

# Package ‘DyAlloc’

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**Type** Package

**Title** Dynamic Allocation

**Version** 0.1.0

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**Description** Provides imbalance scores for each possible treatment group as a new subject enters the clinical trial study by Dynamic Allocation. The treatment allocation probability for each group is calculated and a final group allocation is returned. This package supports three Dynamic Allocation procedures and a final function that wraps all the functions into one. This Dynamic Allocation scheme is an unbalance minimization method proposed by Lebowitsch et al.(2012) <doi: 10.1002/sim.5418>.

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**Encoding** UTF-8

**LazyData** true

**RoxygenNote** 7.1.2

**Suggests** knitr,  
rmarkdown,  
testthat (>= 3.0.0)

**Config/testthat/edition** 3

**VignetteBuilder** knitr

**URL** <https://github.com/ktmiu/DyAlloc>

**BugReports** <https://github.com/ktmiu/DyAlloc/issues>

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DyAlloc	<i>Provides the final treatment group allocation for a new subject entering the study. Incorporates all the previous functions and a practitioner can use this function solely to obtain treatment assignments for the study subjects. The site default is FALSE.</i>
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### Description

Provides the final treatment group allocation for a new subject entering the study. Incorporates all the previous functions and a practitioner can use this function solely to obtain treatment assignments for the study subjects. The site default is FALSE.

### Usage

```
DyAlloc(df, N, covars, weight, newsub, site = FALSE)
```

### Arguments

df	data frame. The profiles of existing subjects in the study.
N	numeric variable. The number of treatment arms
covars	a vector. All the names of covariates in the study.
weight	a vector. The weights for overall study, with-in stratum, (site), and factors/covariates, in this particular order
newsub	a vector. The factor profile of the new subject entering the study.
site	a boolean value. Whether or not to account for site imbalance (default:FALSE)

### Value

A treatment group allocation

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MarImb	<i>Creates a marginal imbalance score for each treatment arm of N treatment groups. This is a low level function to be used in subsequent functions and will most likely not be used directly by a practitioner.</i>
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### Description

Creates a marginal imbalance score for each treatment arm of N treatment groups. This is a low level function to be used in subsequent functions and will most likely not be used directly by a practitioner.

### Usage

```
MarImb(df, N)
```

### Arguments

df	data frame. The profiles of existing subjects in the study.
N	numeric variable. The number of treatment arms in the study.

**Value**

A vector of marginal imbalance scores for each treatment arm is produced (a total of N scores)

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Trt_Prob	<i>Creates a vector of probabilities of being assigned to each treatment group. This function uses the imbalance scores created from the function WeiImb as input. *NOTE: if the imbalance scores are the same, then they have equal probability of being assigned to. E.g. if we get two equal least weighted imbalance scores, they each have a probability of 0.5 for a subject to be assigned to.*</i>
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**Description**

Creates a vector of probabilities of being assigned to each treatment group. This function uses the imbalance scores created from the function WeiImb as input. \*NOTE: if the imbalance scores are the same, then they have equal probability of being assigned to. E.g. if we get two equal least weighted imbalance scores, they each have a probability of 0.5 for a subject to be assigned to.\*

**Usage**

```
Trt_Prob(imbalances, alpha)
```

**Arguments**

imbalances	a vector. Imbalance scores across the N treatment groups (generally, the scores we get from WeiImb would be plugged in here)
alpha	a numeric number. The "second best probability" parameter, generally alpha is set to 0.2. This means that the treat group a subject assign to gets the probability of 0.8.

**Value**

A vector of probabilities of being assigned to each treatment group.

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WeiImb	<i>Creates a weighted imbalance score for each treatment arm *NOTE: the default for site here is FALSE, but one can specify site=TRUE in the argument to account for site imbalance. Note that the weight for site has to be placed in the third element of the 'weight' vector (and can be omitted when site=FALSE)*</i>
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**Description**

Creates a weighted imbalance score for each treatment arm \*NOTE: the default for site here is FALSE, but one can specify site=TRUE in the argument to account for site imbalance. Note that the weight for site has to be placed in the third element of the 'weight' vector (and can be omitted when site=FALSE)\*

**Usage**

```
WeiImb(df, N, covars, weight, newsub, site = FALSE)
```

**Arguments**

df	data frame. The profiles of existing subjects in the study.
N	numeric variable. The number of treatment arms in the study.
covars	a vector. All the names of covariates in the study.
weight	a vector. The weights for overall study, with-in stratum, (site), and factors/covariates, in this particular order
newsub	a vector. The factor profile of the new subject entering the study.
site	a boolean value. Whether or not to account for site imbalance (default:FALSE)

**Value**

A vector of weighted imbalance scores for each treatment arm is produced (a total of N scores)