. Please note that due to rounding, these probabilities are approximate. For finer control, please use m_each.
m	if specified, a two-group design is assumed. m is the total number of units to be assigned to treatment. Should only be specified for a two group design in which exactly m of N units to treatment. If not specified, half of the sample (N/2) will be assigned to treatment. Is null by default. In clustered designs, exactly m of N clusters is assigned to treatment. If not specified, half of the clusters will be assigned to treatment.
m_each	a numeric vector giving the size of each treatment group. Must sum to N. If unspecified, equally sized (rounded) groups will be assumed.
block_var	A vector of length N that includes the blocking variable

block_m	A matrix whose number of rows is equal to the number of blocks and whose number of columns is equal to the number of treatment arms. The rows should respect the alphabetical ordering of the blocks as determined by <code>sort(unique(block_var))</code> . The columns should be in the order of <code>condition_names</code> , if specified.
clust_var	a vector of length N that describes which cluster each unit belongs to.
num_arms	the total number of treatment arms. If unspecified, will be determined from the length of <code>m_each</code> or <code>condition_names</code> .
condition_names	a character vector giving the names of the treatment groups. If unspecified, the treatment groups will be names T1, T2, T3, etc.
design	a string that specifies the design used. Can only take the values "simple", "complete", "block", or "cluster".
return_design	a logical value that specifies whether a dataframe with Z, the probabilities of each condition, and the observed condition probability should be returned. Defaults to FALSE.
prob_each	A vector whose length is equal to the number of treatment assignments. When specified, <code>prob_each</code> assigns the same (within rounding) proportion of each block to each treatment condition, using complete random assignment. <code>prob_each</code> must sum to 1.

Examples

```

N <- 100
Z <- simple_ra(N)
condition_probs(Z=Z, N=N, design = "simple")

Z <- simple_ra(N=N, prob_each = c(.1, .2, .7), condition_names = c("A", "B", "C"))
condition_probs(Z=Z, N=N, prob_each = c(.1, .2, .7), condition_names = c("A", "B", "C"),
  design = "simple", return_design=TRUE)

# Complete designs
N <- 100
Z <- complete_ra(N=N, m = 45)
condition_probs(Z=Z, N=N, m = 45, design = "complete")

Z <- complete_ra(N=N, m_each = c(10, 20, 70))
condition_probs(Z=Z, N=N, m_each = c(10, 20, 70),
  design = "complete", return_design=TRUE)

# Block designs

block_var <- rep(c("A", "B", "C"), times=c(50, 100, 200))
block_m <- rbind(c(30, 20),
  c(50, 50),
  c(100, 100))
Z <- block_ra(block_var=block_var, block_m=block_m)
condition_probs(Z=Z, block_var=block_var, block_m=block_m, design="block")

Z <- block_ra(block_var=block_var, prob_each=c(.1, .1, .8),
  condition_names=c("control", "placebo", "treatment"))
condition_probs(Z=Z, block_var=block_var, prob_each=c(.1, .1, .8),
  condition_names=c("control", "placebo", "treatment"),
  design="block")

```

```
# Cluster designs

clust_var <- rep(letters, times=1:26)
Z <- cluster_ra(clust_var=clust_var, m_each=c(7, 7, 12))
condition_probs(Z=Z, clust_var=clust_var, m_each=c(7, 7, 12),
design="cluster", return_design=TRUE)
```

conduct_ra	<i>Conduct a declared random assignment.</i>
------------	--

Description

Conduct a declared random assignment.

Usage

```
conduct_ra(ra_declaration)
```

Arguments

ra_declaration A random assignment declaration, created by [declare_ra](#).

Examples

```
declaration <- declare_ra(N=100, m_each=c(30, 30, 40))
Z <- conduct_ra(ra_declaration = declaration)
table(Z)
```

declare_ra	<i>Declare a random assignment procedure.</i>
------------	---

Description

Declare a random assignment procedure.

Usage

```
declare_ra(N = NULL, prob = NULL, num_arms = NULL, prob_each = NULL,
m = NULL, m_each = NULL, block_var = NULL, block_m = NULL,
clust_var = NULL, condition_names = NULL, simple = FALSE)
```

Arguments

N	The total number of units in the experimental sample.
prob	The probability of assignment to treatment. If specified, a two-group design is assumed.
num_arms	The total number of treatment arms. If unspecified, will be determined from the number of columns of block_m, the length of prob_each, the length of m_each, or the length of condition_names.
prob_each	A numeric vector giving the probability of assignment to each treatment arm. Must sum to 1. Please note that due to rounding, these probabilities are approximate. For finer control, please use m_each.
m	If specified, a two-group design is assumed. m is the total number of units to be assigned to treatment. Should only be specified for a two group design in which exactly m of N units are assigned to treatment. If not specified (and no other arguments are specified), half of the sample (N/2) will be assigned to treatment (if N is odd, m will be set to either floor(N/2) or ceiling(N/2) with equal probability. m is NULL by default.
m_each	A numeric vector giving the size of each treatment group. Must sum to N. If unspecified, equally sized (rounded) groups will be assumed.
block_var	A vector of length N indicating which block each unit belongs to.
block_m	A matrix of arm sizes with blocks in the rows and treatment conditions in the columns. The rows should respect the alphabetical ordering of the blocks as determined by sort(unique(block_var)). The columns should be in the order of condition_names, if specified.
clust_var	A vector of length N that indicates which cluster each unit belongs to.
condition_names	A character vector giving the names of the treatment groups. If unspecified, the treatment groups will be names T1, T2, T3, etc.
simple	A logical indicating if simple random assignment is intended. Is FALSE by default.
prob_each	A numeric vector whose length is equal to the number of treatment conditions. When specified, prob_each assigns the same (within rounding) proportion of each block to each treatment condition, using complete random assignment. prob_each must sum to 1.

Value

A random assignment declaration.

obtain_condition_probabilities

Obtain the probabilities of units being in the conditions that they are in.

Description

This function is especially useful when units have different probabilities of assignment and the analyst plans to use inverse-probability weights.

Usage

```
obtain_condition_probabilities(ra_declaration, assignment)
```

Arguments

- ra_declaration A random assignment declaration, created by `declare_ra`.
- assignment A vector of random assignments, often created by `conduct_ra`.

Examples

```
# Conduct a block random assignment
block_var <- rep(c("A", "B", "C"), times=c(50, 100, 200))
block_m <- rbind(c(10, 40),
                c(30, 70),
                c(50, 150))
declaration <- declare_ra(block_var = block_var, block_m = block_m)
Z <- conduct_ra(ra_declaration = declaration)
table(Z, block_var)

observed_probabilities <-
  obtain_condition_probabilities(ra_declaration = declaration, assignment = Z)

# Probabilities in the control group:
table(observed_probabilities[Z == 0], block_var[Z == 0])

# Probabilities in the treatment group:
table(observed_probabilities[Z == 1], block_var[Z == 1])
```

randomizr	<i>randomizr</i>
-----------	------------------

Description

randomizr

simple_ra	<i>Simple Random Assignment</i>
-----------	---------------------------------

Description

This function conducts simple random assignment, a procedure in which units are assigned to treatment conditions with a known probability, but the number of units assigned to any condition might vary from one randomization to the next. This function can accomodate any number of treatment arms.

Usage

```
simple_ra(N, prob = NULL, num_arms = NULL, prob_each = NULL,
         condition_names = NULL)
```

Arguments

N	The total number of units in the experimental sample.
prob	The probability of assignment to treatment. If specified, a two-group design is assumed.
num_arms	The total number of treatment arms. If unspecified, will be determined from the length of prob_each or condition_names.
prob_each	A numeric vector giving probabilities of assignment to each treatment group. Must sum to 1. If unspecified, equal probabilities will be assumed.
condition_names	A character vector giving the names of the treatment groups. If unspecified, the treatment groups will be names T1, T2, T3, etc.

Examples

```
# Two Group Designs

Z <- simple_ra(N=100)
table(Z)

Z <- simple_ra(N=100, prob=0.5)
table(Z)

Z <- simple_ra(N=100, prob_each = c(0.3, 0.7),
               condition_names = c("control", "treatment"))
table(Z)

# Multi-arm Designs
Z <- simple_ra(N=100, num_arms=3)
table(Z)

Z <- simple_ra(N=100, prob_each=c(0.3, 0.3, 0.4))
table(Z)

Z <- simple_ra(N=100, prob_each=c(0.3, 0.3, 0.4),
               condition_names=c("control", "placebo", "treatment"))
table(Z)

Z <- simple_ra(N=100, condition_names=c("control", "placebo", "treatment"))
table(Z)
```

simple_ra_probabilities

Probabilities of assignment: Simple Random Assignment

Description

Probabilities of assignment: Simple Random Assignment

Usage

```
simple_ra_probabilities(N, prob = NULL, num_arms = NULL, prob_each = NULL,
                      condition_names = NULL)
```

Arguments

N	the total number of units in the experimental sample (required).
prob	If specified, a two-group design is assumed. prob is the probability of assignment to treatment. Within rounding, $N \times \text{prob}$ subjects will be assigned to treatment.
num_arms	The total number of treatment arms. If unspecified, num_arms will be determined from the length of m_each or condition_names.
prob_each	A numeric giving the probability of assignment to each treatment arm. Must sum to 1. Please note that due to rounding, these probabilities are approximate. For finer control, please use m_each.
condition_names	A character vector giving the names of the treatment groups. If unspecified, the treatment groups will be names T1, T2, T3, etc. An exception is a two-group design in which N only or N and m are specified, in which the condition names are 0 and 1.

Value

A matrix of probabilities of assignment.

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