

# Package: SRSim (via r-universe)

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**Type** Package

**Title** Spontaneous Reporting Simulator (SRSim)

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**Description** A package for simulating spontaneous reporting data as used in the field of pharmacovigilance.

**Depends** R (>= 3.2.3), Rcpp, RcppArmadillo, RcppProgress, dplyr, tidyr, mvtnorm, corpcor, pcalg, Rgraphviz

**LinkingTo** Rcpp, RcppArmadillo, RcppProgress

**License** GPL-3

**Encoding** UTF-8

**LazyData** true

**RoxygenNote** 6.0.1

**URL** <https://github.com/bips-hb/srsim>

**BugReports** <https://github.com/bips-hb/srsim/issues>

**Repository** <https://bips-hb.r-universe.dev>

**RemoteUrl** <https://github.com/bips-hb/srsim>

**RemoteRef** HEAD

**RemoteSha** e53edbd2c1a0e393709809ff863d6433c3b6d538

## Contents

convert2Tables	2
create2x2TablesDAGRcpp	3
f_beta0	4
generateDAG	4
simulateReport	5

simulateSRS . . . . .	6
SRSim . . . . .	7
validReport . . . . .	8

<b>Index</b>	<b>9</b>
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convert2Tables	<i>Create 2 x 2 Tables from DAG based SR data</i>
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## Description

Creates a data frame with all 2 x 2 contingency tables given a simulated data set from simulateSRS. The tables are organized as follows:

	event $j$	not event $j$	<i>total</i>
drug $i$	a	c	a + c
not drug $i$	b	d	b + d
<i>total</i>	a + b	c + d	n_reports

## Usage

```
convert2Tables(sr)
```

## Arguments

sr                    The output generated by the [simulateSRS](#) function

## Value

A data frame where each row represents a 2 x 2 table. The columns represent:

drug_id	The ID of the drug
event_id	The ID of the event
prob_drug	The marginal probability of that drug
prob_event	The marginal probability of that event
or	The increase of the odds ratio when the drug is on the report
associated	TRUE is there is a non-zero correlation, FALSE otherwise
a	Number of times the drug and event appeared together in a report
b	Number of times the event appeared without the drug in a report
c	Number of times the drug appeared without the event in a report
d	Number of times the drug and event both did not appear in a report

## See Also

[simulateSRS](#)

**Examples**

```
sr <- simulateSRS()
tables <- create2x2Tables(sr)
```

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```
create2x2TablesDAGRcpp
```

*Create 2 x 2 Tables*

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**Description**

Creates a data frame containing all 2 x 2 contingency tables from the results generated by [simulateSRS](#). See the R wrapper function [convert2Tables](#) for more information.

**Usage**

```
create2x2TablesDAGRcpp(reports, prob_drugs, prob_events, n_parents, parent_id,
  beta1)
```

**Arguments**

reports	A binary matrix. Each row is a report
prob_drugs	A vector with the marginal probabilities of the drugs
prob_events	A vector with the marginal probabilities of the events
n_parents	A vector with the number of parents for each of the nodes
parent_id	A vector with the id of the parent
beta1	A vector with the regression coefficients for each node

**Value**

A dataframe. A description of the columns can be found in the commentary for the function [convert2Tables](#)

**See Also**

[convert2Tables](#)

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f_beta0	<i>Determining the Intercept</i>
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### Description

f\_beta0 is used by [simulateSRS](#) to find the appropriate intercept for a logistic regression model.

### Usage

```
f_beta0(beta0, margprob, beta1, margprob_parent)
```

### Arguments

beta0	The intercept
margprob	The marginal probability
beta1	The regression coefficient of the parent variable
margprob_parent	The marginal probability of the parent

### Value

The absolute difference between the desired marginal probability and the current marginal probability

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generateDAG	<i>Directed Acyclic Graph for SR Data</i>
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### Description

generateDAG creates a directed acyclic graph used for generating spontaneous reporting data

### Usage

```
generateDAG(n_drugs = 10, n_events = 10, n_innocent_bystanders = 5,
            n_correlated_pairs = 2)
```

### Arguments

n_drugs	Number of drugs (Default: 10)
n_events	Number of adverse events (Default: 10)
n_innocent_bystanders	Number of innocent bystanders (Default: 5)
n_correlated_pairs	Number of drug-event pairs that will be associated (Default: 2)

**Value**

The DAG as an igraph object

**See Also**

[simulateSRS](#)

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simulateReport	<i>Simulate a single Report</i>
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**Description**

Returns a single report for a spontaneous reporting system. Note that this function does not check whether the report is 'valid', see [validReport](#)

**Usage**

```
simulateReport(n_drugs, n_events, n_parents, beta0, beta1, parent_id)
```

**Arguments**

n_drugs	The number of drugs
n_events	The number of events
n_parents	A vector with the number of parents for each of the nodes
beta0	A vector with the intercepts for the logistic regression models
beta1	A vector with the regression coefficients for each node
parent_id	A vector with the id of the parent

**Value**

A binary vector

**Description**

simulateSRS simulates a spontaneous reporting (SR) data set. The relationships between the drugs and the adverse events (AEs) are specified by a directed acyclic graph (DAG), see [generateDAG](#).

Each report to a SRS contains two lists:

1. the drugs to which the patient was (thought to be) exposed to, and
2. the AEs that the patient experienced.

We will represent each report as a binary vector. The first items represent whether the patient was exposed to the drug (1 if he/she was, and 0 otherwise). The second part represents whether the patient experienced the event or not (1 if he/she did, and 0 otherwise). For example, if there are 3 drugs and 4 events in total, a typical report could be

0101100

which represents that the patient was exposed to drug 2 (but not to drug 1 and 3), and experienced event 1 and 2 (but not 3 and 4). The simulation results in a binary matrix where each row is a report.

**Valid Reports** Not any binary sequence is a valid report. Each report should contain at least one drug and at least one event (otherwise it would never be sent to the spontaneous reporting system). While generating reports, we make sure that this is indeed the case. When one does not want to check the validity and wants to allow any binary sequence, one can set `valid_reports` to `FALSE`.

**Usage**

```
simulateSRS(n_reports = 100, n_drugs = 10, n_events = 10,
  alpha_drugs = 1, beta_drugs = 20, alpha_events = 1, beta_events = 20,
  n_innocent_bystanders = 5, bystander_prob = 0.9, n_correlated_pairs = 2,
  theta = 2, valid_reports = TRUE, seed = NULL, verbose = TRUE)
```

**Arguments**

<code>n_reports</code>	Number of reports (Default: 100)
<code>n_drugs</code>	Number of drugs (Default: 10)
<code>n_events</code>	Number of adverse drug events (Default: 10)
<code>alpha_drugs</code>	Alpha parameter for the drug marginal probabilities (Default: 1.0)
<code>beta_drugs</code>	Beta parameter for the drug marginal probabilities (Default: 20.0)
<code>alpha_events</code>	Alpha parameter for the event marginal probabilities (Default: 1.0)
<code>beta_events</code>	Beta parameter for the event marginal probabilities (Default: 20.0)
<code>n_innocent_bystanders</code>	Number of innocent bystanders (Default: 5)

bystander_prob	The conditional probability of the innocent bystander being one when the drug that is actually causing the AE is equal to 1. This parameter corresponds to $\gamma$ in the paper (Default: .9)
n_correlated_pairs	Number of drug-AE pairs that are associated (Default: 2)
theta	Increase in odds-ratio when there is an edge going from a drug to an AE (Default: 2.0). In case theta is a vector of length two, the odds ratio is drawn from a truncated Normal distribution with mean theta[1] and variance theta[2]
valid_reports	If TRUE, only valid reports (with at least one drug and at least one AE) are accepted. (Default: TRUE)
seed	The seed used by the RNG (Default: automatically set)
verbose	Verbosity (Default: TRUE)

**Value**

sr	A binary data frame with the simulated reports. The columns are named drug1, drug2 ..., event1, event2, ...
dag	The directed acyceled graph as an igraph object
nodes	A tibble with all the information on each node/variante: <ul style="list-style-type: none"> <li>• label The label for each node/variante</li> <li>• in_degree The number of edges pointing to the node</li> <li>• id The ID of each node (simple integer)</li> <li>• parent_id The ID of the parent node - if any. Otherwise equal to -1</li> <li>• margprob The marginal probability of the node/variante</li> <li>• beta0 The intercept in the logistic regression model for that node</li> <li>• beta1 The regression coefficient in the logistic regression model for the parent</li> </ul>
prob_drugs	A vector with marginal probabilities of the drugs
prob_events	A vector with marginal probabilities of the events

**See Also**

[convert2Tables](#), [generateDAG](#)

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SRSim

*SRSim*

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**Description**

A package for simulating data from spontaneous reporting systems (SRSs). Spontaneous reporting systems are used to

**Author(s)**

Louis Dijkstra & Marco Garling

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`validReport`*Valid Report*

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**Description**

Checks whether the given report is 'valid'. A report should contain at least one drug and at least one event (otherwise it would never been sent to the spontaneous reporting system anyway).

**Usage**

```
validReport(report, n_drugs, n_events)
```

**Arguments**

<code>report</code>	A logical matrix with one row and <code>n_drugs + n_events</code> columns
<code>n_drugs</code>	The total number of drugs
<code>n_events</code>	The total number of events

**Value**

TRUE when the report is valid, FALSE otherwise



# Index

convert2Tables, [2](#), [3](#), [7](#)  
create2x2TablesDAGRcpp, [3](#)

f\_beta0, [4](#)

generateDAG, [4](#), [6](#), [7](#)

simulateReport, [5](#)

simulateSRS, [2-5](#), [6](#)

SRSim, [7](#)

SRSim-package (SRSim), [7](#)

validReport, [5](#), [8](#)