

# Package ‘SimTimeVar’

January 20, 2025

**Type** Package

**Title** Simulate Longitudinal Dataset with Time-Varying Correlated Covariates

**Version** 1.0.0

**Date** 2017-09-07

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**Description** Flexibly simulates a dataset with time-varying covariates with user-specified exchangeable correlation structures across and within clusters. Covariates can be normal or binary and can be static within a cluster or time-varying. Time-varying normal variables can optionally have linear trajectories within each cluster. See ?make\_one\_dataset for the main wrapper function. See Montez-Rath et al. <[arXiv:1709.10074](https://arxiv.org/abs/1709.10074)> for methodological details.

**LazyData** true

**License** GPL-2

**Imports** metafor, mvtnorm, ICC, miscTools, car, plyr, corpcor, psych, stats, utils

**RoxygenNote** 6.0.1

**NeedsCompilation** no

**Repository** CRAN

**Date/Publication** 2017-09-30 16:22:10 UTC

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add\_one\_categorical     *Generate linear predictor from logistic model*

---

## Description

An internal function not intended for the user. Given a dataset and multinomial regression parameters, generates a categorical variable and adds it to the dataset.

## Usage

```
add_one_categorical(.d, n, obs, cat.parameters)
```

## Arguments

`.d`                    The dataset to which to add the categorical variable.

`n`                     The number of clusters.

`obs`                  The number of observations per cluster.

`cat.parameters`     A dataframe of parameters for generating the categorical variable. See Details.

## Examples

```
# mini dataset with 3 observations per person
data = data.frame( male = rep( rbinom(n=10, size=1, prob=0.5), each=3 ) )
add_one_categorical( data, 10, 3, cat.params)
```

---

`add_time_function_vars`*Creates linear time-function variables*

---

**Description**

Given variable-specific slopes and intercepts for a cluster, creates continuous variables that increase or decrease linearly in time (with normal error with standard deviation error .SD) and adds them to the dataframe.

**Usage**

```
add_time_function_vars(d4, obs, parameters)
```

**Arguments**

<code>d4</code>	The dataframe to which to add the time-function variables.
<code>obs</code>	The number of observations per cluster.
<code>parameters</code>	The parameters matrix.

**Details**

See `make_one_dataset` for additional information.

---

`BN.rBound`*Maximum correlation between binary and normal random variables*

---

**Description**

Given parameter  $p$  for a Bernoulli random variable, returns its maximum possible correlation with an arbitrary normal random variable. Used to adjust correlation matrices whose entries are not theoretically possible.

**Usage**

```
BN.rBound(p)
```

**Arguments**

<code>p</code>	Parameter of Bernoulli random variable.
----------------	---

**Examples**

```
# find the largest possible correlation between a normal  
# variable and a binary with parameter 0.1  
BN.rBound(0.1)
```

---

`cat.params`*An example dataframe for categorical variable parameters*

---

**Description**

An example of how to set up the categorical variable parameters dataframe.

**Usage**`cat.params`**Format**

An object of class `data.frame` with 5 rows and 3 columns.

---

`closest`*Return closest value*

---

**Description**

An internal function not intended for the user. Given a number `x` and vector of permitted values, returns the closest permitted value to `x` (in absolute value).

**Usage**`closest(x, candidates)`**Arguments**

`x`                    The number to be compared to the permitted values.  
`candidates`        A vector of permitted values.

**Examples**`closest( x = 5, candidates = c(-3, 8, 25) )`

---

complete\_parameters     *Fill in partially incomplete parameters matrix*

---

### Description

Fills in "strategic" NA values in a user-provided parameters matrix by (1) calculating SDs for proportions using the binomial distribution; (2) calculating variances based on SDs; and (3) setting within-cluster variances to 1/3 of the across-cluster variances (if not already specified).

### Usage

```
complete_parameters(parameters, n)
```

### Arguments

parameters	Initial parameters matrix that may contain NA values.
n	The number of clusters

### Details

For binary variables, uses binomial distribution to compute across-cluster standard deviation of proportion. Where there are missing values, fills in variances given standard deviations and vice-versa. Where there are missing values in `within.var`, fills these in by defaulting to 1/3 of the corresponding across-cluster variance.

### Examples

```
complete_parameters(params, n=10)
```

---

expand\_matrix     *Longitudinally expand a matrix of single observations by cluster*

---

### Description

An internal function not intended for the user. Given a matrix of single observations for a cluster, repeats each cluster's entry in each `.obs` times.

### Usage

```
expand_matrix(.matrix, .obs)
```

### Arguments

.matrix	The matrix of observations to be expanded.
.obs	The number of observations to generate per cluster.

**Examples**

```
mat = matrix( seq(1:10), nrow=2, byrow=FALSE)
expand_matrix(mat, 4)
```

---

expand_subjects	<i>Longitudinally expand a cluster</i>
-----------------	--

---

**Description**

An internal function not intended for the user. Given a matrix of cluster means for each variable to be simulated, "expands" them into time-varying observations.

**Usage**

```
expand_subjects(mus3, n.OtherNorms, n.OtherBins, n.TBins, wcor, obs, parameters,
zero = 1e-04)
```

**Arguments**

mus3	A matrix of cluster means for each variable.
n.OtherNorms	The number normal variables (not counting those used for generating a time-varying binary variable).
n.OtherBins	The number of static binary variables.
n.TBins	The number of time-varying binary variables.
wcor	The within-cluster correlation matrix.
obs	The number of observations to generate per cluster.
parameters	The parameters dataframe.
zero	A small number just larger than 0.

**Examples**

```
# subject means matrix (normally would be created internally within make_one_dataset)
mus3 = structure(c(1, 0, 1, 0, 0, 0, 1, 1, 1, 1, 1e-04, 1e-04, 0.886306145591761,
1e-04, 1e-04, 1e-04, 1e-04, 0.875187001140343, 0.835990583043838,
1e-04, 1e-04, 1e-04, 1e-04, 1e-04, 1e-04, 1e-04, 1e-04, 1e-04,
1e-04, 1e-04, 69.7139993804559, 61.3137637852213, 68.3375516615242,
57.7893277997516, 66.3744152975352, 63.7829561873355, 66.3864252981679,
68.8513253460358, 67.4120718557, 67.8332265185068, 192.366192293195,
128.048983102048, 171.550401133259, 120.348392753954, 158.840864356998,
170.13484760994, 113.512220330821, 162.715528382999, 138.476877345895,
159.841096973242, 115.026417822477, 109.527137142158, 117.087914485084,
121.153861460319, 109.95973584141, 122.96960673409, 90.5100006255084,
107.523229006601, 108.971677388246, 115.641818648526, -4.33184270434101,
-5.45143483618415, -2.56331188314257, -1.38204452333064, -1.61744564863871,
1.83911233741448, 2.0488338883998, -0.237095062415858, -5.47497506857878,
-3.53078955238741), .Dim = c(10L, 7L))
```

```
expand_subjects( mus3 = mus3, n.OtherNorms = 4, n.OtherBins = 1, n.TBins = 2,
                 wcor = wcor, obs = 3, parameters = complete_parameters(params, n=10) )
```

---

has_drug_suffix	<i>Checks whether string has "_s" suffix</i>
-----------------	--

---

### Description

An internal function not intended for the user.

### Usage

```
has_drug_suffix(var.name)
```

### Arguments

var.name	The string to be checked
----------	--------------------------

### Examples

```
has_drug_suffix("myvariable_s")
has_drug_suffix("myvariable")
```

---

make_one_dataset	<i>Simulate time-varying covariates</i>
------------------	---

---

### Description

Simulates a dataset with correlated time-varying covariates with an exchangeable correlation structure. Covariates can be normal or binary and can be static within a cluster or time-varying. Time-varying normal variables can optionally have linear trajectories within each cluster.

### Usage

```
make_one_dataset(n, obs, n.TBins, pcor, wcor, parameters, cat.parameters)
```

### Arguments

n	The number of clusters.
obs	The number of observations per cluster.
n.TBins	Number of time-varying binary variables.
pcor	The across-subject correlation matrix. See Details.
wcor	The within-subject correlation matrix. See Details.
parameters	A dataframe containing the general simulation parameters. See Details.
cat.parameters	A dataframe containing parameters for the categorical variables. See Details.

## Details

### SPECIFYING THE PARAMETERS MATRIX

The matrix `parameters` contains parameters required to generate all non-categorical variables. It must contain column names `name`, `type`, `across.mean`, `across.SD`, `across.var`, `within.var`, `prop`, and `error.SD`. (To see an example, use `data(params)`.) Each variable to be generated requires either one or two rows in `parameters`, depending on the variable type.

The possible variable types and their corresponding specifications are:

- **Static binary variables** do not change over time within a cluster. For example, if clusters are subjects, `sex` would be a static binary variable. Generating such a variable requires a single row of type `static.binary` with `prop` corresponding to the proportion of clusters for which the variable equals 1 and all other columns set to NA. (The correct standard deviation will automatically be computed later.) For example, if the variable is an indicator for a subject's being male, then `prop` specifies the proportion of males to be generated.
- **Time-varying binary variables** can change within a cluster over time, as for an indicator for whether a subject is currently taking the study drug. These variables require two rows in `parameters`. The first row should be of type `static.binary` with `prop` representing the proportion of clusters for which the time-varying binary variable is 1 at least once (and all other columns set to NA). For example, this row in `parameters` could represent the proportion of subjects who ever take the study drug ("ever-users").

The second row should be of type `subject.prop` with `across.mean` representing, for clusters that ever have a 1 for the binary variable, the proportion of observations within the cluster for which the variable is equal to 1. (All other columns should be set to NA.) For example, this row in `parameters` could represent the proportion of observations for which an ever-user is currently taking the drug. To indicate which pair of variables go together, the `subject.prop` should have the same name as the `static.binary` variable, but with the suffix `_s` appended (for example, the former could be named `drug_s` and the latter `drug`).

- **Normal variables** are normally distributed within a cluster such that the within-cluster means are themselves also normally distributed in the population of clusters. Generating a normal variable requires specification of the population mean (`across.mean`) and standard deviation (`across.SD`) as well as of the within-cluster standard deviation (`within.SD`). To generate a static continuous variable, simply set `within.SD` to be extremely small (e.g.,  $1 * 10^{-7}$ ) and all corresponding correlations in `matrix.wcor` to 0.
- **Time-function variables** are linear functions of time (with normal error) within each cluster such that the within-cluster baseline values are normally distributed in the population of clusters. Generating a time-function variable requires two entries. The first entry should be of type `time.function` and specifies the population mean (`across.mean`) and standard deviation (`across.SD`) of the within-cluster baseline values as well as the error standard deviation (`error.SD`). The second entry should be of type `normal` and should have the same name as the `time.function` entry, but with the `"_s"` suffix. This entry specifies the mean (`across.mean`) and standard deviation (`across.SD`) of the within-cluster slopes.

### SPECIFYING THE CATEGORICAL PARAMETERS MATRIX

The matrix `cat.parameters` contains parameters required to generate the single categorical variable, if any. It must contain column names `level`, `parameter`, and `beta`. (To see an example, use `data(cat.params)`.)



- **The reference level:** Each categorical variable must have exactly one "reference" level. The reference level should have one row in `cat.parameters` for which `parameters` is set to NA and `beta` is set to `ref`. For example, in the example file `cat.params` specifying parameters to generate a subject's race, the reference level is `white`.
- **Other levels:** Other levels of the categorical variable will have one or more rows. One row with `parameter` set to `intercept` and `beta` set to a numeric value represents the intercept term in the corresponding multinomial model. Any subsequent rows, with `parameters` set to names of other variables in the dataset and `beta` set to numeric values, represents other coefficients in the corresponding multinomial models.

### SPECIFYING THE POPULATION CORRELATION MATRIX

Matrix `pcor` specifies the population (i.e., across-cluster) correlation matrix. It should have the same number of rows and columns as `parameters` as well as the same variable names and ordering of variables.

### SPECIFYING THE WITHIN-CLUSTER CORRELATION MATRIX

Matrix `wcor` specifies the within-cluster correlation matrix. The order of the variables listed in this file should be consistent with the order in `params` and `pcor`. However, `static.binary` and `subject.prop` variables should not be included in `wcor` since they are static within a cluster. Static continuous variables should be included, but all the correlations should be set to zero.

### Examples

```
data = make_one_dataset(n=10, obs=10, n.TBins=2, pcor=pcor, wcor=wcor,
parameters=complete_parameters(params, n=10), cat.parameters=cat.params)$data
```

---

`make_one_linear_pred` *Generate linear predictor from logistic model*

---

### Description

An internal function not intended for the user. Given a matrix of regression parameters and a dataset, returns the linear predictor based on the given dataset.

### Usage

```
make_one_linear_pred(m, data)
```

### Arguments

<code>m</code>	Part of the parameter matrix for the linear predictor for a single variable.
<code>data</code>	The dataframe from which to generate.

**Examples**

```
# take part of parameters matrix corresponding to single level of categorical
# variable
m = cat.params[ cat.params$level == "black", ]
data = data.frame( male = rbinom(n=10, size=1, prob=0.5) )
make_one_linear_pred(m, data)
```

---

```
mod.jointly.generate.binary.normal
```

*Return closest value*

---

**Description**

An internal function not intended for the user. Simulates correlated normal and binary variables based on the algorithm of Demirtas and Doganay (2012). See references for further information.

**Usage**

```
mod.jointly.generate.binary.normal(no.rows, no.bin, no.nor, prop.vec.bin,
  mean.vec.nor, var.nor, corr.vec, adjust.corr = TRUE)
```

**Arguments**

<code>no.rows</code>	Number of rows
<code>no.bin</code>	Number of binary variables
<code>no.nor</code>	Number of normal variables
<code>prop.vec.bin</code>	Vector of parameters for binary variables
<code>mean.vec.nor</code>	Vector of means for binary variables
<code>var.nor</code>	Vector of variances for binary variables
<code>corr.vec</code>	Vector of correlations
<code>adjust.corr</code>	Boolean indicating whether theoretically impossible correlations between a binary and a normal variable should be adjusted to their closest theoretically possible value.

**References**

Demirtas, H., & Doganay, B. (2012). Simultaneous generation of binary and normal data with specified marginal and association structures. *Journal of Biopharmaceutical Statistics*, 22(2), 223-236.

---

override_static	<i>Override static variable</i>
-----------------	---------------------------------

---

**Description**

An internal function not intended for the user. For static variables, overrides any time-varying values to ensure that they are actually static.

**Usage**

```
override_static(.static.var.name, .id.var.name = "id", .d, .obs)
```

**Arguments**

.static.var.name	Name of static variable.
.id.var.name	Name of variable defining clusters in dataset.
.d	Dataset
.obs	The number of observations per cluster.

**Examples**

```
# example with 10 subjects each with 3 observations
# generate sex in a way where it might vary within a subject
data = data.frame( id = rep(1:10, each=3),
                  male = rbinom( n=10*3, size=1, prob=0.5 ) )
override_static("male", "id", data, 3)
```

---

override_tbin_probs	<i>Override probabilities for time-varying binary variables</i>
---------------------	---

---

**Description**

An internal function not intended for the user. For clusters assigned to have a given time-varying binary variable always equal to 0, overrides to 0 the corresponding proportion of observations with the binary variable equal to 1.

**Usage**

```
override_tbin_probs(mus0, n.TBins, n.OtherBins, zero = 1e-04)
```

**Arguments**

mus0	The matrix of cluster means.
n.TBins	Number of time-varying binary variables.
n.OtherBins	The number of static binary variables.
zero	A number very close to 0, but slightly larger.

**Examples**

```

# make example subject means matrix for 1 static binary,
# 1 time-varying binary, and 1 normal
# 50 subjects and 5 observations (latter plays into variance)
set.seed(451)
mus0 = mod.jointly.generate.binary.normal( no.rows = 50, no.bin = 2, no.nor = 2,
                                           prop.vec.bin = c( .5, .35 ),
                                           mean.vec.nor = c( .4, 100 ),
                                           var.nor = c( (0.4 * 0.6) / 5, 10 ),
                                           corr.vec = c(0.05, .08, 0, 0, -0.03, 0) )

# note that we have ever-users with non-zero propensities to be on drug: not okay
any( mus0[,1] == 0 & mus0[,3] != 0 )

# fix them
mus1 = override_tbin_probs( mus0, 1, 1 )

# all better!
any( mus1[,1] == 0 & mus1[,3] > 0.0001 )

```

---

params	<i>An example parameters dataframe</i>
--------	--

---

**Description**

An example of how to set up the parameters dataframe.

**Usage**

```
params
```

**Format**

An object of class `data.frame` with 12 rows and 8 columns.

---

pcor	<i>An example across-cluster correlation dataframe</i>
------	--

---

**Description**

An example of how to set up the across-cluster correlation dataframe.

**Usage**

```
pcor
```

**Format**

An object of class `data.frame` with 9 rows and 9 columns.

---

proportionize	<i>Turn a number into a valid proportion</i>
---------------	--

---

**Description**

An internal function not intended for the user. Turns an arbitrary number into a valid proportion by setting the number equal to the closest value in [0,1].

**Usage**

```
proportionize(x, zero = 1e-05, one = 0.999)
```

**Arguments**

x	The number to be turned into a proportion.
zero	A very small number that is just larger than 0.
one	A number that is just smaller than 1.

**Examples**

```
proportionize(-0.03)
proportionize(1.2)
proportionize(.63)
```

---

upper_tri_vec	<i>Turn symmetric matrix into vector</i>
---------------	--

---

**Description**

An internal function not intended for the user. Turns a matrix into a vector of the upper-triangular elements (arranged by row).

**Usage**

```
upper_tri_vec(m)
```

**Arguments**

m	Matrix
---	--------

**Examples**

```
# make a simple correlation matrix
x = rnorm(10); y = rnorm(10); z = rnorm(10)
mat = cor( data.frame(x,y,z) )

# turn into into vector
upper_tri_vec(mat)
```

---

`wcor`*An example within-cluster correlation dataframe*

---

**Description**

An example of how to set up the within-cluster correlation dataframe.

**Usage**

```
wcor
```

**Format**

An object of class `data.frame` with 6 rows and 6 columns.

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