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Description Provides response time distributions (density/PDF, distribution function/CDF, quantile function, and random generation): (a) Ratcliff diffusion model based on C code by Andreas and Jochen Voss and (b) linear ballistic accumulator (LBA) with different distributions underlying the drift rate.

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rtdist-package The rtdists Package

Description

Response Time Distributions.

Details

Package: rtdists
Type: Package
Version: 0.6-6
Date: 2016-07-14
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License: GPL (>=3)
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Provides response time distributions (density/PDF, distribution function/CDF, quantile function, and random generation): (a) Ratcliff diffusion model based on C code by Andreas and Jochen Voss and (b) linear ballistic accumulator (LBA) with different distributions underlying the drift rate.

Author(s)

Henrik Singmann, Scott Brown, Matthew Gretton, Andrew Heathcote, with contributions from Andreas Voss, Jochen Voss, Andrew Terry

Diffusion The Ratcliff Diffusion Model
Diffusion

Description

Density, distribution function, quantile function, and random generation for the Ratcliff diffusion model with following parameters: a (threshold separation), z (starting point), v (drift rate), t0 (non-decision time/response time constant), d (differences in speed of response execution), sv (inter-trial-variability of drift), st0 (inter-trial-variability of non-decisional components), sz (inter-trial-variability of relative starting point), and s (diffusion constant). Note that the parameterization or defaults of non-decision time variability st0 and diffusion constant s differ from what is often found in the literature and that the parameterization of z and sz have changed compared to previous versions (now absolute and not relative).

Usage

diffusion(rt, response = "upper", a, v, t0, z = 0.5 * a, d = 0, sz = 0, sv = 0, st0 = 0, s = 1, precision = 3)

pdiffusion(rt, response = "upper", a, v, t0, z = 0.5 * a, d = 0, sz = 0, sv = 0, st0 = 0, s = 1, precision = 3, maxt = 10000)

qdiffusion(p, response = "upper", a, v, t0, z = 0.5 * a, d = 0, sz = 0, sv = 0, st0 = 0, s = 1, precision = 3, maxt = 10000, interval = c(0, 10), scale_p = FALSE, scale_max = Inf)

rdiffusion(n, a, v, t0, z = 0.5 * a, d = 0, sz = 0, sv = 0, st0 = 0, s = 1, precision = 3)

Arguments

rt a vector of RTs. Or for convenience also a data.frame with columns rt and response (such as returned from rdiffusion or rLBA). See examples.

response character vector. Which response boundary should be tested? Possible values are c("upper", "lower"), possibly abbreviated and "upper" being the default. Alternatively, a numeric vector with values 1=lower and 2=upper. For convenience, response is converted via as.numeric also allowing factors (see examples). Ignored if the first argument is a data.frame.

a threshold separation. Amount of information that is considered for a decision. Large values indicate a conservative decisional style. Typical range: 0.5 < a < 2

v drift rate. Average slope of the information accumulation process. The drift gives information about the speed and direction of the accumulation of information. Large (absolute) values of drift indicate a good performance. If received information supports the response linked to the upper threshold the sign will be positive and vice versa. Typical range: -5 < v < 5

t0 non-decision time or response time constant (in seconds). Lower bound for the duration of all non-decisional processes (encoding and response execution). Typical range: 0.1 < t0 < 0.5

z starting point. Indicator of an a priori bias in decision making. When the relative starting point z deviates from 0.5*a, the amount of information necessary for a decision differs between response alternatives. Default is 0.5*a (i.e., no bias).
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Diffusion

d  differences in speed of response execution (in seconds). Positive values indicate that response execution is faster for responses linked to the upper threshold than for responses linked to the lower threshold. Typical range: -0.1 < d < 0.1. Default is 0.

sz  inter-trial-variability of starting point. Range of a uniform distribution with mean z describing the distribution of actual starting points from specific trials. Minimal impact on the RT distributions, values different from 0 can predict slow errors. Can be fixed to 0 in most applications. Typical range: 0 < sz < 0.5. Default is 0.

sv  inter-trial-variability of drift rate. Standard deviation of a normal distribution with mean v describing the distribution of actual drift rates from specific trials. Minimal impact on the RT distributions, values different from 0 can predict fast errors. Can be fixed to 0 in most applications. Typical range: 0 < sv < 2. Default is 0.

st0  inter-trial-variability of non-decisional components. Range of a uniform distribution with mean t0 + st0/2 describing the distribution of actual t0 values across trials. Accounts for response times below t0. Reduces skew of predicted RT distributions. Can be fixed to 0 in most applications. Typical range: 0 < st0 < 0.2. Default is 0.

s  diffusion constant; standard deviation of the random noise of the diffusion process (i.e., within-trial variability), scales a, v, and sv. Needs to be fixed to a constant in most applications. Default is 1. Note that the default used by Ratcliff and in other applications is often 0.1.

precision  numerical scalar value. Precision of calculation. Corresponds roughly to the number of decimals of the predicted CDFs that are calculated accurately. Default is 3.

maxt  maximum rt allowed, used to stop integration problems. Currently ignored as numerical integration works fine with Inf.

p  vector of probabilities. Or for convenience also a data.frame with columns p and response. See examples.

interval  a vector containing the end-points of the interval to be searched for the desired quantiles (i.e., RTs) in qdiffusion. Default is c(0, 1).

scale_p  logical. Should entered probabilities automatically be scaled by maximally predicted probability? Default is FALSE. Convenience argument for obtaining predicted quantiles. Can be slow as the maximally predicted probability is calculated individually for each p.

scale_max  numerical scalar. Value at which maximally predicted RT should be calculated if scale_p is TRUE.

n  is a desired number of observations.

Details

The Ratcliff diffusion model (Ratcliff, 1978) is a mathematical model for two-choice discrimination tasks. It is based on the assumption that information is accumulated continuously until one of two decision thresholds is hit. For more information, see Voss, Rothermund, and Voss (2004), Voss, Nagler, and Lerche (2013), or Wagenmakers (2009).
All functions are fully vectorized across all parameters as well as the response. This allows for trialwise parameters for each parameter.

For convenience, all functions (with the exception of rdiffusion) allow that the first argument is a data.frame containing the information of the first and second argument in two columns (i.e., rt/p and response). Other columns will be ignored. This allows, for example, to pass the data.frame generated by rdiffusion directly to pdiffusion. See examples.

**Distribution Function (CDF):** For the time being, the cumulative probability function (pdiffusion) uses numerical integration of ddiffusion via integral from package pracma. While this is somewhat slow, it reliably produces correct results. Please report all issues with the CDF to the package maintainer.

**Quantile Function:** Due to the bivariate nature of the diffusion model, the diffusion processes reaching each response boundary only return the defective CDF that does not reach 1. Only the sum of the CDF for both boundaries reaches 1. Therefore, ddiffusion can only return quantiles/RTs for any accumulator up to the maximal probability of that accumulator’s CDF. This can be obtained by evaluating the CDF at Inf.

As a convenience for the user, if scale_p = TRUE in the call to qdiffusion the desired probabilities are automatically scaled by the maximal probability for the corresponding response. Note that this can be slow as the maximal probability is calculated separately for each desired probability. See examples.

Also note that quantiles (i.e., predicted RTs) are obtained by numerically minimizing the absolute difference between desired probability and the value returned from pdiffusion using optimize. If the difference between the desired probability and probability corresponding to the returned quantile is above a certain threshold (currently 0.0001) no quantile is returned but NA. This can be either because the desired quantile is above the maximal probability for this accumulator or because the limits for the numerical integration are too small (default is c(0, 10)).

**Value**

ddiffusion gives the density, pdiffusion gives the distribution function, qdiffusion gives the quantile function (i.e., predicted RTs), and rdiffusion generates random response times and decisions (returning a data.frame with columns rt (numeric) and response (factor)).

The length of the result is determined by n for rdiffusion, equal to the length of rt for ddiffusion and pdiffusion, and equal to the length of p for qdiffusion.

The distribution parameters (as well as response) are recycled to the length of the result. In other words, the functions are completely vectorized for all parameters and even the response boundary.

**Note**

The parameterization of the non-decisional components, t0 and st0, differs from the parameterization used by, for example, Andreas Voss or Roger Ratcliff in that t0 is not the lower bound of the uniform distribution of length st0, but its midpoint.

The default diffusion constant s is 1 and not 0.1 as in most applications of Roger Ratcliff and others.

We have changed the parameterization of the start point z which is now the absolute start point (it was the relative start point in previous versions of rtdists).

RTs need to be sorted (in increasing order) for pdiffusion.
Author(s)


References


Examples

```r
## identical calls (but different random values)
rt1 <- rdiffusion(500, a=1, v=2, t0=0.5)
head(rt1)
rt2 <- rdiffusion(500, a=1, v=2, t0=0.5, d=0, sz=0, sv=0, st0=0)
head(rt2)

# get density for random RTs (possible to specify arguments for pdiffusion in same way):
sum(log(ddiffusion(rt1, rtLresponse, a=1, v=2, t0=0.5))) # response is factor
sum(log(ddiffusion(rt1, as.numeric(rt1$response), a=1, v=2, t0=0.5))) # response is numeric
sum(log(ddiffusion(rt1, as.character(rt1$response), a=1, v=2, t0=0.5))) # response is character
sum(log(ddiffusion(rt1, a=1, v=2, t0=0.5))) # response is data.frame

sum(log(ddiffusion(rt2, rt2$response, a=1, v=2, t0=0.5)))

# can we recover the parameters?
ll_diffusion <- function(pars, rt, response) {
  densities <- tryCatch(
    ddiffusion(rt, response=response,
               a=pars[1], v=pars[2], t0=pars[3],
               sz=pars[4],
               st0=pars[5], sv=pars[6]),
    error = function(e) 0)
  if (any(densities == 0)) return(1e6)
  return(-sum(log(densities)))
}

## Not run:
start <- c(runif(2, 0.5, 3), 0.1, runif(3, 0, 0.5))
names(start) <- c("a", "v", "t0", "sz", "st0", "sv")
```
recov <- nlminb(startL ll_diffusionL lower = 0, rt=rt1$rt, response=rt1$response)
round(recov$par, 3)
# a v t0 sz st0 sv
#0.954 1.764 0.503 0.000 0.000 0.000

## End(Not run)

## Not run:
## replicate Table 1 from Wagenmakers et al. (2007) using rdiffusion:

n <- 1e5 # number of samples
# take parameter values from Table 2 and set s to 0.1
george <- rdiffusion(n, a = 0.12, v = 0.25, t0 = 0.3, s = 0.1)
rich <- rdiffusion(n, a = 0.12, v = 0.25, t0 = 0.25, s = 0.1)
amy <- rdiffusion(n, a = 0.08, v = 0.25, t0 = 0.3, s = 0.1)
mark <- rdiffusion(n, a = 0.08, v = 0.25, t0 = 0.25, s = 0.1)

george$id <- "george"
rich$id <- "rich"
amy$id <- "amy"
mark$id <- "mark"

wag <- rbind(george, rich, amy, mark)
wag$id <- factor(wag$id, levels = c("george", "rich", "amy", "mark"))

opt <- options()
options(digits = 3)
aggregate(cbind(rt, as.numeric(response)-1) ~ id, wag, mean)
# id rt V2
# 1 george 0.517 0.952
# 2 rich 0.467 0.953
# 3 amy 0.422 0.881
# 4 mark 0.372 0.882
options(digits = 1)
aggregate(rt ~ id, wag, var)
# id rt
# 1 george 0.024
# 2 rich 0.024
# 3 amy 0.009
# 4 mark 0.009
options(opt)

## End(Not run)

## plot density:
curve(ddiffusion(x, a=1, v=2, t0=0.5, response = "upper"),
xlim=c(0,3), main="Density of upper responses", ylab="density", xlab="response time")
curve(ddiffusion(x, a=1, v=2, t0=0.5, st0=0.2, response = "upper"),
add=TRUE, lty = 2)
legend("topleft", legend=c("no", "yes"), title = "Starting Point Variability?", lty = 1:2)
# plot cdf:
curve(pdiffusion(x, a=1, v=2, t0=0.5, st0=0.2, response="u"),
    xlim = c(0, 3), ylim = c(0,1),
    ylab = "cumulative probability", xlab = "response time",
    main = "CDF of diffusion model with start point variability")
curve(pdiffusion(x, a=1, v=2, t0=0.5, st0=0.2, response="l"),
    add=TRUE, lty = 2)
legend("topleft", legend=c("upper", "lower"), title="response boundary", lty=1:2)

## Not run:
### qdiffusion can only return values up to maximal predicted probability:
(max_p <- pdiffusion(inf, a=1, v=2, t0=0.5, st0=0.2, sz = 0.1, sv = 0.5, response="u"))
# [1] 0.87
# (Note that with the current integration routine for pdiffusion use Inf and not smaller values.)
qdiffusion(0.87, a=1, v=2, t0=0.5, st0=0.2, sz = 0.1, sv = 0.5, response="u")
# [1] 1.945802
qdiffusion(0.88, a=1, v=2, t0=0.5, st0=0.2, sz = 0.1, sv = 0.5, response="u")
# NA with warning.

# to get predicted quantiles, scale required quantiles by maximally predicted response rate:
qs <- c(1, 3, .5, .7, .9)
qdiffusion(qs*max_p, a=1, v=2, t0=0.5, st0=0.2, sz = 0.1, sv = 0.5, response="u")

# or set scale_p to TRUE which scales automatically by maximum p
# (but can be slow as it calculates max_p for each probability separately)
qdiffusion(qs, a=1, v=2, t0=0.5, st0=0.2, sz = 0.1, sv = 0.5, response="u", scale_p = TRUE)

# qdiffusion also accepts a data.frame as first argument:
t3 <- data.frame(p = rep(c(0.05, 0.1, 0.87), 2), response = rep(c("upper", "lower"), each = 3))
# p response
# 1 0.05 upper
# 2 0.10 upper
# 3 0.87 upper
# 4 0.05 lower
# 5 0.10 lower
# 6 0.87 lower
qdiffusion(t3, a=1, v=2, t0=0.5, st0=0.2, sz = 0.1, sv = 0.5)

## End(Not run)

## LBA and diffusion can be used interchangeably:
rt1 <- rlba(500, A=0.5, b=1, t0 = 0.5, mean_v=c(2.4, 1.6), sd_v=c(1,1.2))
rt2 <- rdiffusion(500, a=1, v=2, t0=0.5)

# data can also be passed as data.frame (same is true for pLBA):
sum(log(dlba(rt1, A=0.5, b=1, t0 = 0.5, mean_v=c(2.4, 1.6), sd_v=c(1,1.2))))
sum(log(dlba(rt2, A=0.5, b=1, t0 = 0.5, mean_v=c(2.4, 1.6), sd_v=c(1,1.2))))
sum(log(ddiffusion(rt1, a=1, v=2, t0=0.5)))
sum(log(ddiffusion(rt2, a=1, v=2, t0=0.5)))
The Linear Ballistic Accumulator (LBA)

Description

Density, distribution function, quantile function, and random generation for the LBA model with the following parameters: \(a\) (upper value of starting point), \(b\) (response threshold), \(t_0\) (non-decision time), and drift rate \((\nu)\). All functions are available with different distributions underlying the drift rate: Normal \((\text{norm})\), Gamma \((\text{gamma})\), Frechet \((\text{frechet})\), and log normal \((\text{lnorm})\). The functions return their values conditional on the accumulator given in the response argument winning.

Usage

\[
\text{dlba}(rt, \text{response}, A, b, t0, ..., st0 = 0, \text{distribution} = \text{c("norm", "gamma", "frechet", "lnorm")}, \text{args.dist} = \text{list()}, \text{silent} = \text{FALSE})
\]

\[
\text{plba}(rt, \text{response}, A, b, t0, ..., st0 = 0, \text{distribution} = \text{c("norm", "gamma", "frechet", "lnorm")}, \text{args.dist} = \text{list()}, \text{silent} = \text{FALSE})
\]

\[
\text{qlba}(p, \text{response}, A, b, t0, ..., st0 = 0, \text{distribution} = \text{c("norm", "gamma", "frechet", "lnorm")}, \text{args.dist} = \text{list()}, \text{silent} = \text{FALSE}, \text{interval} = \text{c(0, 10)}, \text{scale_p} = \text{FALSE}, \text{scale_max} = \text{Inf})
\]

\[
\text{rlba}(n, A, b, t0, ..., st0 = 0, \text{distribution} = \text{c("norm", "gamma", "frechet", "lnorm")}, \text{args.dist} = \text{list()}, \text{silent} = \text{FALSE})
\]

Arguments

- **rt** vector of RTs. Or for convenience also a data.frame with columns rt and response (such as returned from rlba or rdiffusion). See examples.
- **response** integer vector of winning accumulators/responses corresponding to the vector of RTs/p (i.e., used for specifying the response for a given RT/probability). Will be recycled if necessary. Cannot contain values larger than the number of accumulators. First response/accumulator must receive value 1, second 2, and so forth. For convenience, response is converted via as.numeric thereby allowing factors to be passed as well (such as returned from rdiffusion). Ignored if rt or p is a data.frame.
- **A** start point interval or evidence in accumulator before beginning of decision process. Start point varies from trial to trial in the interval \([0, A]\) (uniform distribution). Average amount of evidence before evidence accumulation across trials is \(A/2\).
- **b** response threshold. \((b - A/2)\) is a measure of "response caution".
- **t0** non-decision time or response time constant (in seconds). Lower bound for the duration of all non-decisional processes (encoding and response execution).
... two named drift rate parameters depending on distribution (e.g., mean_v and sd_v for distribution="norm"). The parameters can either be given as a numeric vector or a list. If a numeric vector is passed each element of the vector corresponds to one accumulator. If a list is passed each list element corresponds to one accumulator allowing again trialwise drift rates. The shorter parameter will be recycled as necessary (and also the elements of the list to match the length of rt). See details.

st0 variability of non-decision time, such that t0 is uniformly distributed between t0 and t0 + st0. Default is 0. Can be trialwise, and will be recycled to length of rt.

distribution character specifying the distribution of the drift rate. Possible values are c("norm", "gamma", "frechet", default is "norm".

args.dist list of optional further arguments to the distribution functions (i.e., posdrift or robust for distribution="norm", see single-LBA).

silent logical. Should the number of accumulators used be suppressed? Default is FALSE which prints the number of accumulators.

p vector of probabilities. Or for convenience also a data.frame with columns p and response. See examples.

interval a vector containing the end-points of the interval to be searched for the desired quantiles (i.e., RTs) in qLBA. Default is c(0, 1).

scale_p logical. Should entered probabilities automatically be scaled by maximally predicted probability? Default is FALSE. Convenience argument for obtaining predicted quantiles. Can be slow as the maximally predicted probability is calculated individually for each p.

scale_max numerical scalar. Value at which maximally predicted RT should be calculated if scale_p is TRUE.

n desired number of observations (scalar integer).

Details

For convenience, all functions (with the exception of rdiffusion) allow that the first argument is a data.frame containing the information of the first and second argument in two columns (i.e., rt/p and response). Other columns will be ignored. This allows, for example, to pass the data.frame generated by rLBA directly to pLBA. See examples.

Parameters: The following arguments are allowed as ... drift rate parameters:

- mean_v, sd_v mean and standard deviation of normal distribution for drift rate (norm). See Normal
- shape_v, rate_v, scale_v shape, rate, and scale of gamma (gamma) and scale and shape of Frechet (frechet) distributions for drift rate. See GammaDist or frechet. For Gamma, scale = 1/shape and shape = 1/scale.
- meanlog_v, sdlog_v mean and standard deviation of lognormal distribution on the log scale for drift rate (lnorm). See Lognormal.

As described above, the accumulator parameters can either be given as a numeric vector or a list. If a numeric vector is passed each element of the vector corresponds to one accumulator. If a list is
passed each list element corresponds to one accumulator allowing trialwise driftrates. The shorter parameter will be recycled as necessary (and also the elements of the list to match the length of \( rt \)).

The other LBA parameters (i.e., \( A, b, \) and \( t\theta \), with the exception of \( st\theta \)) can either be a single numeric vector (which will be recycled to reach \text{length}(rt)\ or \text{length}(n)\ for trialwise parameters) or a list of such vectors in which each list element corresponds to the parameters for this accumulator (i.e., the list needs to be of the same length as there are accumulators). Each list will also be recycled to reach \text{length}(rt)\ for trialwise parameters per accumulator.

To make the difference between both paragraphs clear: Whereas for the accumulators both a single vector or a list corresponds to different accumulators, only the latter is true for the other parameters. For those (i.e., \( A, b, \) and \( t\theta \)) a single vector always corresponds to trialwise values and a list must be used for accumulator wise values.

\( st\theta \) can only vary trialwise (via a vector). And it should be noted that \( st\theta \) not equal to zero will considerably slow done everything.

**Quantile Function:** Due to the bivariate nature of the LBA, single accumulators only return defective CDFs that do not reach 1. Only the sum of all accumulators reaches 1. Therefore, \( qLBA \) can only return quantiles/RTs for any accumulator up to the maximal probability of that accumulator’s CDF. This can be obtained by evaluating the CDF at \( \inf \).

As a conveniece for the user, if \( scale_p = TRUE \) in the call to \( qLBA \) the desired probabilities are automatically scaled by the maximal probability for the corresponding response. Note that this can be slow as the maximal probability is calculated separately for each desired probability. See examples.

Also note that quantiles (i.e., predicted RTs) are obtained by numerically minimizing the absolute difference between desired probability and the value returned from \( pLBA \) using \texttt{optimize}. If the difference between the desired probability and probability corresponding to the returned quantile is above a certain threshold (currently 0.0001) no quantile is returned but \texttt{NA}. This can be either because the desired quantile is above the maximal probability for this accumulator or because the limits for the numerical integration are too small (default is \( c(0, 1) \)).

**RNG:** For random number generation at least one of the distribution parameters (i.e., \texttt{mean_v}, \texttt{sd_v}, \texttt{shape_v}, \texttt{scale_v}, \texttt{rate_v}, \texttt{meanlog_v}, and \texttt{sdlog_v}) should be of length \( > 1 \) to receive RTs from multiple responses. Shorter vectors are recycled as necessary. Note that for random number generation from a normal distribution for the driftrate the number of returned samples may be less than the number of requested samples if \texttt{posdrifts==FALSE}.

**Value**

\( dlBA \) returns the density (PDF), \( pLBA \) returns the distribution function (CDF), \( qLBA \) returns the quantile/RT, \( rLBA \) return random response times and responses (in a \texttt{data.frame}).

The length of the result is determined by \( n \) for \( rLBA \), equal to the length of \( rt \) for \( dlBA \) and \( pLBA \), and equal to the length of \( p \) for \( qLBA \).

The distribution parameters (as well as \texttt{response}) are recycled to the length of the result. In other words, the functions are completely vectorized for all parameters and even the response.
Note

These are the top-level functions intended for end-users. To obtain the density and cumulative density the race functions are called for each response time with the corresponding winning accumulator as first accumulator (see `lba-race`).

References


Examples

```r
# generate random LBA data:
rt1 <- rlba(S500, A=0.5, b=1, t0 = 0.5, mean_v=c(2.4, 1.6), sd_v=c(1,1.2))
head(rt1)
prop.table(table(rt1$response))

# original parameters have 'high' log-likelihood:
sum(log(dlba(rt1$rt, rt1$response, A=0.5, b=1, t0 = 0.5, mean_v=c(2.4, 1.6), sd_v=c(1,1.2))))

# data can also be passed as data.frame (same is true for plba):
sum(log(dlba(rt1, A=0.5, b=1, t0 = 0.5, mean_v=c(2.4, 1.6), sd_v=c(1,1.2))))

objective_fun <- function(par, rt, response, distribution = "norm") {
  # simple parameters
  spar <- par[grepl("[12]\$", names(par))]

  # distribution parameters:
  dist_par_names <- unique(sub("[12]\$", "", grep("[12]\$", names(par), value = TRUE)))
  dist_par <- vector("list", length = length(dist_par_names))
  names(dist_par) <- dist_par_names
  for (i in dist_par_names) dist_par[[i]] <- as.list(unname(par[grepl(i, names(par), TRUE)]))
  dist_par$sd_v <- c(1, dist_par$sd_v) # fix first sd to 1

  # get summed log-likelihood:
  d <- do.call(dlba, args = c(rt=list(rt), response=list(response), spar, dist_par, distribution=distribution, silent=TRUE))
  if (any(d < 1e-10)) return(1e6)
  else return(-sum(log(d)))
}

# gives same value as manual calculation above:
objective_fun(c(A=0.5, b=1, t0=0.5, mean_v1=2.4, mean_v2=1.6, sd_v2=1.2),
  rt=rt1$rt, response=rt1$response)
```
LBA

```r
## Not run:
# can we recover the parameters?
init_par <- runif(6)
names(init_par) <- c("A", "b", "t0", "mean_v1", "mean_v2", "sd_v2")
nlminb(objective_fun, start = init_par, rt=rt1$rt, response=rt1$response, lower = 0)

## End(Not run)

# plot cdf (2 accumulators):
curve(plBA(x, response = 1, A=0.5, b=1, t0 = 0.5, mean_v=c(2.4, 1.6), sd_v=c(1,1.2)),
    xlim = c(0, 2), ylim = c(0,1),
    ylab = "cumulative probability", xlab = "response time",
    main = "Defective CDFs of LBA")
curve(plBA(x, response = 2, A=0.5, b=1, t0 = 0.5, mean_v=c(2.4, 1.6), sd_v=c(1,1.2)),
    add=TRUE, lty = 2)
legend("topleft", legend=c("1", "2"), title="Response", lty=1:2)

# plot cdf (3 accumulators):
curve(plBA(x, response = 1, A=0.5, b=1, t0 = 0.5, mean_v=c(2.4, 1.6, 1.0), sd_v=c(1,1.2, 2.0)),
    xlim = c(0, 2), ylim = c(0,1),
    ylab = "cumulative probability", xlab = "response time",
    main = "Defective CDFs of LBA")
curve(plBA(x, response = 2, A=0.5, b=1, t0 = 0.5, mean_v=c(2.4, 1.6, 1.0), sd_v=c(1,1.2, 2.0)),
    add=TRUE, lty = 2)
curve(plBA(x, response = 3, A=0.5, b=1, t0 = 0.5, mean_v=c(2.4, 1.6, 1.0), sd_v=c(1,1.2, 2.0)),
    add=TRUE, lty = 3)
legend("topleft", legend=c("1", "2", "3"), title="Response", lty=1:2)

## qLBA can only return values up to maximal predicted probability:
(max_p <- plBA(Inf, response = 1, A=0.5, b=1, t0 = 0.5, mean_v=c(2.4, 1.6), sd_v=c(1,1.2)))

# [1] 0.6684696

qLBA(0.66, response = 1, A=0.5, b=1, t0 = 0.5, mean_v=c(2.4, 1.6), sd_v=c(1,1.2))

# NA

# to get predicted quantiles, scale required quantiles by maximally predicted response rate:
qs <- c(.1, .3, .5, .7, .9)
qLBA(qs*max_p, response = 1, A=0.5, b=1, t0 = 0.5, mean_v=c(2.4, 1.6), sd_v=c(1,1.2))

# or set scale_p to TRUE which scales automatically by maximum p
# (but can be slow as it calculates max_p for each probability separately)
qLBA(qs, response = 1, A=0.5, b=1, t0 = 0.5, mean_v=c(2.4, 1.6), sd_v=c(1,1.2), scale_p=TRUE)

# qLBA also accepts a data.frame as first argument:
t <- data.frame(p = rep(c(0.05, 0.1, 0.66), 2), response = rep(1:2, each = 3))
# p response
# 1 0.05 1
```
LBA-race

# 2 0.10 1
# 3 0.87 1
# 4 0.05 2
# 5 0.10 2
# 6 0.87 2
qLBA(t, A=0.5, b=1, t0 = 0.5, mean_v=c(2.4, 1.6), sd_v=c(1,1.2))

## LBA and diffusion can be used interchangeably:
rt1 <- rLBA(500, A=0.5, b=1, t0 = 0.5, mean_v=c(2.4, 1.6), sd_v=c(1,1.2))
rt2 <- rdiffusion(500, a=1, v=2, t0=0.5)

# data can also be passed as data.frame (same is true for pLBA):
sum(log(dLBA(rt1, A=0.5, b=1, t0 = 0.5, mean_v=c(2.4, 1.6), sd_v=c(1,1.2))))
sum(log(dLBA(rt2, A=0.5, b=1, t0 = 0.5, mean_v=c(2.4, 1.6), sd_v=c(1,1.2))))
sum(log(ddiffusion(rt1, a=1, v=2, t0=0.5)))
sum(log(ddiffusion(rt2, a=1, v=2, t0=0.5)))

LBA-race

LBA race functions: Likelihood for first accumulator to win.

Description

n1PDF and n1CDF take RTs, the distribution functions of the LBA, and corresponding parameter values and put them throughout the race equations and return the likelihood for the first accumulator winning (hence n1) in a set of accumulators.

Usage

n1PDF(rt, A, b, t0, ..., st0 = 0, distribution = c("norm", "gamma", "frechet", "lnorm"), args.dist = list(), silent = FALSE)
n1CDF(rt, A, b, t0, ..., st0 = 0, distribution = c("norm", "gamma", "frechet", "lnorm"), args.dist = list(), silent = FALSE)

Arguments

rt a vector of RTs.
A, b, t0 LBA parameters, see LBA. Can either be a single numeric vector (which will be recycled to reach length(rt) for trialwise parameters) or a list of such vectors in which each list element corresponds to the parameters for this accumulator (i.e., the list needs to be of the same length as there are accumulators). Each list will also be recycled to reach length(rt) for trialwise parameters per accumulator.

... two named drift rate parameters depending on distribution (e.g., mean_v and sd_v for distribution="norm"). The parameters can either be given as a numeric vector or a list. If a numeric vector is passed each element of the vector
corresponds to one accumulator. If a list is passed each element corresponds
to one accumulator allowing again trialwise drift rates. The shorter parameter
will be recycled as necessary (and also the elements of the list to match the
length of rt). See examples.

\textbf{st0}

parameter specifying the variability of \( t0 \) (which varies uniformly from \( t0 \) to \( t0 + st0 \)). Can be trialwise, and will be recycled to length of rt.

\textbf{distribution}

character specifying the distribution of the drift rate. Possible values are \texttt{c("norm", "gamma", "frechet")}, default is \texttt{"norm"}.

\textbf{args.dist}

list of optional further arguments to the distribution functions (i.e., posdrift or
robust for \texttt{distribution=="norm"}).

\textbf{silent}

logical. Should the number of accumulators used be suppressed? Default is
\texttt{FALSE} which prints the number of accumulators.

\section*{Details}

For a set of \( N \) independent accumulators \( i = 1 \ldots N \), the race likelihood for a given accumulator \( i \) is
given by

\[ L(\text{unit } i\text{ wins}) = f_i(t) \times \prod_{j<i} [S_j(t)] \]

where \( f(t) \) is the PDF (\texttt{dlba\ldots}) and \( S_j(t) = 1 - F_j(t) \) is the survivor function, that is the
complement of the CDF \( F(t) \) (\texttt{plba\ldots}) at time \( t \).

In other words, this is just the PDF/CDF for the winning accumulator at time \( t \) times the probability
that no other accumulators have finished at time \( t \).

\section*{See Also}

For more user-friendly functions that return the PDF or CDF for the corresponding (and not first)
accumulator winning see \texttt{/code/linkLBA}.

\section*{Examples}

```r
## check random generated values against race functions:

## 1. Without st0:
r_lba <- rlBA(1e4, A=0.5, b=1, t0 = 0.5, mean_v=c(1.2, 1), sd_v=0.2)
x <- seq(0.5, 4, length.out = 100) # for plotting
# PDF
y <- n1PDF(x, A=0.5, b=1, t0 = 0.5, mean_v=c(1.2, 1.0), sd_v=0.2) # PDF
hist(r_lba$r[r_lba$response==1], probability = TRUE, breaks = "FD")
lines(x=x,y=y/mean(r_lba$response == 1))
# CDF
plot(ecdf(r_lba$r[r_lba$response==1]))
y <- n1CDF(x, A=0.5, b=1, t0 = 0.5, st0 = 0, mean_v=c(1.2, 1.0), sd_v=0.2)
lines(x=x,y=y/mean(r_lba$response == 1), col = "red", lwd = 4.5, lty = 2)
# KS test
## Not run:
normalised_n1CDF = function(rt,...) n1CDF(rt,...)/n1CDF(rt=Inf,...)
```
ks.test(r_lba$response == 1), normalised_n1CDF, A=0.5, b=1, t0 = 0.5, mean_v=c(1.2, 1.0), sd_v=0.2)

## End(Not run)

## 2. With st0 = 0.2:

r_lba <- rLBA(1e4, A=0.5, b=1, t0 = 0.5, st0 = 0.2, mean_v=c(1.2, 1.0), sd_v=0.2)
x <- seq(0.5, 4, length.out = 100) # for plotting

# PDF
y <- n1PDF(x, A=0.5, b=1, t0 = 0.5, st0 = 0.2, mean_v=c(1.2, 1.0), sd_v=0.2) # PDF
hist(r_lba$response == 1), probability = TRUE, breaks = "FD")
lines(x=x, y=y/mean(r_lba$response == 1))

# CDF
plot(ecdf(r_lba$response == 1))
y <- n1CDF(x, A=0.5, b=1, t0 = 0.5, st0 = 0.2, mean_v=c(1.2, 1.0), sd_v=0.2)
lines(x=x, y=y/mean(r_lba$response == 1), col = "red", lwd = 4.5, lty = 2)

# KS test

## End(Not run)

## Other examples:

xx <- rLBA(10, A=0.5, b=1, t0 = 0.5, mean_v=1.2, sd_v=0.2)

# default uses normal distribution for drift rate:
n1PDF(xx$rt, A=0.5, b=1, t0 = 0.5, mean_v=c(1.2, 1.0), sd_v=0.2)

# other distributions:
n1PDF(xx$rt, A=0.5, b=1, t0 = 0.5, shape_v=c(1.2, 1.0), scale_v=c(0.2, 0.3), distribution = "gamma")
n1PDF(xx$rt, A=0.5, b=1, t0 = 0.5, shape_v=c(1.2, 1.0), scale_v=c(0.2, 0.3), distribution = "frechet")
n1PDF(xx$rt, A=0.5, b=1, t0 = 0.5, meanlog_v = c(0.5, 0.8), sdlog_v = 0.5, distribution = "lnorm")

# add st0:
n1PDF(xx$rt, A=0.5, b=1, t0 = 0.5, mean_v=c(1.2, 1.0), sd_v=0.2, st0 = 0.4)

# use different A parameters for each RT:
n1PDF(xx$rt, A=runif(10, 0.4, 0.6),
   b=1, t0 = 0.5, mean_v=c(1.2, 1.0), sd_v=0.2)

# use different A parameters for each RT and each accumulator:
n1PDF(xx$rt, A=list(runif(10, 0.4, 0.6), runif(10, 0.2, 0.4)),
   b=1, t0 = 0.5, mean_v=c(1.2, 1.0), sd_v=0.2)

### vectorize drift rates:

# vector versus list:
v1 <- n1PDF(xx$rt, A=0.5, b=1, t0 = 0.5, mean_v=c(1.2, 1.0), sd_v=0.2)
v2 <- nPDF(xx$rt, A=0.5, b=1, t0 = 0.5, mean_v=list(1.2, 1.0), sd_v=0.2)
identical(v1, v2)  # TRUE

# drift rate per trial:
nPDF(xx$rt, A=0.5, b=1, t0 = 0.5, mean_v=list(rnorm(10, 1.2), rnorm(10, 1))), sd_v=0.2)

# combine list with vector:
nPDF(xx$rt, A=0.5, b=1, t0 = 0.5, mean_v=list(rnorm(10, 1.2), rnorm(10, 1)), sd_v=c(0.2, 0.1))

# t0 per trial and accumulator:
nPDF(xx$rt, A=0.5, b=1, t0 = c(0.5), mean_v=c(1.2, 1.0), sd_v=0.2)  # per trial only
nPDF(xx$rt, A=0.5, b=1, t0 = list(0.5, 0.6), mean_v=c(1.2, 1.0), sd_v=0.2)  # per drift rate only
nPDF(xx$rt, A=0.5, b=1, t0 = list(c(0.4, 0.5), c(0.5, 0.6)), mean_v=c(1.2, 1.0), sd_v=0.2)

---

**Ratcliff and Rouder (1998, Exp. 1) Luminance Discrimination Data**

**Description**

Responses and response times from an experiment in which three participants were asked to decide whether the overall brightness of pixel arrays displayed on a computer monitor was "high" or "low". In addition, instruction manipulated speed and accuracy between blocks.

**Usage**

`rr98`

**Format**

A data.frame with 24,358 obs. and 12 variables:

- **id** participant id, factor with three levels
- **session** session number, integer
- **block** block number, integer
- **trial** trial number within a block, integer
- **instruction** factor with two levels: "accuracy" for blocks with accuracy instructions; "speed" for blocks with speed instruction
- **source** factor with two levels: distribution strength was drawn from, "dark" and "light"
- **strength** proportion of white to black pixels were varied by 33 equally spaced proportions from zero (all 1,024 pixels were black) to 1 (all 1,024 pixels were white). With 0 darkest and 32 lightest. Integer.
- **response** factor with two levels: "dark" and "light"
- **response_num** numeric response variable such that 1="dark" and 2="light"
The Experiment is described in the following by Ratcliff and Rouder (1998, pp. 349):

In Experiment 1, subjects were asked to decide whether the overall brightness of pixel arrays displayed on a computer monitor was "high" or "low". The brightness of a display was controlled by the proportion of the pixels that were white. For each trial, the proportion of white pixels was chosen from one of two distributions, a high distribution [i.e., light] or a low [i.e., dark] distribution, each with fixed mean and standard deviation. Feedback was given after each trial to tell the subject whether his or her decision had correctly indicated the distribution from which the stimulus had been chosen. Other than this feedback, a subject had no information about the distributions. Because the distributions overlapped substantially, a subject could not be highly accurate. A display with 50 from the high distribution on one trial and the low distribution on another.

Stimuli:

The stimulus display for Experiment 1 was a square that was 64 pixels on each side and subtended 3.8 degree of visual angle on a PC-VGA monitor. [...] In each square, 3,072 randomly chosen pixels were neutral gray, like the background, and the remaining 1,024 pixels were either black or white; the proportion of white to black pixels provided the brightness manipulation. There were 33 equally spaced proportions from zero (all 1,024 pixels were black) to 1 (all 1,024 pixels were white). The two distributions from which the bright and dark stimuli were chosen were centered at .375 (low brightness) and .625 (high brightness), and they each had a standard deviation of .1875.

Procedure: A subject’s task was to decide, on each trial, from which distribution, high or low brightness in Experiment 1, the observed stimulus (stimuli) had been sampled. Subjects made their decision by pressing one of two response keys. On each trial, a 500-ms foreperiod, during which the display consisted solely of neutral gray, was followed by presentation of the stimulus; presentation was terminated by the subject’s response. In Experiment 1, speed-versus-accuracy instructions were manipulated. For some blocks of trials, subjects were instructed to respond as quickly as possible, and a "too slow" message followed every response longer than 550 ms. For other blocks of trials, subjects were instructed to be as accurate as possible, and a "bad error" message followed incorrect responses to stimuli from the extreme ends of the distributions. Experiment 1 had ten 35-min sessions, and Experiments 2 and 3 had four sessions. In Experiment 1, subjects switched from emphasis on speed to emphasis on accuracy every 204 trials. Each session consisted of eight blocks of 102 trials per block, for a total of 8,160 trials per subject. Each session consisted of eight blocks of 102 trials, for a total of 3,264 trials per subject in each experiment. For all trials in each experiment, subjects were instructed to maintain a high level of accuracy while responding quickly, and an "error" message indicated incorrect responses. Responses were followed by a 300-ms blank interval, and the error message was displayed for 300 ms after the blank interval.
Note

The data is already prepared following Ratcliff and Rouder (1998) by removing the following trials:

- the first session for each participant
- the first 20 trials of each session
- the first trial of each block (each change in speed accuracy starts a new block)

To fully replicate the data used by Ratcliff and Rouder (1998) one only needs to remove the trials that are TRUE in column outlier (i.e., RTs outside of (200ms, 2500ms)). The full raw data is also available as part of this package, see:

system.file("extdata", "rr98-data", package = "rtdist") and system.file("extdata", "rr98-data.codes", package = "rtdist")

Source


Examples

data(rr98)
rr98 <- rr98[-rr98$outlier,]  # remove outliers
head(rr98)
# id session block trial instruction source strength response response_num correct rt outlier
# 1 jf 2 1 21 accuracy dark 8 dark 1 TRUE 0.801 FALSE
# 2 jf 2 1 22 accuracy dark 7 dark 1 TRUE 0.680 FALSE
# 3 jf 2 1 23 accuracy light 19 light 2 TRUE 0.694 FALSE
# 4 jf 2 1 24 accuracy dark 21 light 2 FALSE 0.582 FALSE
# 5 jf 2 1 25 accuracy light 19 dark 1 FALSE 0.925 FALSE
# 6 jf 2 1 26 accuracy dark 10 dark 1 TRUE 0.685 FALSE

# See vignette for more examples.

single-LBA

Single accumulator of linear ballistic accumulator (LBA)

Description

Density, distribution function, and random generation for a single accumulator of the LBA model with the following parameters: A (upper value of starting point), b (response threshold), t₀ (non-decision time), and drift rate (v). All functions are available with different distributions underlying the drift rate: Normal (norm), Gamma (gamma), Frechet (frechet), and log normal (lnorm).
Usage

\[
\text{dlba\_norm}(rt, A, b, t0, mean_v, sd_v, \text{posdrift} = \text{TRUE}, \text{robust} = \text{FALSE})
\]

\[
\text{plba\_norm}(rt, A, b, t0, mean_v, sd_v, \text{posdrift} = \text{TRUE}, \text{robust} = \text{FALSE})
\]

\[
\text{rlba\_norm}(n, A, b, t0, mean_v, sd_v, st0 = 0, \text{posdrift} = \text{TRUE})
\]

\[
\text{dlba\_gamma}(rt, A, b, t0, \text{shape}_v, \text{rate}_v, \text{scale}_v)
\]

\[
\text{plba\_gamma}(rt, A, b, t0, \text{shape}_v, \text{rate}_v, \text{scale}_v)
\]

\[
\text{rlba\_gamma}(n, A, b, t0, \text{shape}_v, \text{rate}_v, \text{scale}_v, st0 = 0)
\]

\[
\text{dlba\_frechet}(rt, A, b, t0, \text{shape}_v, \text{scale}_v)
\]

\[
\text{plba\_frechet}(rt, A, b, t0, \text{shape}_v, \text{scale}_v)
\]

\[
\text{rlba\_frechet}(n, A, b, t0, \text{shape}_v, \text{scale}_v, st0 = 0)
\]

\[
\text{dlba\_lnorm}(rt, A, b, t0, \text{meanlog}_v, \text{sdlog}_v, \text{robust} = \text{FALSE})
\]

\[
\text{plba\_lnorm}(rt, A, b, t0, \text{meanlog}_v, \text{sdlog}_v, \text{robust} = \text{FALSE})
\]

\[
\text{rlba\_lnorm}(n, A, b, t0, \text{meanlog}_v, \text{sdlog}_v, st0 = 0)
\]

Arguments

- **rt**: a vector of RTs.
- **A**: start point interval or evidence in accumulator before beginning of decision process. Start point varies from trial to trial in the interval \([0, A]\) (uniform distribution). Average amount of evidence before evidence accumulation across trials is \(A/2\).
- **b**: response threshold. \((b - A/2)\) is a measure of "response caution".
- **t0**: non-decision time or response time constant (in seconds). Lower bound for the duration of all non-decisional processes (encoding and response execution).
- **mean_v, sd_v**: mean and standard deviation of normal distribution for drift rate (\text{norm}). See \text{Normal}
- **posdrift**: logical. Should drift rates be forced to be positive? Default is \text{TRUE}. (Uses truncated normal for random generation).
- **robust**: logical. Should robust normal distributions be used for \text{norm} and \text{lnorm}? Can be helpful in rare cases but is approximately three times slower than the non-robust versions. Default is \text{FALSE}.
- **n**: desired number of observations (scalar integer).
- **st0**: variability of non-decision time, such that \(t0\) is uniformly distributed between \(t0\) and \(t0 + st0\). Only available in random number generation functions \text{rlba\_}.
single-LBA

`shape_v`, `rate_v`, `scale_v`
shape, rate, and scale of gamma (`gamma`) and scale and shape of Frechet (`frechet`) distributions for drift rate. See `GammaDist` or `frechet`. For Gamma, scale = 1/shape and shape = 1/scale.

`meanlog_v`, `sdlog_v`
mean and standard deviation of lognormal distribution on the log scale for drift rate (`lnorm`). See `Lognormal`.

Details
These functions are mainly for internal purposes. We do not recommend to use them. Use the high-level functions described in `link(LBA)` instead.

Value
All functions starting with a `d` return the density (PDF), all functions starting with a `p` return the distribution function (CDF), and all functions starting with a `r` return random response times and responses (in a `data.frame`).

Note
Density (i.e., `dlba_`), distribution (i.e., `plba_`), and random derivative (i.e., `rlba_`) functions are vectorized for all parameters (i.e., in case parameters are not of the same length as `rt`, parameters are recycled). Furthermore, the random derivative functions also accept a matrix of length `n` in which each column corresponds to a accumulator specific value (see `rlba` for a more user-friendly way).

References

Examples
```r
## random number generation using different distributions for v:
rlba_norm(10, A=0.5, b=1, t0 = 0.5, mean_v=c(1.2, 1), sd_v=c(0.2,0.3))
rlba_gamma(10, A=0.5, b=1, t0 = 0.5, shape_v=c(1.2, 1), scale_v=c(0.2,0.3))
rlba_frechet(10, A=0.5, b=1, t0 = 0.5, shape_v=c(1.2, 1), scale_v=c(0.2,0.3))
rlba_lnorm(10, A=0.5, b=1, t0 = 0.5, meanlog_v=c(1.2, 1), sdlog_v=c(0.2, 0.3))

# use somewhat plausible values for plotting:
A <- 0.2
b <- 0.5
t0 <- 0.3
```
# plot density:
curve(dlba_norm(x, A=A, b=b, t0=t0, mean_v = 1.0, sd_v = 0.5), ylim = c(0, 4),
xlim=c(0,3), main="Density/PDF of LBA versions", ylab="density", xlab="response time")
curve(dlba_gamma(x, A=A, b=b, t0=t0, shape_v=1, scale_v=1), add=TRUE, lty = 2)
curve(dlba_frechet(x, A=A, b=b, t0=t0, shape_v=1, scale_v=1), add=TRUE, lty = 3)
curve(dlba_lnorm(x, A=A, b=b, t0=t0, meanlog_v = 0.5, sdlog_v = 0.5), add=TRUE, lty = 4)
legend("topright", legend=c("Normal", "Gamma", "Frechet", "Log-Normal"),
title = expression("Distribution of"~italic(v)), lty = 1:4)

# plot cdf:
curve(plba_norm(x, A=A, b=b, t0=t0, mean_v=1.0, sd_v=1.0),
xlim = c(0, 3), ylim = c(0,1),
ylab = "cumulative probability", xlab = "response time",
main = "Distribution/CDF of LBA versions")
curve(plba_gamma(x, A=A, b=b, t0=t0, shape_v=1, scale_v=1), add=TRUE, lty = 2)
curve(plba_frechet(x, A=A, b=b, t0=t0, shape=1, scale=1), add=TRUE, lty = 3)
curve(plba_lnorm(x, A=A, b=b, t0=t0, meanlog_v=0.5, sdlog_v=0.5), add=TRUE, lty = 4)
legend("bottomright", legend=c("Normal", "Gamma", "Frechet", "Log-Normal"),
title = expression("Distribution of"~italic(v)), lty = 1:4)

---

speed_acc  
*Speed-Accuracy Data from Wagenmakers, Ratcliff, Gomez, & McKoon (2008, Experiment 1)*

**Description**

Responses and response times from an experiment in which instruction manipulated speed and accuracy between blocks. This data was also analyzed by Heathcote and Love (2012) who were the first to use the 17 participants also included here.

**Usage**

`speed_acc`

**Format**

A `data.frame` with 31,522 obs. and 9 variables:

- `id` participant id
- `block` block number
- `condition` accuracy for blocks with accuracy instructions; speed for blocks with speed instruction
- `stim` unique identifier of stimulus, stimuli are nested in frequency conditions
- `stim_cat` category of stimulus, either word or non-word
- `frequency` "high frequency word", "low frequency word", "very low frequency word", or non-words derived from the first three categories
response word, nonword, or not interpretable response (error, i.e., pushed a button, but not the right one and also not the one next to the right button)

rt response time in seconds

censor boolean indicating whether or not a response should be eliminated prior to analysis; uninterpretable response, too fast response (<180 ms), too slow response (>3 sec)

Details

The data excludes the practice blocks but includes all trials. Variable censor can be used for excluding all trials also excluded from the papers using it namely uninterpretable response, too fast response (<180 ms), too slow response (>3 sec). Heathcote and Love (2012, p. 7) describe the data as follows:

We fit the LBA and LNR models to data from Wagenmaker et al.’s (2008) experiment one, where participants made decisions about whether a string of letters constituted a word. These lexical decisions were made about four types of stimuli, non-words (nw) and high-frequency (hf), low-frequency (lf), and very low-frequency (vlf) words. Participants made decisions either under speed or accuracy emphasis instructions in different experimental blocks. Accuracy blocks were preceded by the message “Try to respond accurately” and ”ERROR” was displayed after each wrong response. Speed blocks were preceded by the message ”Try to respond accurately” and ”TOO SLOW” was displayed after each response slower than 0.75 s. We report analyses of data from 17 participants (31,412 data points) in their Experiment 1, including the 15 participants analyzed in Wagenmakers et al. (2008) and two extras (we thank Eric-Jan Wagenmakers for supplying this data).

Source


References


Examples

data(speed_acc)
str(speed_acc)

# remove excluded trials:
speed_acc <- droplevels(speed_acc[!speed_acc$censor,])

# new factors for obtaining values as in table 1, Wagenmakers et al. (2008, p. 152)
speed_acc$freq <- with(speed_acc,
  factor(ifelse(stim_cat == "nonword", "nonword",
    as.character(frequency)),
  levels = c("high", "low", "very_low", "nonword"))
# corr = correct (0 = correct, 1 = error)
speed_acc$corr <- with(speed_acc, 1-as.numeric(stim_cat == response))
str(speed_acc)

## aggregated RTs:
aggregate(rt ~ condition + freq + corr, speed_acc, mean)

## Error Rate:
aggregate(corr ~ condition + freq + corr, speed_acc, mean)
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