

# Package ‘SAMUR’

August 31, 2022

**Type** Package

**Title** Stochastic Augmentation of Matched Data Using Restriction Methods

**Version** 1.1

**Date** 2022-08-30

**Author** Mansour T.A. Sharabiani, Alireza S. Mahani

**Maintainer** Alireza S. Mahani <alireza.s.mahani@gmail.com>

**Description** Augmenting a matched data set by generating multiple stochastic, matched samples from the data using a multi-dimensional histogram constructed from dropping the input matched data into a multi-dimensional grid built on the full data set. The resulting stochastic, matched sets will likely provide a collectively higher coverage of the full data set compared to the single matched set. Each stochastic match is without duplication, thus allowing downstream validation techniques such as cross-validation to be applied to each set without concern for overfitting.

**License** GPL (>= 2)

**Imports** Matching

**NeedsCompilation** no

**Repository** CRAN

**Date/Publication** 2022-08-31 13:00:14 UTC

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samur

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*Stochastic Augmentation of Matched Datasets Using Restriction Methods*


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**Description**

This function generates multiple subsets of the data in which the distribution of covariates is balanced across treatment groups. It works by binning the output of a base matching algorithm into a multidimensional histogram, and drawing - without replacement - from the full data set according to the histogram. This leads to higher data coverage across multiple matched subsets without duplication of cases within each subset.

**Usage**

```

samur(
  formula, data
  , matched.subset = 1:nrow(data)
  , nsmp = 100
  , use.quantile = TRUE, breaks = 10
  , replace = length(unique(matched.subset)) < length(matched.subset)
)
## S3 method for class 'samur'
print(x, ...)

```

**Arguments**

formula	Formula expression used to describe the treatment variable (lhs) and covariates used during matching (rhs).
data	Data frame containing the treatment variables and matched covariates as specified in the formula.
matched.subset	An integer vector representing the indexes of a subset of data that is the output of a base matching algorithm. It cannot contain duplicate values.
nsmp	Number of stochastically matched subsets to generate.
use.quantile	Should numeric covariates be binned using quantiles (TRUE) or not.
breaks	number of breaks to use in binning numeric covariates.
replace	Boolean flag indicating whether or not to perform sampling with replacement.
x	An object of class samur, typically the output of function samur.
...	Arguments passed to/from other methods.

**Value**

An object of class samur, a matrix of size `length(matched.subset)` by `nsmp`, where each column is a matched subset without case duplication. It also has the following attributes:

call	Copy of function call.
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formula	Formula passed to the function.
mdg	Multi-dimensional grid used for binning the matched data subsets.
mdh	Multi-dimensional histogram resulting from binning data[matched.subset, ] according to the grid specified in mdg.
data	Copy of data frame passed to the function.

**Author(s)**

Mansour T.A. Sharabiani, Alireza S. Mahani

**See Also**

[summary.samur](#)

**Examples**

```
## Not run:
library(SAMUR)
library(Matching)
data(lalonde)
myformula <- treat ~ age + educ
myglm <- glm(myformula, lalonde, family="binomial")
X <- myglm$fitted.values
# using M=1 and replace=F to ensure no duplication
bimatch <- Match(Tr = lalonde$treat, X = myglm$fitted.values
  , M = 1, replace = F, caliper = 0.25)
idx <- c(bimatch$index.control, bimatch$index.treated)
my.samur <- samur(formula = myformula, data = lalonde
  , matched.subset = idx, nsmp = 100
  , breaks = 10, use.quantile = TRUE)
summary(my.samur, nboots = 500)

## End(Not run)
```

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summary.samur

*Summarizing Output of SAMUR Augmentation Function*

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**Description**

summary method for class "samur".

**Usage**

```
## S3 method for class 'samur'
summary(object, ...)
## S3 method for class 'summary.samur'
print(x, ...)
```

**Arguments**

object	An object of class "samur", usually the result of a call to <a href="#">samur</a> .
x	An object of class "summary.samur", usually the result of a call to <code>summary.samur</code> .
...	Further arguments to be passed to/from other methods. Current implementation of <code>summary.samur</code> passes arguments to <code>MatchBalance</code> function from <code>Matching</code> package.

**Value**

A list with the following elements:

<code>min.pval.new</code>	A vector of length equal to number of samples ( <code>nsmp</code> ) generated by <a href="#">samur</a> , each representing the minimum p-value from all univariate tests performed by the underlying function <code>MatchBalance</code> . It also has an attributed named <code>min.pval.orig</code> , containing a similar number for the original matched subset, i.e. <code>data[matched.subset, ]</code> .
<code>min.pval.orig</code>	Same number as above, but for original matched subset.
<code>coverage.new</code>	Percent of cases from full data set covered among all stochastic, matched samples.
<code>coverage.orig</code>	Same as above, calculated for the original matched subset.

**Note**

All t-tests used for p-value calculations are "not" paired, since the philosophy of stochastic augmentation relaxes the notion of one-to-one matching.

**Author(s)**

Alireza S. Mahani, Mansour T.A. Sharabiani

**See Also**

[samur](#), [MatchBalance](#)

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