

# 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 study given the profiles of previous subjects. The treatment allocation probability for each group is calculated and a final group allocation is returned.

**License** MIT + file LICENSE

**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 assignment</i>
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**Description**

provides the final treatment group assignment

**Usage**

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

**Arguments**

df	data frame
N	numeric variable
covars	a vector
weight	a vector
newsub	a vector
site	a boolean value

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MarImb	<i>Creates a marginal imbalance score for each treatment arm of N treatment groups</i>
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**Description**

Creates a marginal imbalance score for each treatment arm of N treatment groups

**Usage**

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

**Arguments**

df	data frame
N	numeric variable

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Trt_Prob	<i>Creates a vector of probabilities of being assigned to each treatment group</i>
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**Description**

Creates a vector of probabilities of being assigned to each treatment group

**Usage**

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

**Arguments**

imbalances	a vector
alpha	a numeric number

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WeiImb	<i>Creates a weighted imbalance score for each treatment arm</i>
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**Description**

Creates a weighted imbalance score for each treatment arm

**Usage**

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

**Arguments**

df	data frame
N	numeric variable
covars	a vector
weight	a vector
newsub	a vector
site	a boolean value