The `mc2d` package

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This documentation is intended for readers with:

- A medium level of experience in R. Please refer to *An Introduction to R* available with the R distribution if needed.
- Some knowledge about Monte-Carlo simulation and Quantitative Risk Assessment (QRA).

The definitive reference for all function arguments remains the package documentation. It is recommended to try the examples while reading.

1 Introduction

1.1 What is `mc2d`?

`mc2d` means Two-Dimensional Monte-Carlo (*Monte-Carlo à 2 Dimensions*). This package provides:

- additional probability distributions;
- tools to construct One-Dimensional and Two-Dimensional Monte-Carlo simulations;
- tools to analyse One-Dimensional and Two-Dimensional Monte-Carlo simulations.

In a previous version, distribution-fitting tools were included; they have since been moved to the separate package `fitdistrplus` [3].

`mc2d` was built for QRA in the Food Safety domain but can be used in other frameworks.

1.2 What is Two-Dimensional Monte-Carlo Simulation (briefly)?

The following text and Figure 1 are adapted from [6] and [7]. The principal reference remains [2].

A QRA should reflect the **variability** in the risk and take into account the **uncertainty** associated with the risk estimate. Variability represents temporal, geographical and/or individual heterogeneity of the risk across the population. Uncertainty stems from a lack of perfect knowledge about the QRA model structure and parameters.[1]

A two-dimensional Monte-Carlo simulation separates variability and uncertainty by sampling their respective distributions independently [2]. The method proceeds as follows (see Figure 1):

1. Parameters are divided into four categories: *fixed*, *variable* (variability only), *uncertain* (uncertainty only), and *variable and uncertain*. For the last category, a hierarchical structure is required, e.g.:

   $$r \mid a, b \sim N(a, b)$$

   where the normal distribution represents variability in r conditional on uncertain parameters a and b, with hyper-distributions such as $a \sim \text{Unif}(l_a, u_a)$ and $b \sim \text{Unif}(l_b, u_b)$.
2. A set of uncertain parameters is randomly sampled from their distributions.
3. The model is evaluated with a one-dimensional Monte-Carlo simulation of size N_v, treating uncertain parameters as fixed. Statistics (mean, SD, percentiles) are computed and stored.
4. Steps 2–3 are repeated N_u times.
5. The 50th percentile (median) of each statistic is the point estimate; the 2.5^{th} and 97.5^{th} percentiles constitute the 95% credible interval.

More formally, in its simplest version the framework is a chain of three random variables:

$$p \to \pi \to Y$$

with marginal distribution $[p]$ and conditional distributions $[\pi \mid p]$ and $[Y \mid \pi]$, under the assumption $[p, \pi, Y] = [p][\pi \mid p][Y \mid \pi]$.

- Y is the variable of interest.
- π is the parameter governing the distribution of Y; its uncertainty is characterised through $[\pi \mid p]$.
- p is the parameter governing the uncertainty of π; its distribution $[p]$ is assumed known.

A two-dimensional Monte-Carlo simulation provides a bundle of N_u distributions $[Y \mid \pi = \pi_i]$ where $\pi_i, i = \{1, \ldots, N_u\}$ are drawn from $[\pi \mid p]$.

`mc2d` uses arrays of (at least) two dimensions: the first dimension reflects variability, the second reflects uncertainty.

[1] In the engineering risk community, these are called *aleatoric uncertainty* for variability and *epistemic uncertainty* for uncertainty.

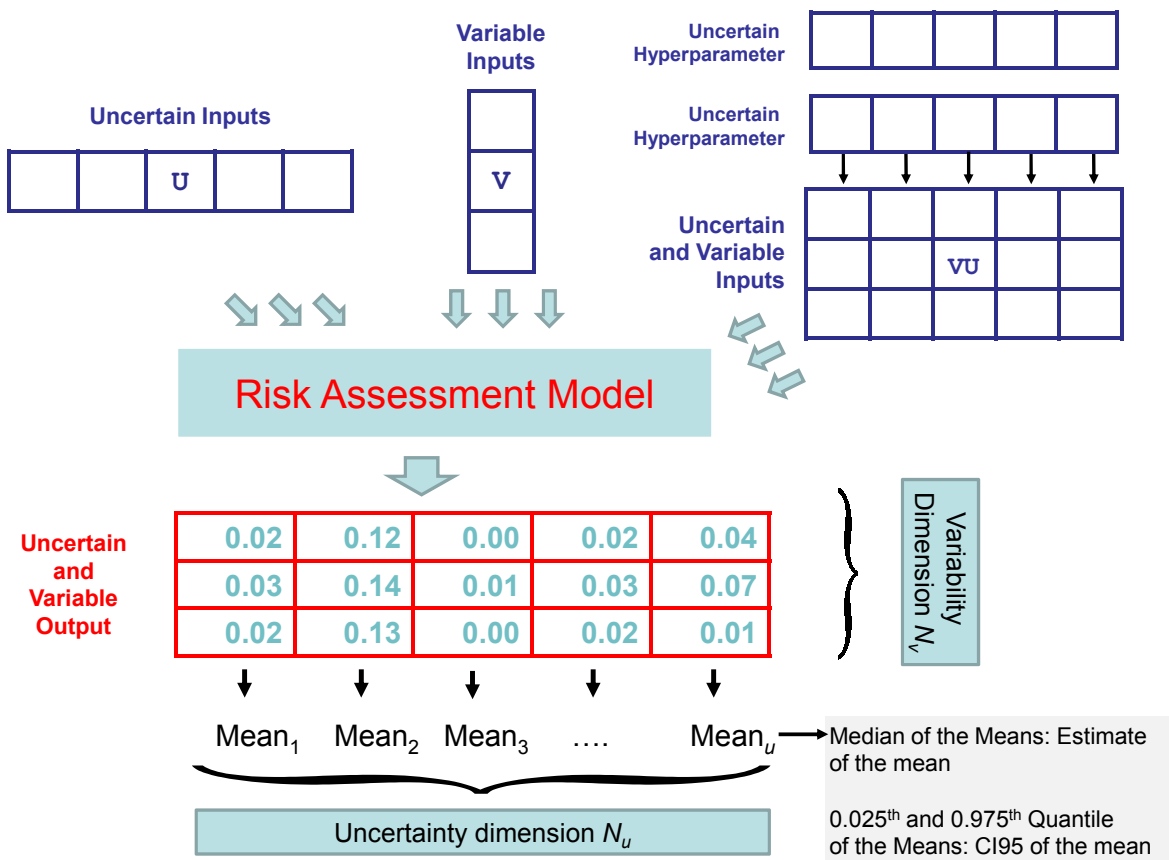


Figure 1: Schematic Representation of a Two-Dimensional Monte-Carlo Simulation.

1.3 A basic example

Quantitative Risk Assessment: *Escherichia coli* O157:H7 infection linked to the consumption of frozen ground beef in <3 year old children.

Warning: the data are fictitious and the model is over-simplified; results should not be interpreted.

The model assumes:

- *E. coli* O157:H7 are randomly distributed in a batch with mean concentration $c = 10$ CFU/g.
- No bacterial growth occurs (product is frozen until cooked just before consumption).
- 2.7% of consumers cook their beef rare, 37.3% medium, and 60.0% well done.
- Bacterial inactivation by cooking: no inactivation (rare), 1/5 surviving (medium), 1/50 surviving (well done).
- Serving size s for <3 year children follows a Gamma distribution: $shape = 3.93$, $rate = 0.0806$.
- The dose-response is a one-hit model with probability of illness per hit $r = 0.001$.

What is the risk of illness in the population that consumed the contaminated lot?

1.3.1 One-Dimensional Monte-Carlo Simulation

All distributions represent variability only:

$$c = 10, \quad i \sim emp(\{1, 1/5, 1/50\}, \{0.027, 0.373, 0.600\}), \quad s \sim \text{Gamma}(3.93, 0.0806)$$

$$n \sim \text{Poisson}(c \times i \times s), \quad r = 0.001, \quad P = 1 - (1 - r)^n$$

```r
library(mc2d)
```

```
## Loading required package: mvtnorm

##
## Attaching package: 'mc2d'

## The following objects are masked from 'package:base':
##
##     pmax, pmin
```

```r
ndvar(1001)
```

```
## [1] 1001
```

```r
conc    <- 10
cook    <- mcstoc(rempiricalD, values = c(1, 1/5, 1/50), prob = c(0.027, 0.373, 0.600))
serving <- mcstoc(rgamma, shape = 3.93, rate = 0.0806)
expo    <- conc * cook * serving
dose    <- mcstoc(rpois, lambda = expo)
r       <- 0.001
risk    <- 1 - (1 - r)^dose
EC1     <- mc(cook, serving, expo, dose, risk)
print(EC1)
```

```
##      node    mode  nsv nsu nva variate  min    mean  median     max Nas type outm
## 1    cook numeric 1001   1   1       1 0.02  0.1165  0.0200   1.000   0    V each
## 2 serving numeric 1001   1   1       1 5.17 48.3735 43.9192 219.976   0    V each
## 3    expo numeric 1001   1   1       1 1.03 56.0684 14.0630 987.649   0    V each
## 4    dose numeric 1001   1   1       1 0.00 56.1618 15.0000 962.000   0    V each
## 5    risk numeric 1001   1   1       1 0.00  0.0508  0.0149   0.618   0    V each
```

```r
summary(EC1)
```

```
## cook :
##        mean    sd  Min 2.5%  25%  50% 75% 97.5% Max  nsv Na's
## NoUnc 0.117 0.176 0.02 0.02 0.02 0.02 0.2     1   1 1001    0
##
## serving :
##       mean   sd  Min 2.5%  25%  50%  75% 97.5% Max  nsv Na's
## NoUnc 48.4 24.3 5.17 14.5 29.8 43.9 62.5   103 220 1001    0
##
## expo :
##       mean   sd  Min 2.5%  25%  50%  75% 97.5% Max  nsv Na's
## NoUnc 56.1 96.2 1.03  3.1 8.17 14.1 79.7   259 988 1001    0
##
## dose :
##       mean   sd Min 2.5% 25% 50% 75% 97.5% Max  nsv Na's
## NoUnc 56.2 96.1   0    2   7  15  79   262 962 1001    0
##
## risk :
##         mean     sd Min  2.5%     25%    50%   75% 97.5%   Max  nsv Na's
## NoUnc 0.0508 0.0753   0 0.002 0.00698 0.0149 0.076 0.231 0.618 1001    0
```

The `print` output shows for each node: the variable mode, `nsv` (variability dimension size), `nsu` (uncertainty dimension size), `nva` (number of variates), basic statistics (min, mean, median, max), number of missing values (`Nas`), the node type (`0` = fixed, `V` = variable, `U` = uncertain, `VU` = variable and uncertain), and the output level `outm`.

This one-dimensional simulation gives a mean risk of approximately 5%, with 2.5% of the population having a risk greater than 20.3%.

1.3.2 Two-Dimensional Monte-Carlo Simulation

Adding uncertainty: the mean concentration c follows $N(10, 2)$ and the parameter r follows $\text{Unif}(0.0005, 0.0015)$:

$$c \sim N(10, 2), \quad i, s \text{ as before}, \quad n \sim \text{Poisson}(c \times i \times s), \quad r \sim \text{Unif}(0.0005, 0.0015), \quad P = 1 - (1 - r)^n$$

```r
ndunc(101)
```

```
## [1] 101
```

```r
conc    <- mcstoc(rnorm,       type = "U",  mean = 10, sd = 2)
cook    <- mcstoc(rempiricalD, type = "V",  values = c(1, 1/5, 1/50), prob = c(0.027, 0.373, 0.600))
serving <- mcstoc(rgamma,      type = "V",  shape = 3.93, rate = 0.0806)
expo    <- conc * cook * serving
```

```r
dose    <- mcstoc(rpois,       type = "VU", lambda = expo)
r       <- mcstoc(runif,       type = "U",  min = 0.0005, max = 0.0015)
risk    <- 1 - (1 - r)^dose
EC2     <- mc(conc, cook, serving, expo, dose, r, risk)
print(EC2, digits = 2)
```

```
##      node    mode  nsv nsu nva variate     min    mean median     max Nas type outm
## 1    conc numeric    1 101   1       1 5.91980 1.0e+01 10.045 1.6e+01   0    U each
## 2    cook numeric 1001   1   1       1 0.02000 1.1e-01  0.020 1.0e+00   0    V each
## 3 serving numeric 1001   1   1       1 2.66586 5.0e+01 44.942 1.6e+02   0    V each
## 4    expo numeric 1001 101   1       1 0.75130 5.4e+01 13.910 1.6e+03   0   VU each
## 5    dose numeric 1001 101   1       1 0.00000 5.4e+01 14.000 1.5e+03   0   VU each
## 6       r numeric    1 101   1       1 0.00052 9.8e-04  0.001 1.5e-03   0    U each
## 7    risk numeric 1001 101   1       1 0.00000 4.7e-02  0.014 8.4e-01   0   VU each
```

```r
summary(EC2)
```

```
## conc :
##        NoVar
## median 10.05
## mean   10.10
## 2.5%    6.03
## 97.5%  14.20
##
## cook :
##        mean    sd  Min 2.5%  25%  50% 75% 97.5% Max  nsv Na's
## NoUnc 0.107 0.166 0.02 0.02 0.02 0.02 0.2   0.2   1 1001    0
##
## serving :
##       mean   sd  Min 2.5% 25%  50%  75% 97.5% Max  nsv Na's
## NoUnc 49.6 24.9 2.67 13.6  31 44.9 63.9   110 161 1001    0
##
## expo :
##        mean    sd   Min 2.5%   25%   50%   75% 97.5%  Max  nsv Na's
## median 53.7  95.6 1.275 3.36  8.10 14.14  75.8   243  960 1001    0
## mean   54.0  96.2 1.282 3.38  8.15 14.22  76.2   244  966 1001    0
## 2.5%   32.2  57.4 0.765 2.02  4.86  8.48  45.5   146  576 1001    0
## 97.5%  75.9 135.2 1.802 4.75 11.45 19.98 107.1   343 1356 1001    0
##
## dose :
##        mean    sd    Min 2.5%   25%  50%   75% 97.5%  Max  nsv Na's
## median 53.5  96.5 0.0000 2.00  8.00 14.0  76.0   245  946 1001    0
## mean   54.1  96.5 0.0495 2.08  7.63 14.4  74.7   252  964 1001    0
## 2.5%   32.3  57.6 0.0000 1.00  4.50  9.0  45.0   152  592 1001    0
## 97.5%  76.4 136.3 1.0000 3.50 11.50 20.5 105.5   364 1407 1001    0
##
## r :
##           NoVar
## median 0.001006
## mean   0.000976
## 2.5%   0.000536
```

```
## 97.5%  0.001480
##
## risk :
##          mean     sd      Min     2.5%     25%     50%    75% 97.5%   Max  nsv Na's
## median 0.0457 0.0714 0.00e+00 0.001925 0.00714 0.01340 0.0658 0.210 0.583 1001    0
## mean   0.0473 0.0728 5.41e-05 0.002032 0.00744 0.01399 0.0702 0.216 0.588 1001    0
## 2.5%   0.0238 0.0397 0.00e+00 0.000653 0.00345 0.00657 0.0336 0.110 0.360 1001    0
## 97.5%  0.0794 0.1133 9.40e-04 0.003996 0.01372 0.02535 0.1234 0.359 0.807 1001    0
```

The `type` argument indicates whether a distribution represents variability (`"V"`, default), uncertainty (`"U"`), or both (`"VU"`). The median of the 101 simulations gives a best estimate of 0.0457 with a 95% credible interval of [0.0238, 0.0794].

2 Basic Principles and Functions

A typical `mc2d` session:

1. Choose an empirical or parametric distribution for each parameter (`fitdistrplus` [3] is a convenient fitting tool).
2. Construct an `mcnode` object for each parameter (`mcdata`, `mcstoc`).
3. Group `mcnode` objects into an `mc` object (`mc`).
4. Study the `mc` object via summaries, graphs, and sensitivity analysis (`summary.mc`, `plot.mc`, `tornado`, `tornadounc`).

2.1 Preliminary Step

Load `mc2d` at the start of your R session with `library(mc2d)`. Set the default Monte-Carlo dimensions with `ndvar()` (variability) and `ndunc()` (uncertainty).

2.2 The `mcnode` Object

2.2.1 `mcnode` Object Structure

An `mcnode` is the basic element of an `mc` object — it is associated with one variable, while an `mc` is a set of associated variables.

An `mcnode` is an array of dimension ($nsv \times nsu \times nvariates$).[2] Four types exist:

- `V` **mcnode** (Variability): dimension ($nsv \times 1 \times nvariates$).
- `U` **mcnode** (Uncertainty): dimension ($1 \times nsu \times nvariates$).
- `VU` **mcnode** (Variability and Uncertainty): dimension ($nsv \times nsu \times nvariates$).
- `0` **mcnode** (Neither): dimension ($1 \times 1 \times nvariates$). Not needed in the univariate context but useful for multivariate nodes (Section 3).

Ways to construct an `mcnode`:

1. `mcstoc` — from random number generating functions.

[2] In this section we only consider univariate nodes with $nvariates = 1$.

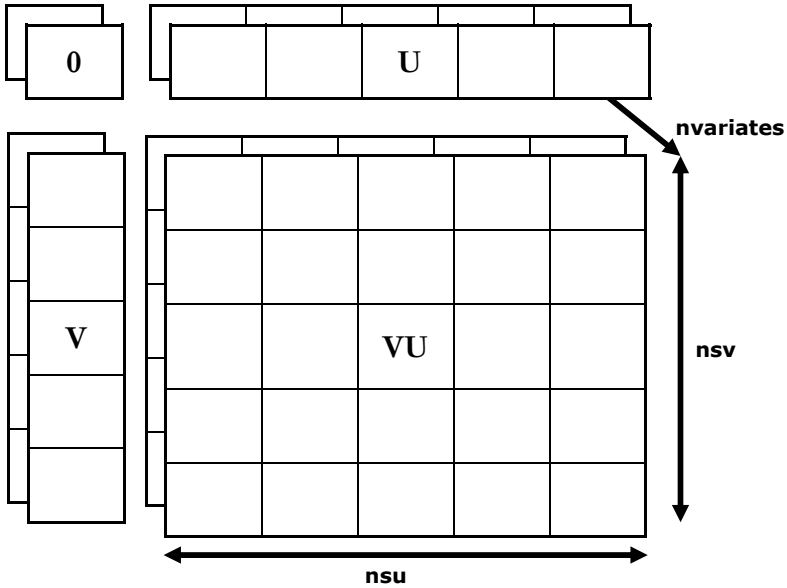


Figure 2: Structure of the various ‘mcnode‘ objects.

2. `mcdata` — from data.
3. Direct operations on `mcnode` objects.
4. `mcprobtree` — from a mixture of distributions (probability tree).
5. Functions such as `==`, `>`, `is.na`, `is.finite` applied to an existing `mcnode`.

2.2.2 The `mcstoc` function

```
mcstoc(func=runif, type=c("V","U","VU","O"), ...,
       nsv=ndvar(), nsu=ndunc(), nvariates=1, outm="each",
       nsample="n", seed=NULL, rtrunc=FALSE, linf=-Inf, lsup=Inf, lhs=FALSE)
```

- `func`: random-data function or its name as a character. Table 1 lists available distributions.
- `type`: type of `mcnode` to build. Default: `"V"`.
- `...`: arguments passed to `func` (except the sample size). *All must be named.*
- `nsv`, `nsu`: number of samples in variability/uncertainty dimensions.
- `nvariates`: number of variates (Section 3).
- `outm`: default output for multivariate nodes (Section 3).
- `nsample`: name of the sample-size argument of `func` (usually `"n"`; use `"nn"` for `rhyper` and `rwilcox`).
- `seed`: random seed. If `NULL`, seed is unchanged.
- `rtrunc`: truncate the distribution between `linf` and `lsup`.
- `lhs`: use Latin Hypercube Sampling.

In our example, `mcstoc` specified `conc` (normal), `cook` (empirical discrete), `serving` (gamma), and `dose` (Poisson with `mcnode` argument `lambda`).

Table 1: Available distributions

Package	Distribution	Function	Size arg.	Other parameters	trunc	lhs
‘stats‘	beta	‘rbeta‘	‘n‘	‘shape1, shape2, ncp‘	Y	Y
	binomial	‘rbinom‘	‘n‘	‘size, prob‘	Y	Y
	Cauchy	‘rcauchy‘	‘n‘	‘location, scale‘	Y	Y
	chi-squared	‘rchisq‘	‘n‘	‘df, ncp‘	Y	Y
	exponential	‘rexp‘	‘n‘	‘rate‘	Y	Y
	F	‘rf‘	‘n‘	‘df1, df2, ncp‘	Y	Y
	gamma	‘rgamma‘	‘n‘	‘shape, rate (or scale)‘	Y	Y
	geometric	‘rgeom‘	‘n‘	‘prob‘	Y	Y
	hypergeometric	‘rhyper‘	‘nn‘	‘m, n, k‘	Y	Y
	lognormal	‘rlnorm‘	‘n‘	‘meanlog, sdlog‘	Y	Y
	logistic	‘rlogis‘	‘n‘	‘location, scale‘	Y	Y
	neg. binomial	‘rnbinom‘	‘n‘	‘size, prob (or mu)‘	Y	Y
	normal	‘rnorm‘	‘n‘	‘mean, sd‘	Y	Y
	Poisson	‘rpois‘	‘n‘	‘lambda‘	Y	Y
	Student’s t	‘rt‘	‘n‘	‘df, ncp‘	Y	Y
	uniform	‘runif‘	‘n‘	‘min, max‘	Y	Y
	Weibull	‘rweibull‘	‘n‘	‘shape, scale‘	Y	Y
	Wilcoxon	‘rwilcox‘	‘nn‘	‘m, n‘	Y	Y
‘mc2d‘	Bernoulli	‘rbern‘	‘n‘	‘prob‘	Y	Y
	emp. discrete	‘rempiricalD‘	‘n‘	‘values, prob‘	Y	Y
	emp. cont.	‘rempiricalC‘	‘n‘	‘min, max, values, prob‘	Y	Y
	PERT	‘rpert‘	‘n‘	‘min, mode, max, shape‘	Y	Y
	triangular	‘rtriang‘	‘n‘	‘min, mode, max‘	Y	Y
	gen. beta	‘rbetagen‘	‘n‘	‘shape1,shape2,min,max,ncp‘	Y	Y
	multinomial	‘rmultinomial‘	‘n‘	‘size, prob‘	N	N
	Dirichlet	‘rdirichlet‘	‘n‘	‘alpha‘	N	N
	mv. normal	‘rmultinormal‘	‘n‘	‘mean, sigma‘	N	N
	beta subjective	‘rbetasubj‘	‘n‘	‘min, mode, mean, max‘	Y	Y
	min. info.	‘rmqi‘	‘n‘	‘mqi, mqi.quantile, ...‘	Y	Y

```r
conc    <- mcstoc(rnorm,       type = "U",  mean = 10, sd = 2)
cook    <- mcstoc(rempiricalD, type = "V",  values = c(1, 1/5, 1/50), prob = c(0.027, 0.373, 0.600))
serving <- mcstoc(rgamma,      type = "V",  shape = 3.93, rate = 0.0806)
dose    <- mcstoc(rpois,       type = "VU", lambda = expo)
r       <- mcstoc(runif,       type = "U",  min = 0.0005, max = 0.0015)
```

A normal distribution $N(2, 3)$ truncated on $[1.5, 2]$ with Latin Hypercube Sampling:[3]

```r
x <- mcstoc(rnorm, mean = 2, sd = 3, rtrunc = TRUE, linf = 1.5, lsup = 2, lhs = TRUE)
summary(x)
```

```
## node :
##       mean    sd Min 2.5%  25%  50%  75% 97.5% Max  nsv Na's
## NoUnc 1.75 0.144 1.5 1.51 1.63 1.75 1.88  1.99   2 1001    0
```

Additional distributions in `mc2d`: `rbern` (Bernoulli), `rempiricalD` (empirical discrete), `rpert` [8], `rtriang`, `rdirichlet`, `rmultinormal`, `rmqi` (min. quantile info.). The multinomial distribution is vectorized as `rmultinomial` (use instead of `stats::rmultinom`).

2.2.3 The `mcdata` function

```r
mcdata(data, type=c("V","U","VU","0"), nsv=ndvar(), nsu=ndunc(), nvariates=1, outm="each")
```

See the function documentation for accepted data sizes and types. Example — placing `TRUE` in a `"U"` node for half the simulations:

```r
nu  <- ndunc()
tmp <- (1:nu) > (nu/2)
mcdata(tmp, type = "U")
```

```
##   node    mode nsv nsu nva variate min  mean median max Nas type outm
## 1    x logical   1 101   1       1   0 0.505      1   1   0    U each
```

2.2.4 Operations on an `mcnode`

`mcnode` objects support arithmetic operations with coherent type propagation (Table 2).[4]

- `0` + `0` = `0`; `0` + `V` = `V`; `0` + `U` = `U`; `0` + `VU` = `VU`
- `V` + `V` = `V`; `V` + `U` = `VU`[5]; `V` + `VU` = `VU`[6]
- `U` + `U` = `U`; `U` + `VU` = `VU`[7]; `VU` + `VU` = `VU`

[3] The mean and SD of the non-truncated distribution are not preserved after truncation.
[4] These rules differ from standard R recycling rules.
[5] `U` is recycled by row; `V` classically by column.
[6] `V` recycled by column.
[7] `U` recycled by row.

Table 2: ‘mcnode‘ combination types

	0	V	U	VU
0	0	V	U	VU
V	V	V	VU	VU
U	U	VU	U	VU
VU	VU	VU	VU	VU

```
expo <- conc * cook * serving   # U * V * V → VU
risk <- 1 - (1 - r)^dose        # U * VU → VU
```

2.2.5 The mcprobtree function

`mcprobtree` builds an `mcnode` as a mixture of distributions. If the microbiologists are 75% sure that $conc \sim N(10, 2)$ and 25% sure that $conc \sim U(8, 12)$:[8]

```
conc1    <- mcstoc(rnorm,  type = "U", mean = 10, sd = 2)
conc2    <- mcstoc(runif,  type = "U", min = 8, max = 12)
whichdist <- c(0.75, 0.25)
concbis   <- mcprobtree(whichdist, list("0" = conc1, "1" = conc2), type = "U")
```

`mcprobtree` can also generate samples from a mixture for variability.

2.2.6 Other functions for constructing an mcnode

Comparison operators (`==`, `<`, `<=`, `>=`, `>`) generate an `mcnode` when applied to one. Special functions `is.na`, `is.nan`, `is.finite`, `is.infinite` are also implemented.

```
cook < 1
```

```
##   node    mode  nsv nsu nva variate min  mean median max Nas type outm
## 1    x logical 1001   1   1       1   0 0.975      1   1   0    V each
```

```
suppressWarnings(tmp <- log(mcstoc(runif, min = -1, max = 1)))
tmp
```

```
##   node    mode  nsv nsu nva variate   min  mean median    max Nas type outm
## 1    x numeric 1001   1   1       1 -7.08 -1.08 -0.777 -0.001 481    V each
```

```
is.na(tmp)
```

```
##   node    mode  nsv nsu nva variate min  mean median max Nas type outm
## 1    x logical 1001   1   1       1   0 0.481      0   1   0    V each
```

[8] Alternatives for `whichdist`: `mcstoc(rempiricalD, type="U", values=c(0,1), prob=c(75,25))` or `mcstoc(rbern, type="U", prob=0.25)`.

2.2.7 Specifying a correlation between mcnodes

A Spearman rank correlation structure between 2 or more nodes can be specified with `cornode`, which uses the Iman & Conover method [4].[9]

```
cornode(cook, serving, target = 0.5, result = TRUE)
```

```
## output Rank Correlation per variates
## variates: 1
## [1] 1.000 0.396 0.396 1.000
```

```
## $cook
##   node    mode  nsv nsu nva variate  min  mean median max Nas type outm
## 1    x numeric 1001   1   1       1 0.02 0.107   0.02   1   0    V each
##
## $serving
##   node    mode  nsv nsu nva variate  min mean median max Nas type outm
## 1    x numeric 1001   1   1       1 2.67 49.6   44.9 161   0    V each
```

Correlations can be specified between `V`, `U`, or `VU` nodes, or between one `V` node and multiple `VU` nodes. A multivariate normal distribution (`rmultinormal`) is another way to specify correlations assuming normality.

2.3 The mc Object

Once `mcnode` objects are constructed, group them into an `mc` object for analysis. An `mc` is a list of `mcnodes`. It can be constructed with `mc()`, `evalmcmod()`, or within `evalmccut()`.

2.3.1 The mc function

```
mc(..., name=NULL, devname=FALSE)
```

`...` are `mcnode` or `mc` objects. In our example:

```
EC2 <- mc(conc, cook, serving, expo, dose, r, risk)
print(EC2)
summary(EC2)
```

2.3.2 The mcmodel and evalmcmod functions

`mcmodel` wraps a model expression for later evaluation with `evalmcmod`. Use this once the model is validated, to re-run it with different dimensions or seeds in one line.

```
modelEC3 <- mcmodel({
  conc    <- mcstoc(rnorm,       type = "U",  mean = 10, sd = 2)
  cook    <- mcstoc(rempiricalD, type = "V",  values = c(1, 1/5, 1/50), prob = c(0.027, 0.373, 0.600))
  serving <- mcstoc(rgamma,      type = "V",  shape = 3.93, rate = 0.0806)
```

[9] The resulting correlation (~0.4) is an approximation because a discrete distribution (`cook`: 3 categories) is correlated with a continuous distribution (`serving`).

```r
  r       <- mcstoc(runif,       type = "U",  min = 0.0005, max = 0.0015)
  expo    <- conc * cook * serving
  dose    <- mcstoc(rpois,       type = "VU", lambda = expo)
  risk    <- 1 - (1 - r)^dose
  mc(conc, cook, serving, expo, dose, r, risk)
})
modelEC3
```

```
## expression({
##     conc <- mcstoc(rnorm, type = "U", mean = 10, sd = 2)
##     cook <- mcstoc(rempiricalD, type = "V", values = c(1, 1/5,
##         1/50), prob = c(0.027, 0.373, 0.6))
##     serving <- mcstoc(rgamma, type = "V", shape = 3.93, rate = 0.0806)
##     r <- mcstoc(runif, type = "U", min = 5e-04, max = 0.0015)
##     expo <- conc * cook * serving
##     dose <- mcstoc(rpois, type = "VU", lambda = expo)
##     risk <- 1 - (1 - r)^dose
##     mc(conc, cook, serving, expo, dose, r, risk)
## })
## attr(,"class")
## [1] "mcmodel"
```

Notes:

- The model is wrapped between `{` and `}`.
- Any valid R code is allowed inside.[10]
- The model must end with an `mc()` call.

```
evalmcmod(expr, nsv=ndvar(), nsu=ndunc(), seed=NULL)
```

```r
EC3 <- evalmcmod(modelEC3, nsv = 100, nsu = 10,   seed = 666)
EC4 <- evalmcmod(modelEC3, nsv = 100, nsu = 1000, seed = 666)
```

2.3.3 The `mcmodelcut` and `evalmccut` functions

For high-dimensional models that exceed R's memory limit, `evalmccut` evaluates the model in a loop over the uncertainty dimension, computing and storing statistics at each step.[11]

```r
modEC4 <- mcmodelcut({
  ## First block: unidimensional nodes
  {
    cook    <- mcstoc(rempiricalD, type = "V",  values = c(0, 1/5, 1/50), prob = c(0.027, 0.373, 0.6))
    serving <- mcstoc(rgamma,      type = "V",  shape = 3.93, rate = 0.0806)
    conc    <- mcstoc(rnorm,       type = "U",  mean = 10, sd = 2)
    r       <- mcstoc(runif,       type = "U",  min = 5e-04, max = 0.0015)
  }
  ## Second block: two-dimensional nodes → mc object
```

[10] The simulation dimensions can be referenced via `ndvar()` and `ndunc()` if needed.
[11] Using a `tornado` inside the model should be avoided as it slows `evalmccut` considerably.

```r
  {
    expo <- conc * cook * serving
    dose <- mcstoc(rpois, type = "VU", lambda = expo)
    risk <- 1 - (1 - r)^dose
    res  <- mc(conc, cook, serving, expo, dose, r, risk)
  }
  ## Third block: statistics
  {
    list(
      sum    = summary(res),
      plot   = plot(res, draw = FALSE),
      minmax = lapply(res, range),
      tor    = tornado(res),
      et     = sapply(res, sd)
    )
  }
})
res <- evalmccut(modEC4, nsv = 10001, nsu = 101, seed = 666)
summary(res)
```

2.4 Analysing an mc Object

2.4.1 The summary function

```
summary(object, probs=c(0,0.025,0.25,0.5,0.75,0.975,1), lim=c(0.025,0.975), ...)
```

Quantiles in `probs` are evaluated in the variability dimension; then the median and `lim` quantiles are evaluated across those statistics.

```r
tmp <- summary(EC2, probs = c(0.995, 0.999), digits = 12)
tmp$risk
```

```
##          mean     sd 99.5% 99.9%  nsv Na's
## median 0.0457 0.0714 0.464 0.525 1001    0
## mean   0.0473 0.0728 0.465 0.523 1001    0
## 2.5%   0.0238 0.0397 0.265 0.318 1001    0
## 97.5%  0.0794 0.1133 0.681 0.761 1001    0
## attr(,"type")
## [1] "VU"
```

2.4.2 The hist function

```
hist(x, griddim=NULL, xlab=names(x), ylab="Frequency", main="", ...)
```

Provides histograms of each `mcnode` in the `mc` object. Note: variability and uncertainty are collapsed, so the histogram may be approximate.

```r
hist(EC2)
```

From `mc2d` version 0.2-0, `gghist` provides a `ggplot2`-based histogram, returning a `ggplot2` object that can be further customised with `+` operators.

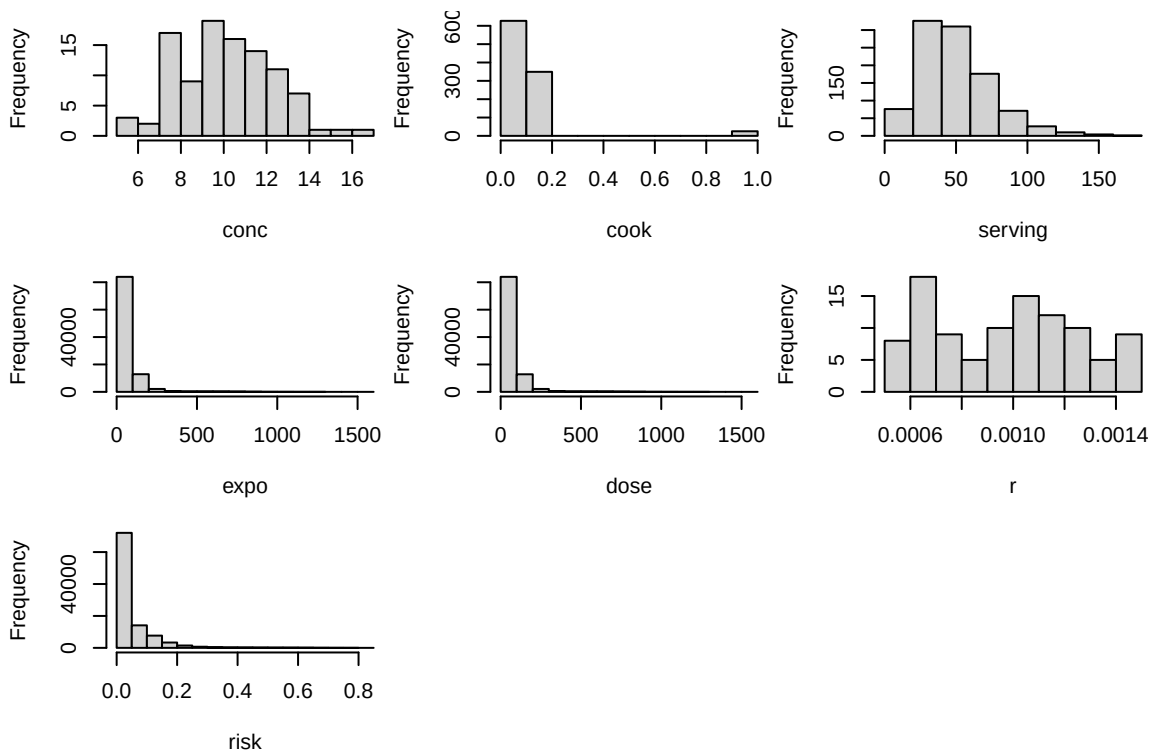


Figure 3: The `hist` function.

2.4.3 The `plot` function

```
plot(x, prec=0.001, stat=c("median","mean"), lim=c(0.025,0.25,0.75,0.975),
     na.rm=TRUE, griddim=NULL, xlab=NULL, ylab="Fn(x)", main="",
     draw=TRUE, paint=TRUE, ...)
```

Plots the empirical CDF with uncertainty envelope. The 0.25 and 0.75 quantiles (default `lim`) form the inner envelope.

```
plot(EC2)
```

From `mc2d` version 0.2-0, `ggplotmc` provides a `ggplot2`-based version.

`spaghetti` draws individual empirical CDF step-functions, one per uncertainty sample, instead of the summary envelope produced by `plot`. The `maxlines` argument caps the number of lines drawn.

```
spaghetti(x, griddim=NULL, xlab=names(x), ylab="F(n)", main="", maxlines=100, ...)
```

```
spaghetti(EC2)
```

`ggspaghetti` provides the same plot via `ggplot2`.

All `mcnode` objects support the same `print`, `summary`, `plot`, and `hist` methods. `ggplotmc`, `gghist`, and `ggspaghetti` on an `mcnode` allow post-processing of the graph.

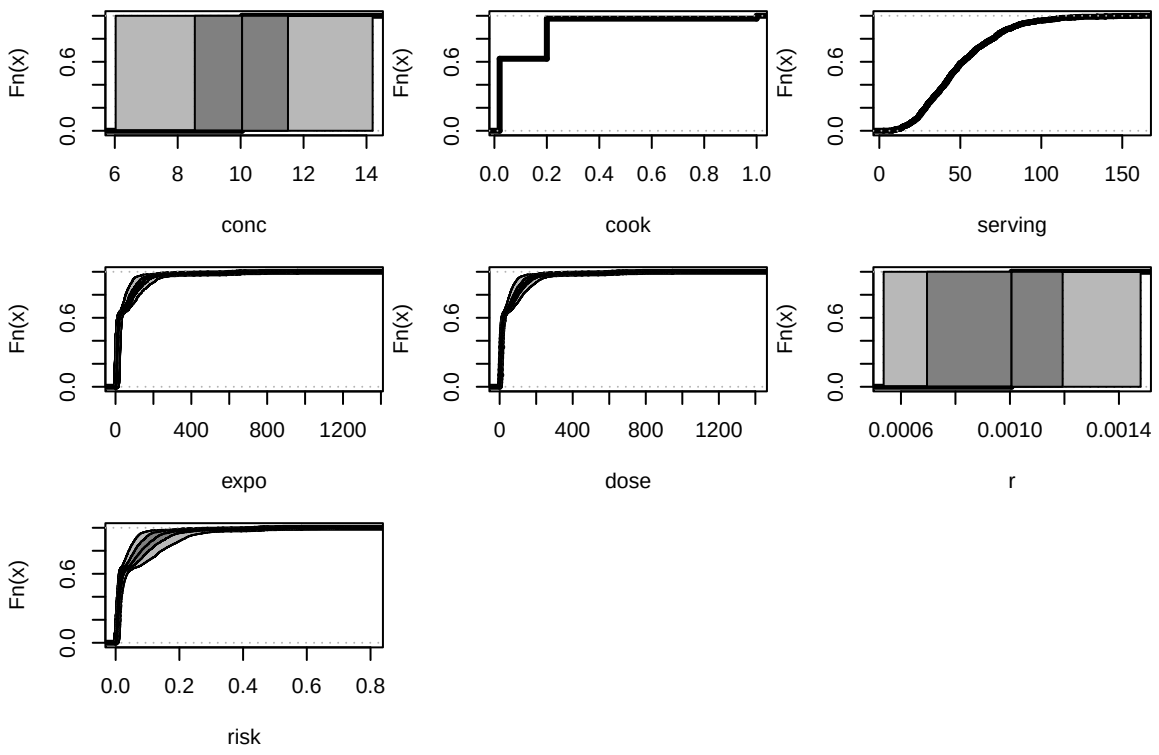


Figure 4: The `plot` function.

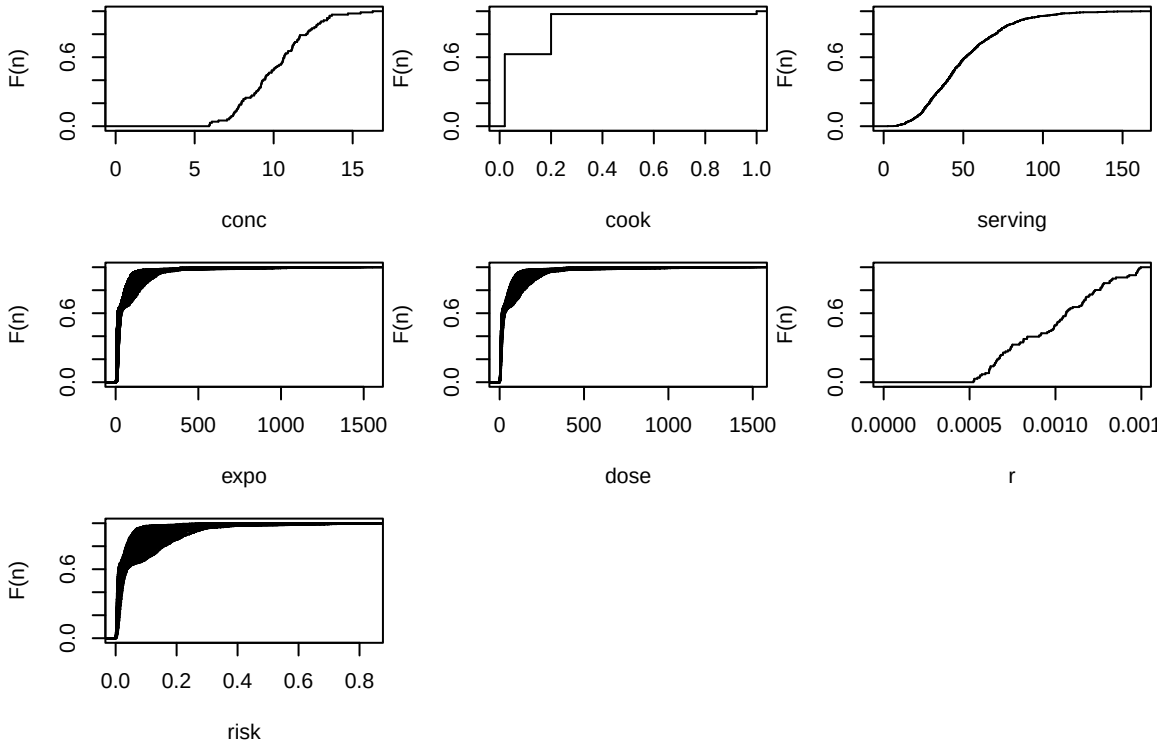


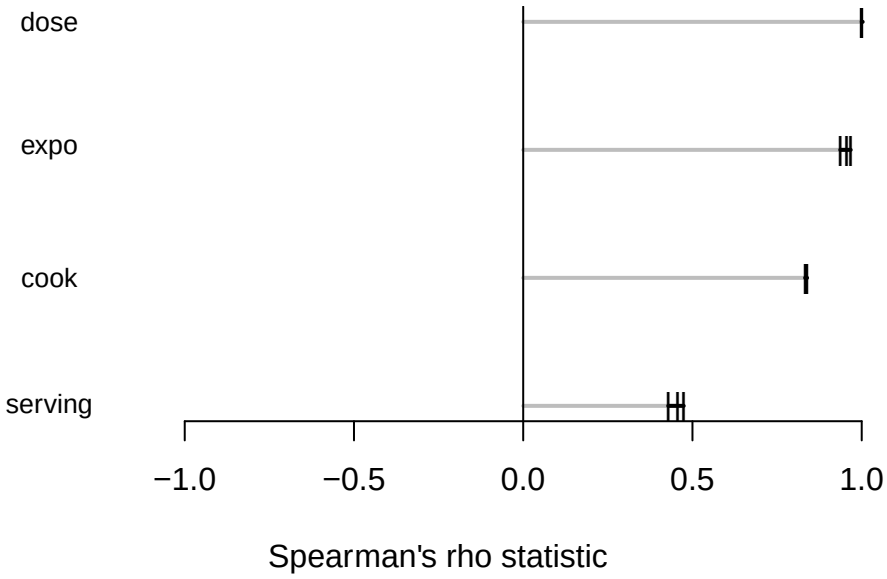
Figure 5: The `spaghetti` function.

2.4.4 The `tornado` function

```
tornado(x, output=length(x), use="all.obs", method=c("spearman","kendall","pearson"),
        lim=c(0.025,0.975))
```

Computes Spearman (default) rank correlation between nodes. `output` specifies the output node (default: last). `tornado` creates a `tornado` object with a `plot` method.

```
torEC2 <- tornado(EC2)
plot(torEC2)
```



From `mc2d` version 0.2-0, `ggtornado` provides a `ggplot2`-based version.

2.4.5 The `tornadounc` function

```
tornadounc(mc, output=length(mc), quant=c(0.5,0.75,0.975),
           use="all.obs", method=c("spearman","kendall","pearson"), ...)
```

Examines the impact of uncertainty on an output estimate. Computes Spearman rank correlation between statistics of `mcnode` objects in the variability dimension. `quant` specifies which quantiles to use.

```
tornadounc(EC2, output = "risk", quant = .99)
```

```
## Tornado on uncertainty
## Spearman's rho statistic
## Output:  risk
```

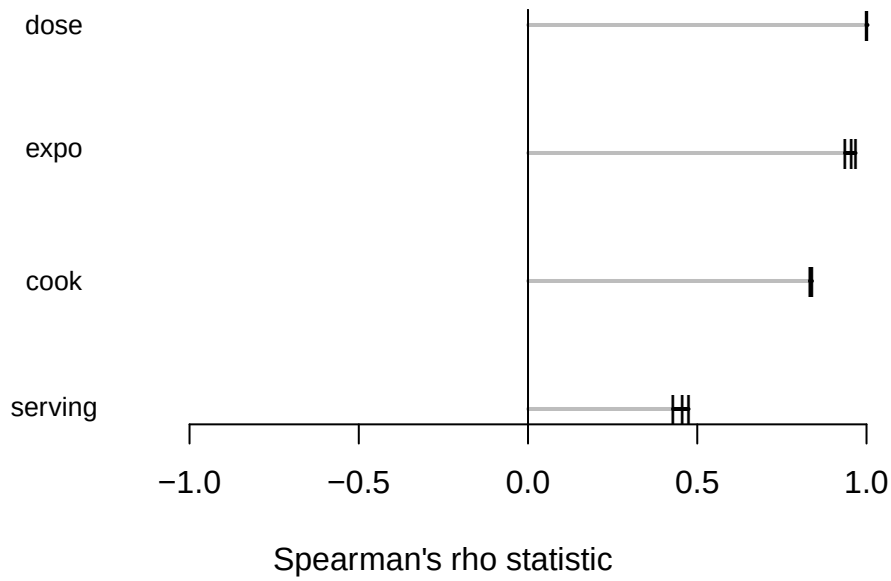


Figure 6: The `plot.tornado` function.

```
## $risk
##            conc mean expo sd expo 99% expo mean dose sd dose 99% dose     r
## mean risk 0.612     0.612   0.612    0.612     0.610   0.609    0.614 0.813
## sd risk   0.611     0.611   0.611    0.611     0.609   0.608    0.613 0.813
## 99% risk  0.611     0.611   0.611    0.611     0.609   0.608    0.616 0.811
```

The output shows the impact of uncertain `U` nodes and statistics (mean, median, 99th percentile) computed in the variability dimension of `VU` nodes.

2.4.6 The `mcratio` function

Provides variability, uncertainty, and combined measures [5]. Given:

- **A** = median of uncertainty for the median of variability
- **B** = median of uncertainty for the 97.5th percentile of variability
- **C** = 97.5th percentile of uncertainty for the median of variability
- **D** = 97.5th percentile of uncertainty for the 97.5th percentile of variability

Ratios: Variability = B/A; Uncertainty = C/A; Overall Uncertainty = D/A.

```
mcratio(risk)
```

```
##           A    B      C     D VariabilityR UncertaintyR Over.Unc.R
## risk 0.0134 0.21 0.0254 0.359         15.6         1.89       26.8
```

2.5 Other Functions and mc Objects

mc objects are simply lists of three-dimensional arrays. $ extracts an mcnode. unmc removes attributes and collapses unit dimensions to return vectors, matrices, or arrays.

```
tmp  <- unmc(EC2, drop = TRUE)
dimu <- ncol(tmp$risk)
coef <- sapply(1:dimu, function(x) lm(tmp$risk[, x] ~ tmp$dose[, x])$coef)
apply(coef, 1, summary)
```

```
##         (Intercept) tmp$dose[, x]
## Min.        0.00117      0.000461
## 1st Qu.     0.00335      0.000593
## Median      0.00592      0.000773
## Mean        0.00702      0.000752
## 3rd Qu.     0.00966      0.000861
## Max.        0.02083      0.001140
```

3 Multivariate Nodes

The nvariates dimension is the third dimension of an mcnode. It is mandatory for multivariate distributions, and useful in other situations.

Note that:

```
mcstoc(runif, nvariates = 3, min = c(1, 2, 3), max = 4)
```

```
##   node    mode  nsv nsu nva variate  min mean median max Nas type outm
## 1    x numeric 1001   1   3       1 1.04 3.02   3.21   4   0    V each
## 2    x numeric 1001   1   3       2 1.00 3.00   3.18   4   0    V each
## 3    x numeric 1001   1   3       3 1.01 2.97   3.14   4   0    V each
```

does **not** produce a node with 3 variates each having a different lower limit — the vector c(1,2,3) is recycled along the variability dimension (standard R behaviour). Use instead:

```
lim <- mcdata(c(1, 2, 3), type = "0", nvariates = 3)
mcstoc(runif, nvariates = 3, min = lim, max = 4)
```

```
##   node    mode  nsv nsu nva variate min mean median max Nas type outm
## 1    x numeric 1001   1   3       1   1 2.50   2.51   4   0    V each
## 2    x numeric 1001   1   3       2   2 2.95   2.90   4   0    V each
## 3    x numeric 1001   1   3       3   3 3.51   3.51   4   0    V each
```

3.1 Multivariate Nodes for Multivariate Distributions

The primary use of multivariate nodes is for multivariate distributions: Dirichlet, multinomial, multivariate normal, and empirical.

Example 1. Three-member families each buy 500 g of ground beef. The proportions eaten by the baby, older brother, and mother follow a Dirichlet ($\alpha = (2, 3, 5)$) distribution.

```r
(p <- mcstoc(rdirichlet,    type = "U",  nvariates = 3, alpha = c(2, 3, 5)))
```

```
##   node    mode nsv nsu nva variate     min  mean median   max Nas type outm
## 1    x numeric   1 101   3       1 0.00389 0.184  0.173 0.486   0    U each
## 2    x numeric   1 101   3       2 0.04085 0.290  0.281 0.593   0    U each
## 3    x numeric   1 101   3       3 0.21786 0.526  0.519 0.851   0    U each
```

```r
s  <- mcstoc(rmultinomial, type = "VU", nvariates = 3, size = 500, prob = p)
summary(s)
```

```
## node :
## [[1]]
##         mean    sd   Min  2.5%   25%   50%   75% 97.5% Max  nsv Na's
## median  86.6  8.41  62.0  70.0  81.0  87.0  92.0 103.0 119 1001    0
## mean    92.0  8.14  66.7  76.4  86.4  91.8  97.4 108.1 120 1001    0
## 2.5%    15.8  3.78   6.0   9.0  13.0  16.0  18.0  23.5  30 1001    0
## 97.5%  208.3 11.07 176.5 188.0 201.0 208.0 215.5 230.0 250 1001    0
##
## [[2]]
##         mean    sd   Min 2.5% 25%   50%   75% 97.5% Max  nsv Na's
## median 140.4 10.06 108.0  120 134 140.0 147.0 160.0 171 1001    0
## mean   145.1  9.48 115.1  127 139 144.9 151.4 163.8 177 1001    0
## 2.5%    35.7  5.73  18.5   25  32  35.5  39.5  47.5  56 1001    0
## 97.5%  285.4 11.37 250.5  264 278 285.5 293.0 307.0 318 1001    0
##
## [[3]]
##        mean    sd Min 2.5% 25% 50% 75% 97.5% Max  nsv Na's
## median  259 10.76 225  238 252 260 267   282 298 1001    0
## mean    263 10.58 228  242 256 263 270   283 297 1001    0
## 2.5%    119  8.99  90  100 112 118 125   138 152 1001    0
## 97.5%   395 11.41 360  378 390 396 402   412 428 1001    0
```

Example 2. Each family member eats a normal distribution of steak (100, 150, 250 g mean) with positive correlation between the children's servings and negative with the mother's.

```r
sigma <- matrix(c(10, 2, -5, 2, 10, -5, -5, -5, 10), ncol = 3)
(x   <- mcstoc(rmultinormal, type = "V", nvariates = 3, mean = c(100, 150, 250),
               sigma = as.vector(sigma)))
```

```
##   node    mode  nsv nsu nva variate   min mean median max Nas type outm
## 1    x numeric 1001   1   3       1  89.3  100    100 110   0    V each
## 2    x numeric 1001   1   3       2 140.6  150    150 160   0    V each
## 3    x numeric 1001   1   3       3 239.9  250    250 262   0    V each
```

```r
cor(x[, 1, ])
```

```
##        [,1]   [,2]   [,3]
## [1,]  1.000  0.166 -0.475
## [2,]  0.166  1.000 -0.521
## [3,] -0.475 -0.521  1.000
```

Both `mean` and `sigma` can be variable or uncertain.[12] Example with uncertain mean:

```
m   <- mcdata(c(100, 150, 250), type = "O", nvariates = 3)
mun <- mcstoc(rnorm,        type = "U",  nvariates = 3, mean = m, sd = 20)
x   <- mcstoc(rmultinormal, type = "VU", nvariates = 3, mean = mun, sigma = as.vector(sigma))
cor(x[, 1, ])
```

```
##        [,1]   [,2]   [,3]
## [1,]  1.000  0.187 -0.467
## [2,]  0.187  1.000 -0.543
## [3,] -0.467 -0.543  1.000
```

Example 3. Non-parametric bootstrap: 6 individuals eat 100 g, 12 eat 150 g, 6 eat 170 g, and 6 eat 200 g [2].

```
val <- c(100, 150, 170, 200)
pr  <- c(6, 12, 6, 6)
out <- c("min", "mean", "max")
(x  <- mcstoc(rempiricalD, type = "U",  outm = out, nvariates = 30, values = val, prob = pr))
```

```
##   node    mode nsv nsu nva variate min mean median max Nas type outm
## 1    x numeric   1 101  30      NA 100  100    100 100   0    U  min
## 2    x numeric   1 101  30      NA 137  155    155 169   0    U mean
## 3    x numeric   1 101  30      NA 200  200    200 200   0    U  max
```

```
mcstoc(rempiricalD, type = "VU", values = x)
```

```
##   node    mode  nsv nsu nva variate min mean median max Nas type outm
## 1    x numeric 1001 101   1       1 100  155    150 200   0   VU each
```

The `outm` option controls which statistics to show: `"none"`, `"each"` (default), or a vector of function names applied across all 30 variates.

3.2 Multivariate Nodes as a Third Dimension for Multiple Options

Assume uncertainty in `conc`: 75% sure $conc \sim N(10, 2)$, 25% sure $conc \sim U(8, 12)$. Build a bivariate node and propagate both hypotheses simultaneously.

```
conc1 <- mcstoc(rnorm,  type = "U",  mean = 10, sd = 2)
conc2 <- mcstoc(runif,  type = "U",  min = 8, max = 12)
conc  <- mcdata(c(conc1, conc2), type = "U", nvariates = 2)

cook    <- mcstoc(rempiricalD, type = "V",  values = c(1, 1/5, 1/50), prob = c(0.027, 0.373, 0.600))
serving <- mcstoc(rgamma,      type = "V",  shape = 3.93, rate = 0.0806)
expo    <- conc * cook * serving
dose    <- mcstoc(rpois,       type = "VU", nvariates = 2, lambda = expo)
r       <- mcstoc(runif,       type = "U",  min = 0.0005, max = 0.0015)
risk    <- 1 - (1 - r)^dose
EC5     <- mc(conc, risk)
summary(EC5)
```

[12] `rmultinormal` is a vectorized version of `rmvnorm` from `mvtnorm`.

```
## conc :
## [[1]]
##        NoVar
## median  9.99
## mean    9.87
## 2.5%    6.11
## 97.5%  13.07
##
## [[2]]
##        NoVar
## median  9.99
## mean   10.01
## 2.5%    8.19
## 97.5%  11.91
##
##
## risk :
## [[1]]
##          mean     sd Min     2.5%     25%     50%    75% 97.5%   Max  nsv Na's
## median 0.0463 0.0716   0 0.001433 0.00650 0.01317 0.0667 0.229 0.672 1001    0
## mean   0.0472 0.0720   0 0.001658 0.00689 0.01365 0.0687 0.235 0.659 1001    0
## 2.5%   0.0261 0.0428   0 0.000635 0.00372 0.00713 0.0370 0.133 0.440 1001    0
## 97.5%  0.0760 0.1082   0 0.003346 0.01174 0.02345 0.1150 0.369 0.856 1001    0
##
## [[2]]
##          mean     sd      Min     2.5%     25%     50%    75% 97.5%   Max  nsv Na's
## median 0.0485 0.0743 0.00e+00 0.001774 0.00697 0.01402 0.0691 0.241 0.693 1001    0
## mean   0.0481 0.0733 1.12e-05 0.001760 0.00705 0.01395 0.0700 0.240 0.671 1001    0
## 2.5%   0.0259 0.0428 0.00e+00 0.000563 0.00351 0.00701 0.0364 0.134 0.458 1001    0
## 97.5%  0.0769 0.1094 0.00e+00 0.002908 0.01247 0.02305 0.1155 0.377 0.856 1001    0
```

(Remember to specify `nvariates = 2` in `mcstoc` for `dose` — `mc2d` cannot infer it.)

3.3 Multivariate Nodes as a Third Dimension for Multiple Contaminants

Two contaminants with uncertain concentrations $N(10, 2)$ and $N(14, 2)$:[13]

```r
mconc   <- mcdata(c(10, 14), type = "0",  nvariates = 2)
conc    <- mcstoc(rnorm,       type = "U",  nvariates = 2, mean = mconc, sd = 2)
cook    <- mcstoc(rempiricalD, type = "V",  values = c(1, 1/5, 1/50), prob = c(0.027, 0.373, 0.600))
serving <- mcstoc(rgamma,      type = "V",  shape = 3.93, rate = 0.0806)
expo    <- conc * cook * serving
dose    <- mcstoc(rpois,       type = "VU", nvariates = 2, lambda = expo)
dosetot <- mcapply(dose, margin = "variates", fun = sum)
r       <- mcstoc(runif,       type = "U",  min = 0.0005, max = 0.0015)
risk    <- 1 - (1 - r)^dosetot
EC6     <- mc(conc, risk)
summary(EC6)
```

```
## conc :
```

[13] A correlation between contaminants could be specified via `rmultinormal`.

```
## [[1]]
##        NoVar
## median 10.25
## mean   10.00
## 2.5%    5.61
## 97.5%  13.68
##
## [[2]]
##        NoVar
## median  14.1
## mean    14.0
## 2.5%    10.3
## 97.5%   17.8
##
##
## risk :
##          mean     sd     Min    2.5%     25%    50%    75% 97.5%   Max  nsv Na's
## median 0.1017 0.1245 0.00116 0.00588 0.01782 0.0326 0.1671 0.415 0.845 1001    0
## mean   0.1051 0.1265 0.00117 0.00617 0.01865 0.0347 0.1734 0.421 0.828 1001    0
## 2.5%   0.0611 0.0798 0.00000 0.00314 0.00997 0.0187 0.0955 0.259 0.638 1001    0
## 97.5%  0.1525 0.1729 0.00276 0.00970 0.02912 0.0530 0.2590 0.581 0.951 1001    0
```

4 Another Example: A QRA of Waterborne Cryptosporidiosis in France

Adapted from [6]. Goal: evaluate the risk of infection with *Cryptosporidium parvum* from consumption of tap water given n oocysts/100 l observed in a storage reservoir (simplified model).

4.1 Tap Water Consumption Model

We have raw data on daily tap water consumption from 1,180 consumers (`inca`, histogram below). We could use the empirical distribution directly:

```r
ndvar(1001)
```

```
## [1] 1001
```

```r
ndunc(101)
```

```
## [1] 101
```

```r
mcstoc(rempiricalD, type = "V", values = inca)
```

```
##   node    mode  nsv nsu nva variate min mean median max Nas type outm
## 1    x numeric 1001   1   1       1   0  0.4    0.3 3.2   0    V each
```

Instead, we use `fitdistrplus` [3]. The data include many zeros (days without tap water consumption). We model them as a mixture.

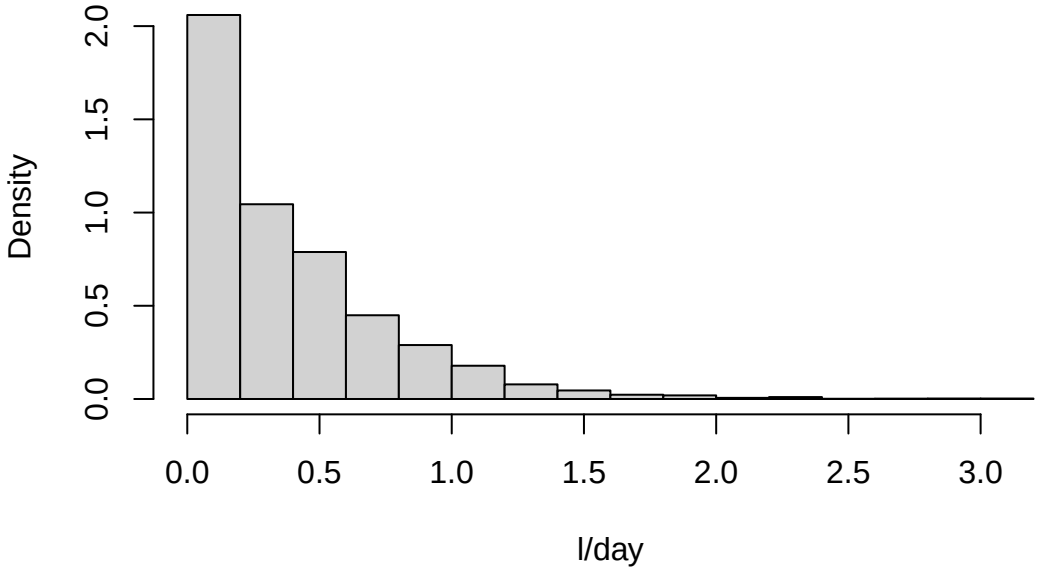


Figure 7: Histogram of daily tap water intake.

```
library(fitdistrplus)
```

```
## Loading required package: MASS
```

```
## Loading required package: survival
```

```
pzero    <- sum(inca == 0) / length(inca)
inca_non_0 <- inca[inca != 0]
descdist(inca_non_0)
```

```
## summary statistics
## ------
## min:  0.0221   max:  3.2
## median:  0.48
## mean:  0.566
## estimated sd:  0.385
## estimated skewness:  1.75
## estimated kurtosis:  7.99
```

From the shape descriptor plot above, we try a lognormal distribution:

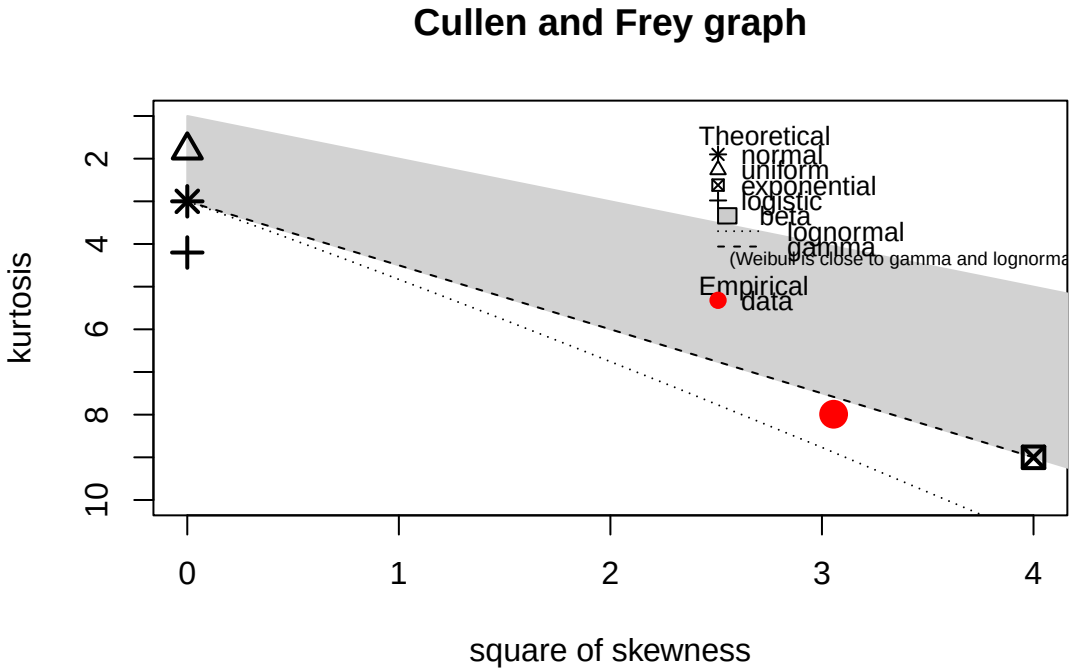


Figure 8: Graph from `descdist`.

```
Adj_water <- fitdist(inca_non_0, "lnorm", method = "mle")
meanlog   <- Adj_water$est[1]
sdlog     <- Adj_water$est[2]
summary(Adj_water)
```

```
## Fitting of the distribution ' lnorm ' by maximum likelihood
## Parameters :
##         estimate Std. Error
## meanlog   -0.784    0.00891
## sdlog      0.674    0.00630
## Loglikelihood:  -1374   AIC:  2752   BIC:  2765
## Correlation matrix:
##           meanlog     sdlog
## meanlog  1.00e+00 -2.23e-12
## sdlog   -2.23e-12  1.00e+00
```

The fit is satisfactory. Uncertainty around the MLE estimates could be incorporated via `bootdist`:

```
Boot       <- bootdist(Adj_water, bootmethod = "param", niter = ndunc())
Mean_conso <- mcdata(Boot$estim$meanlog, type = "U")
Sd_conso   <- mcdata(Boot$estim$sdlog,   type = "U")
conso1     <- mcstoc(rlnorm, type = "VU", meanlog = Mean_conso, sdlog = Sd_conso)
```

For simplicity, we ignore that uncertainty and use `mcprobtree` to build the mixture:

```r
conso0 <- mcdata(0, type = "V")
conso1 <- mcstoc(rlnorm, type = "V", meanlog = meanlog, sdlog = sdlog)
v      <- mcprobtree(c(pzero, 1 - pzero), list("0" = conso0, "1" = conso1), type = "V")
summary(v)
```

```
## node :
##        mean    sd Min 2.5% 25%   50%   75% 97.5%  Max  nsv Na's
## NoUnc 0.394 0.419   0    0   0 0.313 0.597  1.41 2.98 1001    0
```

4.2 The Dose-Response Model

Bootstrap from data `datDR` [1]. A function `DR` with argument `n` is defined and passed to `mcstoc`:

```r
datDR <- list(dose = c(30, 100, 300, 500, 1000, 10000, 100000, 1000000),
              pi   = c(2, 4, 2, 5, 2, 3, 1, 1),
              ni   = c(5, 8, 3, 6, 2, 3, 1, 1))

estDR <- function(pos, ref) {
  suppressWarnings(
    -glm(cbind(ref$ni - pos, pos) ~ ref$dose + 0,
         binomial(link = "log"))$coefficients)
}

ml <- 1 - exp(-estDR(datDR$pi, datDR) * datDR$dose)

DR <- function(n) {
  boot <- matrix(rbinom(length(datDR$dose) * n, datDR$ni, ml), nrow = length(datDR$dose))
  apply(boot, 2, estDR, ref = datDR)
}
r <- mcstoc(DR, type = "U")
summary(r)
```

```
## node :
##          NoVar
## median 0.00536
## mean   0.00600
## 2.5%   0.00274
## 97.5%  0.01113
```

4.3 The Model

```r
Rr <- mcstoc(rbeta, type = "U", shape1 = 2.65, shape2 = 3.64)
w  <- mcstoc(rbeta, type = "V", shape1 = 2.6,  shape2 = 3.4)
```

Given $O_o = 2$ oocysts observed in 100 l, the expected number of oocysts in the sample `l`:

```r
Oo <- 2
l  <- (Oo + mcstoc(rnbinom, type = "U", size = Oo + 1, prob = Rr)) / 100
```

The expected number drunk by individuals and the risk ($\times$10000):

```r
Or <- l * v * w
P  <- 10000 * (1 - exp(-r * Or))
summary(P)
```

```
## node :
##         mean    sd Min 2.5% 25%   50%   75%  97.5%   Max  nsv Na's
## median 0.486 0.572   0    0   0 0.321 0.713  2.026  3.97 1001    0
## mean   0.687 0.809   0    0   0 0.454 1.008  2.864  5.61 1001    0
## 2.5%   0.162 0.191   0    0   0 0.107 0.238  0.675  1.32 1001    0
## 97.5%  2.411 2.837   0    0   0 1.594 3.538 10.047 19.67 1001    0
```

This can be compared to Table 2 in [6]. Results for $O_o = \{0, 1, 2, 5, 10, 20, 50, 100, 1000\}$ can be obtained in one step using:

```r
Oo <- mcdata(c(0, 1, 2, 5, 10, 20, 50, 100, 1000), type = "O", nvariates = 9)
```

As a Conclusion

We hope that `mc2d` will help risk assessors to construct and analyse their models, and to develop two-dimensional simulations. *Please report any bugs to rpouillot@yahoo.fr.*

References

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