Package 'sensR'

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Description Provides methods for sensory discrimination methods; duotrio, tetrad, triangle, 2-AFC, 3-AFC, A-not A, same-different, 2-AC and degree-of-difference.
This enables the calculation of d-primes, standard errors of d-primes, sample size and power computations, and comparisons of different d-primes. Methods for profile likelihood confidence intervals and plotting are included. Most methods are described in Brockhoff, P.B. and Christensen, R.H.B. (2010) <doi:10.1016/j.foodqual.2009.04.003>.

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URL https://github.com/aigorahub/sensR

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NeedsCompilation no

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AnotA *Analysis of A-not-A tests*

Description

Computation of dprime and it's uncertainty for the monadic A-not-A test together with the one-tailed P-value of the difference test (Fisher's Exact test).

Usage

```
AnotA(x1, n1, x2, n2, ...)

## S3 method for class 'anota'
confint(object, parm, level = 0.95, ...)

## S3 method for class 'anota'
plot(x, main = TRUE, length = 1000, ...)
```

Arguments

x1	the number of (correct) A-answers on A-samples
n1	the total number of A-samples
x2	the number of A-answers on not-A-samples
n2	the number of not-A-samples
object	an anota object
parm	currently not used
level	the desired confidence level
x	an anota object
main	should the plot have a main title?
length	the discretization of the curves
...	additional arguments passed to glm for AnotA; not used for confint and plot

Details

The AnotA function uses the glm and fisher.test functions of the stats package. Note that all arguments have to be positive integers.

Value

For AnotA an object of class anota (which has a print method). This is a list with elements

coefficients	named vector of coefficients (d-prime)
res.glm	the glm-object from the fitting process

vcov	variance-covariance matrix of the coefficients
se	named vector with standard error of the coefficients (standard error of d-prime
data	a named vector with the data supplied to the function
p.value	one-sided p-value from Fisher's exact test (fisher.test)
test	a string with the name of the test (A-Not A) for the print method
call	the matched call

For plot a figure of the distributions of sensory intensity is produced, and for confint a 2-by-2 matrix of confidence intervals is returned.

Author(s)

Rune Haubo B Christensen and Per Bruun Brockhoff

References

Brockhoff, P.B. and Christensen, R.H.B. (2010). Thurstonian models for sensory discrimination tests as generalized linear models. Food Quality and Preference, 21, pp. 330-338.

See Also

print.discrim, discrim, discrimPwr, discrimSim, discrimSS, findcr

Examples

```
# data: 10 of the A-samples were judged to be A
#       20 A-samples in total
#       3 of the not-A samples were judged to be A
#       20 not-A-samples in total

AnotA(10, 20, 3, 20)
(m1 <- AnotA(10, 20, 3, 20))

## plot distributions of sensory intensity:
plot(m1)

## likelihood based confidence intervals:
confint(m1)


## Extended example plotting the profile likelihood
xt <- cbind(c(3, 10), c(20 - 3, 20 - 10))
lev <- gl(2, 1)
summary(res <- glm(xt ~ lev,
                   family = binomial(link = probit)))
N <- 100
dev <- double(N)
level <- c(0.95, 0.99)
delta <- seq(1e-4, 5, length = N)
for(i in 1:N)
```

```
  dev[i] <- glm(xt ~ 1 + offset(c(0, delta[i])),
                family = binomial(probit))$deviance
plot(delta, exp(-dev/2), type = "l",
     xlab = expression(delta),
     ylab = "Normalized Profile Likelihood")
## Add Normal approximation:
lines(delta, exp(-(delta - coef(res)[2])^2 /
                 (2 * vcov(res)[2,2])), lty = 2)
## Add confidence limits:
lim <- sapply(level, function(x)
              exp(-qchisq(x, df=1)/2) )
abline(h = lim, col = "grey")
```

AUC *AUC computation*

Description

This is the default AUC function for scalar d-primes, which will compute Area Under the ROC curve (ROC is an acronym for receiver operating characteristic) assuming a normal distribution for the underlying percepts.

Usage

```
## Default S3 method:
AUC(d, se.d, scale = 1, CI.alpha = 0.05, ...)

## S3 method for class 'anota'
AUC(d, CI.alpha = 0.05, ...)
```

Arguments

d	a unit lenght vector with the value of d-prime for which AUC is to be computed or a anota object from the fitting of a A-not A test with AnotA
scale	a unit length vector giving the ratio of scale (ie. standard deviation) of the latent distribution for the no-class items relative to that of the yes-class items
se.d	standard error of d (d-prime). If provided, the function will compute confidence limits of value of AUC—cf. in section value.
CI.alpha	the type I level of the confidence interval of AUC
...	additional arguments passed integrate

Details

The AUC is computed using the standard normal distribution function pnorm.

Confidence limits are based on a normal approximation of d and not of AUC. The limits are computed, if an estimate of the standard error of d is provided. Note that the limits do not take the uncertainty in estimating the scale nor that of estimating the standard error of d into account.

A print method is implemented for objects of class AUC.

Value

A list with components. If se.d is supplied to the default method or if a discrim object is supplied, the object contains the latter three additional elements.

value	the estimated value of AUC
res.int	the result from the call to integrate
lower	the lower confidence limit
upper	the upper confidence limit
CI.alpha	echoes the provided CI.alpha

Author(s)

Rune Haubo B Christensen

Examples

```
## Compute AUC from d-prime and confindence interval for the AUC:
fm1 <- AnotA(8, 25, 1, 25)
AUC(d=fm1$coef, se.d=fm1$se)
## The AUC-method for AnotA-objects can be used for convenience:
AUC(fm1)
```

---

betabin — *Beta-binomial and chance-corrected beta-binomial models for over-dispersed binomial data*

Description

Fits the beta-binomial model and the chance-corrected beta-binomial model to (over-dispersed) binomial data.

Usage

```
betabin(data, start = c(.5,.5),
        method = c("duotrio", "tetrad", "threeAFC", "twoAFC",
          "triangle", "hexad", "twofive", "twofiveF"),
        vcov = TRUE, corrected = TRUE, gradTol = 1e-4, ...)

## S3 method for class 'betabin'
summary(object, level = 0.95, ...)
```

Arguments

data	matrix or data.frame with two columns; first column contains the number of success and the second the total number of cases. The number of rows should correspond to the number of observations.
start	starting values to be used in the optimization
vcov	logical, should the variance-covariance matrix of the parameters be computed?
method	the sensory discrimination protocol for which d-prime and its standard error should be computed
corrected	should the chance corrected or the standard beta binomial model be estimated?
gradTol	a warning is issued if max|gradient| < gradTol, where 'gradient' is the gradient at the values at which the optimizer terminates. This is not used as a termination or convergence criterion during model fitting.
object	an object of class "betabin", i.e. the result of `betabin()`.
level	the confidence level of the confidence intervals computed by the summary method
...	`betabin`: The only recognized (hidden) argument is `doFit` (boolean) which by default is `TRUE`. When `FALSE` `betabin` returns an environment which facilitates examination of the likelihood surface via the (hidden) functions `sensR:::getParBB` and `sensR:::setParBB`. Not used in `summary.betabin`.

Details

The beta-binomial models are parameterized in terms of mu and gamma, where mu corresponds to a probability parameter and gamma measures over-dispersion. Both parameters are restricted to the interval (0, 1). The parameters of the standard (i.e. corrected = FALSE) beta-binomial model refers to the mean (i.e. probability) and dispersion on the scale of the observations, i.e. on the scale where we talk of a probability of a correct answer (Pc). The parameters of the chance corrected (i.e. corrected = TRUE) beta-binomial model refers to the mean and dispersion on the scale of the "probability of discrimination" (Pd). The mean parameter (mu) is therefore restricted to the interval from zero to one in both models, but they have different interpretations.

The summary method use the estimate of mu to infer the parameters of the sensory experiment; Pc, Pd and d-prime. These are restricted to their allowed ranges, e.g. Pc is always at least as large as the guessing probability.

Confidens intervals are computed as Wald (normal-based) intervals on the mu-scale and the confidence limits are subsequently transformed to the Pc, Pd and d-prime scales. Confidence limits are

restricted to the allowed ranges of the parameters, for example no confidence limits will be less than zero.

Standard errors, and therefore also confidence intervals, are only available if the parameters are not at the boundary of their allowed range (parameter space). If parameters are close to the boundaries of their allowed range, standard errors, and also confidence intervals, may be misleading. The likelihood ratio tests are more accurate. More accurate confidence intervals such as profile likelihood intervals may be implemented in the future.

The summary method provides a likelihood ratio test of over-dispersion on one degree of freedom and a likelihood ratio test of association (i.e. where the null hypothesis is "no difference" and the alternative hypothesis is "any difference") on two degrees of freedom (chi-square tests). Since the gamma parameter is tested on the boundary of the parameter space, the correct degree of freedom for the first test is probably 1/2 rather than one, or somewhere in between, and the latter test is probably also on less than two degrees of freedom. Research is needed to determine the appropriate no. degrees of freedom to use in each case. The choices used here are believed to be conservative, so the stated p-values are probably a little too large.

The log-likelihood of the standard beta-binomial model is

$$\ell(\alpha,\beta;x,n)=\sum_{j=1}^{N}\left\{\log\binom{n_j}{x_j}-\log Beta(\alpha,\beta)+\log Beta(\alpha+x_j,\beta-x_j+n_j)\right\}$$

and the log-likelihood of the chance corrected beta-binomial model is

$$\ell(\alpha,\beta;x,n)=\sum_{j=1}^{N}\left\{C+\log\left[\sum_{i=0}^{x_j}\binom{x_j}{i}(1-p_g)^{n_j-x_j+i}p_g^{x_j-i}Beta(\alpha+i,n_j-x_j+\beta)\right]\right\}$$

where

$$C=\log\binom{n_j}{x_j}-\log Beta(\alpha,\beta)$$

and where $\mu=\alpha/(\alpha+\beta)$, $\gamma=1/(\alpha+\beta+1)$, $Beta$ is the Beta function, cf. `beta`, N is the number of independent binomial observations, i.e.~the number of rows in `data`, and p_g is the guessing probability, `pGuess`.

The variance-covariance matrix (and standard errors) is based on the inverted Hessian at the optimum. The Hessian is obtained with the `hessian` function from the numDeriv package.

The gradient at the optimum is evaluated with `gradient` from the numDeriv package.

The bounded optimization is performed with the "L-BFGS-B" optimizer in `optim`.

The following additional methods are implemented objects of class `betabin`: `print`, `vcov` and `logLik`.

Value

An object of class `betabin` with elements

`coefficients`	named vector of coefficients
`vcov`	variance-covariance matrix of the parameter estimates if `vcov = TRUE`
`data`	the data supplied to the function

call	the matched call
logLik	the value of the log-likelihood at the MLEs
method	the method used for the fit
convergence	0 indicates convergence. For other error messages, see optim.
message	possible error message - see optim for details
counts	the number of iterations used in the optimization - see optim for details
corrected	is the chance corrected model estimated?
logLikNull	log-likelihood of the binomial model with prop = pGuess
logLikMu	log-likelihood of a binomial model with prop = sum(x)/sum(n)

Author(s)

Rune Haubo B Christensen

References

Brockhoff, P.B. (2003). The statistical power of replications in difference tests. Food Quality and Preference, 14, pp. 405–417.

See Also

triangle, twoAFC, threeAFC, duotrio, tetrad twofive, twofiveF, hexad

Examples

```
## Create data:
x <- c(3,2,6,8,3,4,6,0,9,9,0,2,1,2,8,9,5,7)
n <- c(10,9,8,9,8,6,9,10,10,10,9,9,10,10,10,10,9,10)
dat <- data.frame(x, n)

## Chance corrected beta-binomial model:
(bb0 <- betabin(dat, method = "duotrio"))
summary(bb0)
## Un-corrected beta-binomial model:
(bb <- betabin(dat, corrected = FALSE, method = "duotrio"))
summary(bb)
vcov(bb)
logLik(bb)
AIC(bb)
coef(bb)
```

clls-deprecated *Cumulative Link Location-Scale Models*

Description

IMPORTANT: This function and its methods are no longer supported. The user is adviced to use clm() from package ordinal instead.

Fits a cumulative link location-scale model to an ordered response variable. When the scale part is left unspecified, the model reduces to a cumulative link model assuming a constant scale. With the default logistic link function, the model reduces to the famous *Proportional Odds Model*. With the probit link and a single two-level factor in both location and scale parts, the model is known as the *Binormal* model in the Signal Detection Theory and the Psychometric literature.

Usage

```
clls(location, scale, data, weights, start, ..., subset,
         na.action, contrasts = NULL, Hess = FALSE, model = TRUE,
         method = c("logistic", "probit", "cloglog", "cauchit"))
```

Arguments

location	a formula expression as for regression models, of the form `response ~ predictors`. The response should be a factor (preferably an ordered factor), which will be interpreted as an ordinal response, with levels ordered as in the factor. The model must have an intercept: attempts to remove one will lead to a warning and be ignored. An offset may be used. See the documentation of `formula` for other details.
scale	a optional formula expression as for the location part, of the form `~ predictors`, ie. with an empty left hand side. If left unspecified, the model assumes a constant scale and reduces to the cumulative link model. An offset may be used. See the documentation of `formula` for other details.
data	an optional data frame in which to interpret the variables occurring in `formula`.
weights	optional case weights in fitting. Default to 1.
start	initial values for the parameters. This is in the format `c(beta, theta, sigma)`: see the Values section.
...	additional arguments to be passed to `optim`, most often a `control` argument.
subset	expression saying which subset of the rows of the data should be used in the fit. All observations are included by default.
na.action	a function to filter missing data.
contrasts	a list of contrasts to be used for some or all of the factors appearing as variables in the model formula.
Hess	logical for whether the Hessian (the observed information matrix) should be returned. Use this if you intend to call `summary` or `vcov` on the fit.
model	logical for whether the model matrix should be returned.

method	logistic or probit or complementary log-log or cauchit (corresponding to a Cauchy latent variable).

Details

The implementation is highly inspired by polr in package MASS and should give compatible results, if scale is left unspecified.

Note that standard errors are appropriate for tau = log sigma and not for sigma, because the profile likelihood is usually more symmetric for tau than for sigma. Therefore vcov will give the variance-covariance matrix of the parameters with tau rather than sigma and summary.clls will report standard errors for log sigma. Notice also that a relevant test for sigma is $H_0 : sigma = 1$, so the relevant test for log sigma is $H_0 : log(sigma) = 0$. This is reflected in the z value for sigma returned by summary.clls.

There are methods for the standard model-fitting functions, including summary, vcov, anova, and an extractAIC method.

Value

A object of class "clls". This has components

coefficients	the coefficients of the location (beta), the intercepts (theta) and the scale (sigma).
beta	the parameter estimates of the location part.
theta	the intercepts/thresholds for the class boundaries.
sigma	the parameter estimates of the scale part.
tau	parameter estimates of the scale part on the log scale; ie. tau = log sigma.
deviance	the residual deviance.
fitted.values	a matrix, with a column for each level of the response with the fitted probabilities.
fitted.case	a vector of same length as response, with the fitted probabilities on a case-by-case basis.
lev	the names of the response levels.
terms.location	a terms structure describing the location part.
terms.scale	a terms structure describing the scale part.
df.residual	the number of residual degrees of freedoms, calculated using the weights.
edf	the (effective) number of degrees of freedom used by the model
n, nobs	the (effective) number of observations, calculated using the weights.
call	the matched call.
method	the matched method used.
convergence	the convergence code returned by optim.
niter	the number of function and gradient evaluations used by optim.
Hessian	if Hess is true, the observed Fisher information matrix.
location	if model is true, the model.frame for the location part.
scale	if model is true, the model.frame for the scale part.

References

Agresti, A. (2002) *Categorical Data.* Second edition. Wiley.

Christensen, R.H.B., Cleaver, G. and Brockhoff, P.B. (2011). Statistical and Thurstonian models for the A-not A protocol with and without sureness. *Food Quality and Preference*, 22(6), pp.542-549.

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S.* Fourth edition. Springer.

See Also

polr, optim, glm, multinom.

Examples

```
old <- options(contrasts = c("contr.treatment", "contr.poly"))
## Extend example from polr in package MASS:
## Fit model from polr example:
data(housing, package = "MASS")
fm1 <- clls(Sat ~ Infl + Type + Cont, weights = Freq, data = housing)
fm1
summary(fm1)
## With probit link:
summary(update(fm1, method = "probit"))

## Allow scale to depend on Cont-variable
summary(fm2 <- update(fm1, scale =~ Cont))
anova(fm1, fm2)
## which seems to improve the fit
options(old)
```

---

clm2twoAC *Extract 2-AC coefficient table from a cumulative link model*

Description

The Thurstonian model for the 2-AC protocol can be formulated as a cumulative link model (see the references). This function extracts the 2-AC model parameter estimates, standard errors, z-value and p-values from a cumulative link (mixed) model fitted with clm or clmm from package ordinal.

Usage

```
clm2twoAC(object, ...)
```

Arguments

object	a clm or clmm object
...	not currently used.

Value

A `data.frame` with the coefficient table. The two first rows contain the estimates of `tau` and `d.prime` while the remaining rows contain optional regression variables for `d.prime`.

Author(s)

Rune Haubo B Christensen

References

Christensen R.H.B., Lee H-S and Brockhoff P.B. (2012). Estimation of the Thurstonian model for the 2-AC protocol. Food Quality and Preference, 24(1), pp.119-128.

See Also

twoAC, twoACpwr

Examples

```
## Example of a simple 2-AC model. First the conventional way:
twoAC(c(2, 2, 6))

## The using a cumulative link model (clm from package ordinal):
if(require(ordinal)) {
    response <- gl(3,1)
    fit.clm <- clm(response ~ 1, weights = c(2, 2, 6), link = "probit")
    clm2twoAC(fit.clm)
    ## Alternatively we could get estimates and standard errors "by hand":
    tab <- coef(summary(fit.clm))
    theta <- tab[,1]
    (tau <- (theta[2] - theta[1])/sqrt(2))
    (d.prime <- (-theta[2] - theta[1])/sqrt(2))
    VCOV <- vcov(fit.clm)
    (se.tau <- sqrt((VCOV[1,1] + VCOV[2,2] - 2*VCOV[2,1])/2))
    (se.d.prime <- sqrt((VCOV[1,1] + VCOV[2,2] + 2*VCOV[2,1])/2))

    ## Extended example with a regression model for d.prime
    ## (see the referenced paper for details):
    n.women <- c(2, 2, 6)*10
    n.men <- c(1, 2, 7)*10
    wt <- c(n.women, n.men)
    response <- gl(3,1, length = 6)
    gender <- gl(2, 3, labels = c("women", "men"))
    fm2 <- clm(response ~ gender, weights = wt, link = "probit")
    clm2twoAC(fm2)
}
```

`confint.twoAC` *Confidence intervals and profile likelihoods for parameters in 2AC models*

Description

Computes confidence intervals from the profiled likelihood and the Wald approximation in the 2AC model, or plots the profile likelihood function for d.prime.

Usage

```
## S3 method for class 'twoAC'
confint(object, parm, level = 0.95,
        type = c("likelihood", "Wald"), ...)

## S3 method for class 'profile.twoAC'
confint(object, parm = "d.prime", level = 0.95, ...)

## S3 method for class 'twoAC'
profile(fitted, alpha = 1e-3, nSteps = 1e2, range, ...)

## S3 method for class 'profile.twoAC'
plot(x, level = c(0.95, 0.99), Log = FALSE,
      relative = TRUE, fig = TRUE, n = 1e3, ..., ylim = NULL)
```

Arguments

`object`	a fitted `twoAC` object or a `profile.twoAC` object.
`fitted`	a fitted `twoAC` object.
`x`	a `profile.twoAC` object.
`type`	the type of confidence interval required. `"profile"` is the most accurate.
`parm`	For `confint.profile.twoAC`: has to be `"d.prime"`. For `confint.twoAC`: for `type = "Wald"` a specification of which parameters the confidence interval is required for. Ignored for `type = "profile"`.
`level`	the confidence level required.
`alpha`	determines the range of profiling. By default the likelihood is profiled in the 99.9% Wald confidence interval region.
`range`	if supplied, `d.prime` will be profiled between `min(range)` and `max(range)`. This over-rules the automatic range computation.
`nSteps`	the number of profile steps.
`Log`	should the profile likelihood be plotted on the log-scale?
`relative`	should the relative or the absolute likelihood be plotted?
`fig`	should the profile likelihood be plotted?

n	the no. points used in the spline interpolation of the profile likelihood.
ylim	overrules default y-limits on the plot of the profile likelihood.
...	not currently used.

Details

These confint methods call the appropriate profile method, then finds the confidence intervals by interpolation of the profile traces. If the profile object is already available, this should be used as the main argument rather than the fitted model object itself.

In plot.profile.twoAC: at least one of Log and relative arguments have to be TRUE.

Value

confint: A matrix (or vector) with columns giving lower and upper confidence limits for each parameter. These will be labelled as (1-level)/2 and 1 - (1-level)/2 in % (by default 2.5% and 97.5%). Profile likelihood confindence intervals are only available for d.prime and not tau.

profile.twoAC: a data.frame with the profile of d.prime.

plot.profile.twoAC invisibly returns the spline approcimation to the profile.

Author(s)

Rune Haubo B Christensen

References

Christensen R.H.B., lee H-S and Brockhoff P.B. (2012). Estimation of the Thurstonian model for the 2-AC protocol. Food Quality and Preference, 24(1), pp.119-128.

See Also

profile and confint

Examples

```
(fm1 <- twoAC(c(2, 2, 6)))
confint(fm1)
confint(fm1, type = "Wald")

pr1 <- profile(fm1)
confint(pr1)

pr1 <- profile(fm1, alpha = 1e-5)
old <- par(mfrow = c(2,2))
plot(pr1)
plot(pr1, Log = FALSE, relative = TRUE)
plot(pr1, Log = TRUE, relative = TRUE)
plot(pr1, Log = TRUE, relative = FALSE)
par(old)
```

discrim *Sensory discrimination analysis*

Description

Computes the probability of a correct answer (Pc), the probability of discrimination (Pd) and d-prime, their standard errors, confidence intervals and a p-value of a difference or similarity test for one of the four common discrimination protocols.

Usage

```
discrim(correct, total, d.prime0, pd0, conf.level = 0.95,
           method = c("duotrio", "tetrad", "threeAFC", "twoAFC",
             "triangle", "hexad", "twofive", "twofiveF"),
           double = FALSE,
           statistic = c("exact", "likelihood", "score", "Wald"),
           test = c("difference", "similarity"), ...)

## S3 method for class 'discrim'
print(x, digits = max(3, getOption("digits")-3), ...)
```

Arguments

correct	the number of correct answers; non-negativescalar integer
total	the total number of answers (the sample size); positive scalar integer
d.prime0	The value of d-prime under the null hypothesis; numerical non-zero scalar
pd0	the probability of discrimination under the null hypothesis; numerical scalar between zero and one
conf.level	the confidence level for the confidence intervals
method	the discrimination protocol. Eight allowed values: "twoAFC", "threeAFC", "duotrio", "tetrad", "triangle", "twofive", "twofiveF", "hexad"
double	should the 'double' variant of the discrimination protocol be used? Logical scalar. Currently not implemented for "twofive", "twofiveF", and "hexad".
test	the type of test
statistic	the statistic to be used for hypothesis testing and confidence intervals
x	an object of class "discrim"
digits	number of digits in resulting table of results
...	not currently used

Details

The degree of product difference/discrimination under the null hypothesis can be specified on *either* the d-prime scale or on the pd (proportion of discriminators) scale. This is done by using either the `d.prime0` *or* the `pd0` arguments. If unspecified, they default to zero and the conventional difference test of "no difference" is obtained.

For a similarity test either `d.prime0` *or* `pd0` have to be specified *and* and a non-zero, positive value should to be given. Here, `d.prime0` or `pd0` define the `limit of similarity` or `equivalence`.

The probability under the null hypothesis is given by `pd0 + pg * (1 - pd0)` where `pg` is the guessing probability which is defined by the discrimination protocol given in the `method` argument.

All estimates are restricted to their allowed ranges, e.g. Pc is always as least as large as the guessing probability. Similarly confidence limits are also restricted to the allowed range of the parameters.

Standard errors are not defined when the parameter estimates are at the boundary of their allowed range, so these will be reported as `NA` in such cases.

If `double = "TRUE"`, the 'double' variants of the discrimination methods is used. For example in a double-triangle test each participant will perform two individual triangle tests and only obtain a correct answer in the double-triangle test if both of the answers to the individual triangle tests are correct. The guessing probability for the double methods are lower than in the conventional discrimination methods. If p_g is the guessing probability of the conventional discrimination method, then p_g^2 is the guessing probability of the double variant of that discrimination method. All the double discrimination methods have their own psychometric functions.

The `"Wald"` statistic is *NOT* recommended for practical use—it is included here for completeness and to allow comparisons.

For `statistic = "score"`, the confidence interval is computed from Wilson's score interval, and the p-value for the hypothesis test is based on Pearson's chi-square test, cf. `prop.test`.

Value

An object of class `discrim` with elements

`coefficients`	matrix of estimates, standard errors and confidence intervals
`data`	a named vector with the data supplied to the function
`p.value`	the p-value of the hypothesis test
`call`	the matched call
`test`	the type of test
`method`	the discrimination protocol
`double`	logical scalar; `TRUE` if a double discrimination method is used, otherwise `FALSE`
`statistic`	the statistic used for confidence intervals and p-value
`pd0`	the probability of discrimination under the null hypothesis
`alt.scale`	the scale for the alternative hypothesis, e.g.~`"d.prime"` or `"pd"`
`conf.level`	the confidence level
`stat.value`	for `statistic != "exact"` the value of the test statistic used to calculate the p-value
`df`	for `statistic == "score"` the number of degrees of freedom used for the Pearson chi-square test to calculate the p-value
`profile`	for `statistic == "likelihood"` the profile likelihood on the scale of Pc

Author(s)

Rune Haubo B Christensen and Per Bruun Brockhoff

References

Brockhoff, P.B. and Christensen, R.H.B (2010). Thurstonian models for sensory discrimination tests as generalized linear models. Food Quality and Preference, 21, pp. 330-338.

Bi, J. (2001) The double discrimination methods. Food Quality and Preference, 12, pp. 507-513.

See Also

discrimPwr, discrimSim, discrimSS, samediff, AnotA, findcr, profile, plot.profile confint

Link functions / discrimination protocols: triangle, twoAFC, threeAFC, duotrio, tetrad, twofive, twofiveF, hexad,

Examples

```
## Running the simple discrimination (difference) tests:
discrim(10, 15, method = "twoAFC")
discrim(10, 15, method = "threeAFC", statistic = "likelihood")
discrim(10, 15, method = "tetrad", statistic = "likelihood")
discrim(10, 15, method = "duotrio", conf.level = 0.90)
discrim(10, 15, method = "triangle", statistic = "score")

# Example of double duotrio discrimination test from Bi (2001):
discrim(35, 100, method = "duotrio", double=TRUE, statistic = "exact")
# Critical value for a sample size of 100 and a guessing probability of 1/4:
findcr(100, p0=1/4) # 33


## plot the distributions of sensory intensity:
m1 <- discrim(10, 15, method = "twoAFC")
plot(m1)

## A similarity test where less than chance successes are obtained:
discrim(22, 75, method = "triangle", d.prime0 = 1, test = "similarity")
```

---

discrimPwr *Sensory discrimination power analysis*

Description

Computes the power of a difference or similarity test for a sensory discrimination experiment using the binomial distribution. d.primePwr is a convenience function that calls discrimPwr but has arguments in terms of d-prime rather than pd, the probability of discrimination.

Usage

```
discrimPwr(pdA, pd0 = 0, sample.size, alpha = 0.05, pGuess = 1/2,
           test = c("difference", "similarity"),
           statistic = c("exact", "normal", "cont.normal"))

d.primePwr(d.primeA, d.prime0 = 0, sample.size, alpha = 0.05,
           method = c("duotrio", "tetrad", "threeAFC", "twoAFC",
             "triangle", "hexad", "twofive", "twofiveF"),
           double = FALSE,
           test = c("difference", "similarity"),
           statistic = c("exact", "normal", "cont.normal"))
```

Arguments

pdA	the probability of discrimination for the model under the alternative hypothesis; scalar between zero and one
d.primeA	d-prime for the model under the alternative hypothesis; non-negative numerical scalar
pd0	the probability of discrimination under the null hypothesis; scalar between zero and one
d.prime0	d-prime under the null hypothesis; non-negative numerical scalar
sample.size	the sample size; a scalar positive integer
alpha	the type I level of the test; scalar between zero and one
method	the discrimination protocol for which the power should be computed
double	should the 'double' variant of the discrimination protocol be used? Logical scalar. Currently not implemented for "twofive", "twofiveF", and "hexad".
pGuess	the guessing probability for the discrimination protocol, e.g. 1/2 for duo-trio and 2-AFC, 1/3 for triangle, tetrad and 3-AFC, 1/10 for two-out-of-five and hexad and 2/5 for two-out-of-five with forgiveness; scalar between zero and one
test	the type of one-sided binomial test (direction of the alternative hypothesis): "difference" corresponds "greater" and "similarity" corresponds to "less"
statistic	should power determination be based on the 'exact' binomial test, the normal approximation to this, or the normal approximation with continuity correction?

Details

The power of the standard one-tailed difference test where the null hypothesis is "no difference" is obtained with `pd0 = 0`.

The probability under the null hypothesis is given by `pd0 + pg * (1 - pd0)` where pg is the guessing probability `pGuess`. Similarly, the probability of the alternative hypothesis is given by `pdA + pg * (1 - pdA)`

Value

The power; a numerical scalar.

Author(s)

Rune Haubo B Christensen and Per Bruun Brockhoff

References

Brockhoff, P.B. and Christensen, R.H.B (2010). Thurstonian models for sensory discrimination tests as generalized linear models. Food Quality and Preference, 21, pp. 330-338.

Bi, J. (2001) The double discrimination methods. Food Quality and Preference, 12, pp. 507-513.

See Also

findcr, discrim, discrimSim, AnotA, discrimSS

Examples

```
## Finding the power of a discrimination test with d-prime = 1,
## a sample of size 30 and a type I level of .05:
pd <- coef(rescale(d.prime = 1, method = "twoAFC"))$pd
discrimPwr(pd, sample.size = 30)
d.primePwr(1, sample.size = 30, method = "twoAFC")
## Obtaining the equivalent normal approximation with and without
## continuity correction:
discrimPwr(pd, sample.size = 30, statistic = "cont.normal")
discrimPwr(pd, sample.size = 30, statistic = "normal")

# Example from Bi (2001) with n=100 and 35 correct answers in a
# double duotrio test:
p1 <- 0.35
# Estimate of d-prime quoted by Bi(2001) was 1.06:
dp <- psyinv(p1, method="duotrio", double=TRUE)
# Power using normal approximation w/o continuity adjustment quoted by Bi(2001):
d.primePwr(dp, sample.size = 100, method="duotrio",
           double=TRUE, stat="normal") # 0.73
# d.primePwr(dp, sample.size = 100, method="duotrio", double=TRUE,
#            stat="cont.normal")

# Power of exact test:
d.primePwr(dp, sample.size = 100, method="duotrio",
           double=TRUE, stat="exact") # 0.697

## A similarity example:
discrimPwr(pdA = 0.1, pd0 = 0.2, sample.size = 100, pGuess = 1/3,
           test = "similarity")
```

discrimR *Replicated Thurstonian Model for discrimination analysis*

Description

The model is a synthesis of a mixture and a mixed effect model. The random effect distribution for the cluster term (often individuals) is a point mass for delta = 0 and a continuous distribution for delta > 0.

The function fits the model and computes d-prime for an average subject, 2) the variance among subjects, 3) the "posterior" probability of a subject being a discriminator (with delta > 0), 4) the "posterior" expectation on the random effect (ie. the subject-specific delta) and 5) the probability that a randomly chosen individual is a discriminator (ie. the probability mass at delta = 0 in the random effects distribution)

Warning: This function is preliminary; see the details for further information.

Usage

```
discrimR(formula, data, weights, cluster, start, subset, na.action,
           contrasts = NULL, hess = FALSE, ranef = FALSE, zi = FALSE,
           method = c("duotrio", "probit", "threeAFC", "triangle",
             "twoAFC"), ...)
```

Arguments

formula	A formula where the lhs is the binomial response. An indicator vector or a matrix with two column; successes and failures like in a call to glm with a binomial family. The rhs should be 1; no other predictors are currently allowed, but extending this is ongoing work.
data	The data.frame in which to look for variables.
weights	Possible weights
cluster	The clustering variable; should be a factor.
start	Optional starting values; recommended in the current implementation
subset	...
na.action	...
contrasts	...
hess	Should the hessian of the parameters be computed?
ranef	Should the random effect estimates be computed?
zi	Should the posterior probabilities of a subject being a discriminator be computed?
method	Should correspond to the actual test applied.
...	Additional arguments to optim. control=list(trace=TRUE, REPORT=1) is recommended, so the reduction in deviance and convergence can be followed.

Details

This function is preliminary and improving it is ongoing work. The computational methods are expected to change completely. This will hopefully facilitate methods for more general rhs-formulae with additional predictors.

Currently no methods or extractor functions have been written, so the user will have to select the relevant elements from the fitted object (see below). Implementation of methods and extractor functions will occur in due course.

Value

A list with the following elements:

`fpar`	The fixed effect parameter, ie. delta (for an average individual)
`rpar`	A vector with two elements: The first element is the variance component (standard deviation) on the log-scale, where optimization is performed. The second element is the variance component (standard deviation) on the original scale.
`deviance`	Deviance for the model
`se`	standard errors for 1) the fixed effect parameter and 2) the variance component on the log-scale
`convergence`	Convergence message from `optim`
`lli`	Log-likelihood contributions from each of the observations.
`ranef`	The random effect estimates for the levels of the clustering factor (often individual)
`zi`	posterior probabilities of a subject being a discriminator
`p`	The probability that a randomly chosen individual is a discriminator (ie. the probability mass for delta > 0 in the random effects distribution)
`fitted`	Fitted values
`Y`	The scaled response vector on which optimization is performed.
`call`	the matched call

Author(s)

Rune Haubo B Christensen

See Also

`triangle`, `twoAFC`, `threeAFC`, `duotrio`, `discrimPwr`, `discrimSim`, `discrimSS`, `samediff`, `AnotA`, `findcr`

Examples

```
freq <- c(10,8,10,9,8,9,9,1,10,10,8,2,6,7,6,7,6,4,5,5,3,3,9,9,5,5,8,8,9,9)
tmp <- data.frame(id = factor(1:30), n = rep(10, 30), freq = freq)
head(tmp)
str(tmp)
```

```
fm <- discrimR(cbind(freq, n - freq) ~ 1, tmp, cluster = id,
                    start = c(.5, .5), method = "twoAFC",
                    ranef = TRUE, zi = TRUE, hess = TRUE,
                    control=list(trace=TRUE, REPORT=1))

names(fm)
fm[1:4]
```

`discrimSim` *Simulates replicated difference tests*

Description

Simulates the outcome of `sample.size` replicated sensory difference tests (for any one of eight protocols: 2-AFC, 3-AFC, duotrio, tetrad, triangle, two-out-of-five, two-out-of-five with forgiveness and hexad tests) for a given d-prime value and a given overdispersion (default 0).

Usage

```
discrimSim(sample.size, replicates, d.prime, sd.indiv = 0,
           method = c("duotrio", "halfprobit", "probit", "tetrad",
             "triangle", "twoAFC", "threeAFC", "hexad", "twofive", "twofiveF"),
           double = FALSE)
```

Arguments

`sample.size`	the sample size - number of subjects
`replicates`	number of replications per subject
`d.prime`	the value of d-prime
`method`	the discrimination protocol
`sd.indiv`	the individual variability in d-prime values. A value of 0 (default) corresponds to complete independence
`double`	should the 'double' variant of the discrimination protocol be used? Logical scalar. Currently not implemented for "twofive", "twofiveF", and "hexad".

Details

The d-prime for each subject is a random draw from a normal distribution with mean `d.prime` and standard deviation `sd.indiv`. All negative values are set to zero.

Value

A vector of length `sample.size` with the number of correct answers for each subject.

Author(s)

Rune Haubo B Christensen and Per Bruun Brockhoff

References

Brockhoff, P.B. and Christensen, R.H.B. (2010). Thurstonian models for sensory discrimination tests as generalized linear models. Food Quality and Preference, 21, pp. 330-338.

See Also

triangle, twoAFC, threeAFC, duotrio, tetrad, twofive, twofiveF, hexad, discrimPwr, discrim, AnotA, discrimSS, samediff, findcr

Examples

```
## Running simulations:
discrimSim(sample.size = 10, replicates = 3, d.prime = 2,
           method = "triangle", sd.indiv = 1)
```

---

discrimSS *Sensory discrimination sample size calculation*

Description

Computes the sample size for a difference or similarity test for a sensory discrimination experiment using the binomial distribution. `d.primeSS` is a convenience function that calls `discrimSS` but has arguments in terms of d-prime rather than pd, the expected proportion of discriminators.

Usage

```
discrimSS(pdA, pd0 = 0, target.power = 0.90, alpha = 0.05,
          pGuess = 1/2, test = c("difference", "similarity"),
          statistic = c("exact", "stable.exact", "both.exact",
           "normal", "cont.normal"))

d.primeSS(d.primeA, d.prime0 = 0, target.power = 0.90, alpha = 0.05,
          method = c("duotrio", "tetrad", "threeAFC", "twoAFC",
            "triangle", "hexad", "twofive", "twofiveF"),
          double = FALSE,
          test = c("difference", "similarity"),
          statistic = c("exact", "stable.exact", "both.exact",
           "normal", "cont.normal"))
```

Arguments

`pdA`	the probability of discrimination for the model under the alternative hypothesis; scalar between zero and one
`d.primeA`	d-prime for the model under the alternative hypothesis; non-negative numerical scalar

pd0	the probability of discrimination under the null hypothesis; scalar between zero and one
d.prime0	d-prime under the null hypothesis; non-negative numerical scalar
target.power	the desired power for the test
alpha	the type I level of the test; scalar between zero and one
method	the discrimination protocol for which the sample size should be computed
double	should the 'double' variant of the discrimination protocol be used? Logical scalar. Currently not implemented for "twofive", "twofiveF", and "hexad".
pGuess	the guessing probability for the discrimination protocol, e.g. 1/2 for duo-trio and 2-AFC, 1/3 for triangle, tetrad and 3-AFC, 1/10 for two-out-of-five and hexad and 2/5 for two-out-of-five with forgiveness;; scalar between zero and one
test	the type of one-sided binomial test (direction of the alternative hypothesis): "difference" corresponds "greater" and "similarity" corresponds to "less"
statistic	options are explained in the Details section below

Details

For difference tests pdA or d.primeA (the sensory difference under the alternative hypothesis) has to be larger than pd0 or d.prime0 (the sensory difference under the null hypothesis). The sample size of the standard one-tailed difference test where the null hypothesis of "no difference" is obtained with pd0 = 0 or d.prime0 = 0.

For similarity tests it is required that pd0 > pdA or equivalently that d.prime0 > d.primeA. Here, the interval [0, pdA] or [0, d.primeA] is the similarity region covering sensory differences for which we would say that the products are similar.

The probability of a correct answer under the null hypothesis is given by pd0 + pGuess * (1 - pd0). Similarly, the probability of a correct answer under the alternative hypothesis is given by pdA + pGuess * (1 - pdA).

The statistic argument:

- "exact" is the conventional sample size for the exact binomial test: The smallest sample size that gives the desired power (target.power) at the given significance level. Ususally slightly higher sample sizes will not have the desired power, however. This is due to the non-monotonic behavior of power as a function of sample size.
- "stable.exact" is so-called stable exact sample size proposed by Ennis and Jesionka (2011) which has the property that no larger sample sizes has a power less than the target.power.
- "both.exact" returns both exact and stable.exact sample sizes
- "normal" is the normal approximation to the exact binomial sample size without any continuity adjustment. This usually provides a sample size that is smaller than the sample size for the exact binomial test.
- "cont.normal" is the continuity adjusted normal approximation to the sample size for the exact binomial test. This sample size is usually closer to the exact sample size than the unadjusted approximation and usually higher than the unadjusted approximation.

If the sample size based on the continuity adjusted normal approximation is larger than 10,000, the function returns the normal approximation and issues a warning.

Value

The sample size; an integer.

Author(s)

Per Bruun Brockhoff and Rune Haubo B Christensen

References

Brockhoff, P.B. and Christensen, R.H.B (2010). Thurstonian models for sensory discrimination tests as generalized linear models. Food Quality and Preference, 21, pp. 330-338.

Ennis, J.M. and V. Jesionka (2011). The power of sensory discrimination methods revisited. Journal of Sensory Studies, 26, pp. 371-382.

See Also

AnotA, discrimPwr, samediff, findcr

Examples

```
## Finding the smallest necessary sample size:
discrimSS(pdA = 0.5, pd0 = 0, target.power = 0.80, alpha = 0.05,
   pGuess = 1/2, test = "difference", statistic = "exact")
## The stable-exact sample size is larger:
discrimSS(pdA = 0.5, pd0 = 0, target.power = 0.80, alpha = 0.05,
   pGuess = 1/2, test = "difference", statistic = "stable.exact")

## Give identical results:
pd <- coef(rescale(d.prime = 1, method = "twoAFC"))$pd
discrimSS(pdA = pd, pd0 = 0, target.power = 0.90, alpha = 0.05,
   pGuess = 1/2, test = "difference", statistic = "exact")
d.primeSS(1, target.power = 0.90, method = "twoAFC")

## A similarity example:
discrimSS(pdA = 0.1, pd0 = 0.2, target.power = 0.80, alpha = 0.05,
   pGuess = 1/2, test = "similarity", statistic = "exact")
```

---

dod *Thurstonian Degree-of-Difference (DOD) model*

Description

Fits the Thurstonian Degree-of-Difference (DOD) model and performs hypothesis/significance tests of d-prime (Thurstonian delta). One-sided difference and similarity tests as well as two-sided tests of d-prime are available. The user may choose from a number of tests statistics.

Usage

```
dod(same, diff, d.prime0 = 0, conf.level = 0.95,
    statistic = c("likelihood", "Pearson", "Wilcoxon", "Wald"),
    alternative = c("difference", "similarity", "two.sided",
    "less", "greater"), control=dodControl(), ...)

## S3 method for class 'dod'
print(x, digits = max(3, getOption("digits") - 3), ...)
```

Arguments

same	the answers to same-pairs; either 1) a numeric vector of counts of length equal to the number of response categories ordered appropriately or 2) a factor where the levels indicate the response categories.
diff	the answers to different-pairs in the same format as same.
d.prime0	the value of d.prime under the null hypothesis. In the standard no-difference test d.prime0 = 0, while it has to be positive for similarity tests and two-sided tests.
conf.level	the confidence level for the confidence intervals
statistic	the statistic to be used for hypothesis testing
alternative	the nature of the alternative hypothesis in the hypothesis/significance test for d-prime. Note that "greater" is an alias for "difference" and "less" is an alias for "similarity"
control	options to control the fitting process specfied via a call to dodControl.
x	an object of class "dod".
digits	number of digits in resulting table of results.
...	not currently used.

Details

dod will report the likelihood based confidence interval for d.prime unless statistic = "Wald" in which case the standard symmetric Wald type confidence interval is reported. This interval can be highly inaccurate and so is not recommened for practical use.

The p-value for the standard one-tailed difference test of "no difference" is obtained with d.prime0 = 0 corresponding to the default setting.

The standard error of d-prime is not defined when the parameter estimate is zero (or numerically close) and it will be reported as NA in this case.

The "Wald" statistic is *NOT* recommended for practical use—it is only included here for completeness and to allow comparisons with other software etc.

Value

An object of class dod.

Author(s)

Rune Haubo B Christensen

References

Ennis, J.M. and R.H.B. Christensen (2015) A Thurstonian comparison of the tetrad and degree of difference tests. *Food Quality and Preference*, 40, pp.263-269.

Christensen, R.H.B, J.M. Ennis, D.M. Ennis and P.B Brockhoff (2012) A Thurstonian model for the Degree of Difference test with extensions to unequal variance, sequence effects and replicated data. Talk at Sensometrics conference, Rennes, France, July 11th.

See Also

dodSim, dodPwr, dodControl, dod_fit, optimal_tau

Examples

```
## DOD example data:
same.pairs <- c(25, 22, 33, 20)
diff.pairs <- c(18, 22, 30, 30)

## Fit Thurstonian dod-model and perform difference test:
dod(same=same.pairs, diff=diff.pairs)

## Can choose another test statistic (e.g. Wilcoxon):
dod(same=same.pairs, diff=diff.pairs, statistic="Wilcox")

## A similarity test (with simulated data):
set.seed(121)
(Data2 <- dodSim(d.prime=0, ncat=4, sample.size=200, method.tau="equi.prob"))
dod(same=Data2[1, ], diff=Data2[2, ], d.prime0=1.2,
    alternative="similarity")

## Extract parameters from a dod fit:
fm <- dod(same=same.pairs, diff=diff.pairs)
coef(fm)
```

---

dodControl *Control settings for the dod function*

Description

Specify control setting when fitting the the Thurstonian Degree-of-Difference (DOD) model using dod and dod_fit.

Usage

```
dodControl(grad.tol = 1e-4,
           integer.tol = 1e-8,
           get.vcov = TRUE,
           get.grad = TRUE,
           test.args = TRUE,
           do.warn=TRUE,
           optCtrl=list())
```

Arguments

grad.tol	tolerance for the maximum absolute gradient of the parameters are convergence.
integer.tol	tolerance for when to give a warning about non-integer counts in data.
get.vcov	compute the variance-covariance matrix of the parameters (and the standard error of d-prime)?
get.grad	compute the gradient of the parameters?
test.args	test admissibility of arguments to dod and dod_fit?
do.warn	if FALSE warnings from the fitting process are suppressed.
optCtrl	control parameters passed on to the nlminb optimizer.

Value

An list of class dodControl with the appropriate control settings for dod and dod_fit.

Author(s)

Rune Haubo B Christensen

See Also

dod, dod_fit, dodSim, dodPwr, optimal_tau,

Examples

```
## DOD example data:
same.pairs <- c(25, 22, 33, 20)
diff.pairs <- c(18, 22, 30, 30)

## Fit Thurstonian dod-model and perform difference test:
dod(same=same.pairs, diff=diff.pairs)

## Display the fitting process using the trace argument to nlminb:
ctrl <- dodControl(optCtrl=list(trace=TRUE))
dod(same=same.pairs, diff=diff.pairs, control=ctrl)
```

dodPwr *Power of the Degree-of-Difference (DOD) method*

Description

Computes the power of the Degree-of-Difference (DOD) method by simulation

Usage

```
dodPwr(d.primeA, d.prime0=0, ncat = 4, sample.size, nsim = 1e3,
       alpha = 0.05,
       method.tau=c("LR.max", "equi.prob", "se.min", "user.defined"),
       statistic=c("likelihood", "Wilcoxon", "Pearson", "Wald"),
       alternative = c("difference", "similarity", "two.sided",
       "less", "greater"),
       tau=NULL, ...)
```

Arguments

d.primeA	the value of d-prime under the alternative hypothesis; non-negative numerical scalar.
d.prime0	the value of d-prime under the null hypothesis.
ncat	the number of response categories in the DOD model
sample.size	the sample size in each simulation for each of the same-pairs and different pairs. Can be a single scalar value or a 2-vector.
nsim	the number of simulations.
alpha	the significance level.
method.tau	the method with which to choose the boundary parameters - see dodSim for details on the methods.
statistic	the statistic to be used for hypothesis testing.
alternative	the nature of the alternative hypothesis in the hypothesis/significance test for d-prime. Note that "greater" is an alias for "difference" and "less" is an alias for "similarity".
tau	if method.tau = "user.defined" a vector of boundary parameters in the DOD model, otherwise not used.
...	parsed on to wilcox.test when appropriate.

Value

The simulation based estimate of the power with the following attributes:

se(power)	the estimated standard error of the estimated power. This is based on the formula sqrt(pow * (1 - pow) / n), where pow is the estimated power and n is the number of simulations used to estimate the power.

`n.used` the number of simulations used to estimate the power. This is usually equal to nsim, but can sometimes be smaller than nsim due to non-convergences to which the Wald test is especially prone.

Author(s)

Rune Haubo B Christensen

References

Ennis, J.M. and R.H.B. Christensen (2015) A Thurstonian comparison of the tetrad and degree of difference tests. *Food Quality and Preference*, 40, pp.263-269.

See Also

dod, dod_fit, dodSim, optimal_tau, dodControl

Examples

```
## NOTE: The number of simulations (nsim) is set unrealistically low in
## the examples below to reduce the computation time for automatic
## package checks. nsim between 1e3 and 1e4 is usually sufficient and
## the latter often on the safe side. The standard error of the
## estimated power ('se(power)') reported by dodPwr() measures the
## accuracy of the estimated power and indicates if nsim needs to be
## increased.

## Estimate power of the conventional difference test (no-difference
## under the null hypothesis):
set.seed(125)
dodPwr(d.primeA=1, d.prime0=0, ncat=4, sample.size=100, nsim=50,
       alpha=.05, method.tau="LR.max", statistic="likelihood")
##  [1] 0.62
##  attr(,"se(power)")
##  [1] 0.1825346
##  attr(,"n.used")
##  [1] 50
## Here the boundary parameters are chosen automatically so as to
## maximize the likelihood ratio test statistic, and so this setting
## amounts to a highest achievable power scenario given d-prime = 1.

## Using another (and faster) statistic:
dodPwr(d.primeA=1, d.prime0=0, ncat=4, sample.size=100, nsim=1e3,
       alpha=.05, method.tau="LR.max", statistic="Wilcox")


## Not automatically run to reduce computation time.

## Power of a similarity test:
set.seed(127)
dodPwr(d.primeA=0, d.prime0=1, ncat=4, sample.size=100, nsim=1e2,
       alpha=.05, method.tau="LR.max", statistic="Pearson",
```

```
       alternative="similarity")
##  [1] 0.71
##  attr(,"se(power)")
##  [1] 0.1434922
##  attr(,"n.used")
##  [1] 100

## Same as above, but with a given set of boundary parameters:
dodPwr(d.primeA=0, d.prime0=1, sample.size=100, nsim=1e2,
       alpha=.05, method.tau="user.defined", statistic="Pearson",
       alternative="similarity", tau=1:3)

## Using parallel computing to speed up computations:
if(require(parallel)) {
    ## Use detectCores() to get an appropriate number of cores for
    ## practical use - for the example here we fix it at 2:
    ## cl <- makeCluster(detectCores())
    cl <- makeCluster(getOption("cl.cores", 2))
    dvec <- c(0, .2, .5, .7, 1, 1.2, 1.5, 1.75)
    system.time(
        res <- parLapply(cl, dvec, fun=function(dp) {
            library(sensR)
            x <- dodPwr(dp, 0, sample.size=100, nsim=1e4, stat="Wil")
            c("power"=x, "se"=attr(x, "se(power)"))
        })
        )
    stopCluster(cl)
    names(res) <- dvec
    mat <- do.call(cbind, res)
    round(mat[1:2, ], 3)
    ## Example output:
    ##            0   0.2   0.5   0.7     1   1.5  1.75     2
    ##  power 0.051 0.058 0.123 0.238 0.578 0.983 1.000 1.000
    ##  se    0.022 0.023 0.033 0.043 0.049 0.013 0.002 0.001
}

## Realistically one should use more simulations, e.g. nsim=1e4.
```

---

dodSim *Simulate data from the Degree-of-Difference model*

Description

Simulate data from the Degree-of-Difference model for a given value of d-prime. The boundary parameters can either be specified by the user, or be chosen automatically so as to 1) maximize the likelihood ratio statistic, 2) ensure responses in each category is equally probable across same-pairs and different-pairs or 3) minimize the standard error of d-prime.

Usage

```
dodSim(d.prime, ncat=4, sample.size = c(100, 100),
       method.tau = c("equi.prob", "LR.max", "se.min", "user.defined"),
       tau = NULL, d.prime0 = 0, ...)
```

Arguments

d.prime	the value of d-prime.
ncat	the number of response categories.
sample.size	the sample size for same-pairs and different-pairs. The sample size can be a scalar number in which case the sample sizes for both same-pairs and different-pairs are taken to equal that number.
method.tau	the method with which to choose the boundary parameters. If "user.defined", the user has to specify the tau argument, otherwise the set of boundary parameters are chosen automatically (see the Details section below).
tau	if method.tau = "user.defined" the set of boundary parameters, otherwise not used.
d.prime0	if method.tau = "LR.max" the value of d-prime under the null hypothesis, otherwise not used.
...	passed on to optimal_tau.

Details

In principle both d-prime and all boundary parameters have to be specified in order to be able to simulate from the DOD model. However, since it can be difficult to decide which boundary parameters to use for simulation, dodSim offers ways to choose these parameters automatically according to the following three criteria:

equi.prob the boundary parameters are chosen such that responses in each category are equally probable across same-pairs and different-pairs.

LR.max the boundary parameters are chosen such that the likelihood ratio statistic for the test of d-prime is maximized. This choice maximizes the power of the likelihood ratio test and is in a sense an optimal choice of boundary parameters.

se.min the boundary parameters are chosen such that the standard error of d-prime is minimized. This method also maximizes the power of the Wald test of d-prime when the null hypothesis is no-difference (d-prime = 0). This method can be numerical unstable for small and large d-prime values (approximately d.prime < 0.5 and d.prime > 5).

Experience shows that the asymptotic properties of the DOD model are not too sensitive to the choice of boundary parameters: power, standard error of d-prime and confidence intervals seem to be fairly constant irrespectively which of the above three criteria are used to choose the boundary parameters.

Value

A 2-by-ncat matrix of counts with same-pairs in the first row and different-pairs in the second row. First/last column corresponds to "same"/"different" on the response scale.

Author(s)

Rune Haubo B Christensen

See Also

dod, dod_fit, dodControl, optimal_tau, dodPwr

Examples

```
## Simulate data from the DOD model with the equi.prob method:
set.seed(125)
(Data <- dodSim(d.prime=1, sample.size=100, method.tau="equi.prob"))

## Simulate data that maximizes the likelihood ratio statistic:
set.seed(125)
dodSim(d.prime=1, sample.size=100, method.tau="LR.max")

## Simulate with user-defined values for the boundary parameters:
dodSim(d.prime=1.5, sample.size=c(100, 100),
       method.tau="user.defined", tau=1:4)

## Simulate using different sample sizes for same-pairs and
## different-pairs:
dodSim(d.prime=1, ncat=3, sample.size=c(75, 125),
       method.tau="se.min")
```

---

dod_fit *Direct fitter of the Thurstonian Degree-of-Difference (DOD) model*

Description

Fits the Thurstonian Degree-of-Difference (DOD) model. This function is for programming use. The ordinary user probably wants the dod function, which is for interactive use. dod_fit only estimates the DOD model and performs no hypothesis or significance tests.

Usage

```
dod_fit(same, diff, tau=NULL, d.prime=NULL, control=dodControl(),
        ...)
```

Arguments

same	the answers to same-pairs; either 1) a numeric vector of counts of length equal to the number of response categories ordered appropriately or 2) a factor where the levels indicate the response categories.

diff	the answers to different-pairs in the same format as same.
tau	optional vector of boundary parameters. If specified, dod_fit will not optimize over the tau parameters.
d.prime	optional d-prime value. If specified, dod_fit will not optimize over d.prime.
control	options to control the fitting process specfied via a call to dodControl.
...	not currently used.

Details

The standard error of d-prime is not defined when the parameter estimate is zero (or numerically close) and it will be reported as NA in this case.

Value

An object of class dod_fit.

Author(s)

Rune Haubo B Christensen

See Also

dod, dodSim, optimal_tau, dodPwr, dodControl

Examples

```
## DOD example data:
same.pairs <- c(25, 22, 33, 20)
diff.pairs <- c(18, 22, 30, 30)

## Fit Thurstonian dod-model and perform difference test:
fm <- dod_fit(same=same.pairs, diff=diff.pairs)
names(fm)

## Estimate d-prime for given tau:
fm <- dod_fit(same=same.pairs, diff=diff.pairs, tau=1:3)

## Estimate tau for given d-prime:
fm <- dod_fit(same=same.pairs, diff=diff.pairs, d.prime=1)
```

dod_utils *Utility functions for the Degree-of-Difference model*

Description

Various utility functions supporting the Degree-of-Difference (DOD) model.

Usage

```
optimal_tau(d.prime, d.prime0 = 0, ncat=3,
            method=c("equi.prob", "LR.max", "se.min"),
            tau.start=NULL, equi.tol = 1e-4, grad.tol = 1e-2,
            do.warn=TRUE)

par2prob_dod(tau, d.prime)

dod_nll(tau, d.prime, same, diff, integer.tol=1e-8)

dod_null(same, diff, integer.tol=1e-8)

dod_null_tau(same, diff)
```

Arguments

d.prime	the value of d-prime; non-negative numerical scalar.
d.prime0	d-prime under the null hypothesis; only used in optimal_tau when method = "LR.max".
ncat	the number of response categories in the DOD model.
method	the method with which to choose the boundary parameters — see dodSim for details on the methods.
tau.start	optional vector of starting values.
equi.tol	convergence tolerence for the "equi.prob" method.
grad.tol	gradient convergence tolerence.
do.warn	issue warning if estimation of optimal tau does not converge?
same	The answers to same-pairs; either 1) a numeric vector of counts of length equal to the number of response categories ordered appropriately or 2) a factor where the levels indicate the response categories.
diff	the answers to different-pairs in the same format as same.
tau	vector of boundary parameters in the DOD model.
integer.tol	tolerence for when same or diff arguments are considered non-integer counts: a warning is issued if non-integer counts are encountered.

Value

optimal_tau	computes optimal boundary parameters (tau) using various criteria.
par2prob_dod	computes the multinomial probability vectors from DOD model parameters.
dod_nll	implements the negative log-likelihood function for the DOD model.
dod_null	implements the negative log-likelihood function for the DOD model where d-prime = 0.
dod_null_tau	Estimates tau for the DOD model where d-prime = 0.

Author(s)

Rune Haubo B Christensen

See Also

dod, dod_fit, dodSim, dodPwr, dodControl

Examples

```
## Compute optimal boundary parameters using the LR.max criterion for
## d.prime=1 with 4 categories:
dp <- 1
(Tau <- optimal_tau(d.prime=dp, d.prime0 = 0, ncat=4,
                    method="LR.max")$tau)
##  [1] 1.244642 2.109140 3.098985
## This set of boundary parameters optimize the power of the DOD test
## with d.prime = 1 under the alternative hypothesis.

## Compute the probability that an observation will fall in each of
## the (here 2*4=8) response categories given values of tau and d.prime:
par2prob_dod(tau=Tau, d.prime=dp)
##              [,1]      [,2]      [,3]       [,4]
##  p.same 0.6211921 0.2429480 0.1074307 0.02842911
##  p.diff 0.5124361 0.2571691 0.1596425 0.07075227

## Compute the negative log-likelihood given data and parameters:
Same <- c(10, 20, 30, 20)
Diff <- c(10, 10, 20, 40)
dod_nll(tau=Tau, d.prime=dp, same=Same,
        diff=Diff)
##  [1] 334.0986

## Compute the negative log-likelihood under the null hypothesis
## (where d.prime = 0):
dod_null(same=Same, diff=Diff)
##  [1] 208.8154
##  ## The boundary parameters for this:
(Tau0 <- dod_null_tau(same=Same, diff=Diff))
##  [1] 0.2224709 0.5688675 1.2546147

## Some equalities:
```

```
stopifnot(
    dod_nll(tau=Tau0, d.prime=0, same=Same, diff=Diff) ==
    dod_null(same=Same, diff=Diff))
stopifnot(
    dod_null(same=Same, diff=Diff) ==
    -dod_fit(same=Same, diff=Diff, d.prime=0)$logLik
    )
stopifnot(
    dod_nll(same=Same, diff=Diff, tau=Tau, d.prime=dp) ==
    -dod_fit(same=Same, diff=Diff, tau=Tau, d.prime=dp)$logLik
    )
stopifnot(all(
    dod_null_tau(same=Same, diff=Diff) ==
    dod_fit(Same, Diff, d.prime=0)$tau))
```

`dprime_compare` *Test the 'any-differences' hypothesis and estimate common d-prime*

Description

This function will test the 'any-differences' hypothesis (conceptually a one-way ANOVA test for d-primes) with one of the Wald, Pearson or likelihood ratio chi-square test statistics. The common d-prime is estimated with ML or weighted average.

Usage

```
dprime_compare(correct, total, protocol, conf.level = 0.95,
   statistic = c("likelihood", "Pearson", "Wald.p", "Wald.d"),
   estim = c("ML", "weighted.avg"))
```

Arguments

`correct`	a numeric vector of the number of correct answers; one element for each test.
`total`	a numeric vector of the total number of trials; one element for each test.
`protocol`	a character vector or factor naming the protocol used; one element for each test. Currently the following protocols are supported: `"triangle"`, `"duotrio"`, `"threeAFC"`, `"twoAFC"`, `"tetrad"`.
`conf.level`	the confidence level for the estimated common d-prime.
`statistic`	the test statistic for testing the 'any-differences' hypothesis.
`estim`	The estimation method for the common d-prime.

Details

The vectors `correct`, `total` and `protocol` have to be of the same length.

The function has a print method.

Value

an object of class "dprime_compare" with the following elements

stat.value	the value of the (chi-square) test statistic for the 'any-differences' hypothesis.
df	the degrees of freedom for the stat.value test statistic.
p.value	the p-value for the 'any-differences' test.
statistic	the name of the test statistic for the 'any-differences' test.
data	the data table produced by dprime_table.
coefficients	'table' with estimated common d-prime, standard error and confidence limits storred as a one-row data.frame.
conf.level	confidence level for the common d-prime.
conf.int	the confidence interval for the common d-prime.
estim	the estimation method for the common d-prime.
conf.method	the statistical method/test statistic used to compute the confidence interval for the common d-prime.

Author(s)

Rune Haubo B Christensen

See Also

dprime_test, dprime_table, posthoc.dprime_compare.

Examples

```
## Make some fake data:
n <- rep(40, 4)
x <- c(25, 25, 30, 35)
protocol <- c("triangle", "duotrio", "threeAFC", "twoAFC")
## Look at the data table with d-primes etc.:
dprime_table(x, n, protocol)

## 'any differences' test:
## ML estimation and test with likelihood statistic:
(dpc <- dprime_compare(x, n, protocol))
## Other estimation/statistic options:
dprime_compare(x, n, protocol, estim="weighted.avg")
dprime_compare(x, n, protocol, statistic="Pearson")
dprime_compare(x, n, protocol, statistic="Wald.p")
dprime_compare(x, n, protocol, statistic="Wald.d")
```

dprime_table *Summary table of several discrimination experiments using the simple-binomial protocols (Duo-Trio, Triangle, Tetrad, 2-AFC and 3-AFC)*

Description

This function provides a summary table with the following quantities: no. correct trials (`correct`), total number of trials (`total`), the protocol (`protocol`), probability of a correct answer (`pHat`), standard error of pHat (`se.pHat`), d-prime (`dprime`), and standard error of d-prime (`se.dprime`).

Usage

```
dprime_table(correct, total, protocol, restrict.above.guess = TRUE)
```

Arguments

`correct`	a numeric vector of the number of correct answers; one element for each test.
`total`	a numeric vector of the total number of trials; one element for each test.
`protocol`	a character vector or factor naming the protocol used; one element for each test. Currently the following protocols are supported: `"triangle"`, `"duotrio"`, `"threeAFC"`, `"twoAFC"`, `"tetrad"`.
`restrict.above.guess`	controls if `pHat` should be restricted at or above the guessing probability for the given protocol. This also affects `se.pHat`. Note that `dprime` is zero and `se.dprime` is `NA` when `pHat` is at or below the guessing probability of the given protocol.

Details

The vectors `correct`, `total` and `protocol` have to be of the same length.

Value

a data.frame with columns:

`correct`	numeric vector of no. correct.
`total`	numeric vector of no. trials.
`protocol`	character vector naming the protocols used.
`pHat`	Estimate of the probability of correct answers.
`se.pHat`	standard error of `pHat`.
`dprime`	estimate of d-prime.
`se.dprime`	standard error of `dprime`.

Author(s)

Rune Haubo B Christensen

See Also

dprime_compare, dprime_test, posthoc.dprime_compare.

Examples

```
n <- rep(40, 4)
x <- c(25, 25, 30, 35)
protocol <- c("triangle", "duotrio", "threeAFC", "twoAFC")
dprime_table(x, n, protocol)
```

---

dprime_test *Test of simple hypothesis with the common d-prime*

Description

This function tests the hypothesis that the common d-prime is equal to or greater/less than a certain value, e.g. zero in a Wald or likelihood root test.

Usage

```
dprime_test(correct, total, protocol, conf.level = 0.95, dprime0 = 0,
    statistic = c("likelihood", "Wald"),
    alternative = c("difference", "similarity", "two.sided", "less", "greater"),
    estim = c("ML", "weighted.avg"))
```

Arguments

correct	a numeric vector of the number of correct answers; one element for each test.
total	a numeric vector of the total number of trials; one element for each test.
protocol	a character vector or factor naming the protocol used; one element for each test. Currently the following protocols are supported: "triangle", "duotrio", "threeAFC", "twoAFC", "tetrad".
conf.level	the confidence level for the confidence interval of the estimated common d-prime.
dprime0	Value of d-prime under the Null hypothesis. Non-negative numeric scalar.
statistic	the test statistic for computing the confidence interval as well as p-value.
alternative	the direction of the hypothesis test. "difference" and "similarity" are just alternative ways of specifying "greater" and "less" respectively.
estim	The estimation method for the common d-prime.

Details

The vectors correct, total and protocol have to be of the same length.

The function has a print method.

Value

an object of class "dprime_test" with the following elements

p.value	the p-value for the 'any-differences' test.
alternative	character naming the direction of the hypothesis test.
statistic	the name of the test statistic.
data	the data table produced by dprime_table.
conf.level	confidence level for the common d-prime.
conf.int	the confidence interval for the common d-prime.
estim	the estimation method for the common d-prime.
conf.method	the statistical method/test statistic used to compute the confidence interval for the common d-prime.

Author(s)

Rune Haubo B Christensen

See Also

dprime_compare, dprime_table, posthoc.dprime_compare.

Examples

```
n <- rep(40, 4)
x <- c(25, 25, 30, 35)
protocol <- c("triangle", "duotrio", "threeAFC", "twoAFC")
## Look at the data table with d-primes etc.:
dprime_table(x, n, protocol)

## Test of common d':
dprime_test(x, n, protocol)

## Another setting:
dprime_test(x, n, protocol, dprime0=2, statistic="Wald",
            alternative="less", estim="weighted.avg")
```

---

duotrio *Create duotrio binomial family*

Description

Creates af copy of the binomial family with the inverse link function changed to equal the duotrio psychometric function and correspondingly changed link function and derivative of the inverse link function.

Usage

```
duotrio()
```

Value

A binomial family object for models. Among other things it inludes the psychometric function as `linkinv` and the inverse psychometric function (for direct dprime computation) as `linkfun`

Note

Several functions in this package makes use of the function, but it may also be used on its own—see the example below.

Author(s)

Per Bruun Brockhoff

References

Brockhoff, P.B. and Christensen, R.H.B. (2010). Thurstonian models for sensory discrimination tests as generalized linear models. Food Quality and Preference, 21, pp. 330-338.

See Also

triangle, twoAFC, threeAFC, tetrad, discrim, discrimPwr, discrimSim, AnotA, discrimSS, samediff, findcr

Examples

```
## Estimating d-prime using glm for a Duotrio test:
xt <- matrix(c(10, 5), ncol = 2) ## data: 10 correct answers, 5 incorrect
res <- glm(xt ~ 1, family = duotrio)
summary(res)
## Equivalent to (Estimate and Std. Error):
discrim(10, 15, method="duotrio")


## Extended example plotting the profile likelihood
## data: 10 correct answers, 5 incorrect
xt <- matrix(c(10, 5), ncol = 2)
summary(res <- glm(xt ~ 1, family = duotrio))
N <- 100
dev <- double(N)
delta <- seq(1e-4, 5, length = N)
for(i in 1:N)
  dev[i] <- glm(xt ~ -1 + offset(delta[i]),
                family = duotrio)$deviance
plot(delta, exp(-dev/2), type = "l",
     xlab = expression(delta),
     ylab = "Normalized Profile Likelihood")
## Add Normal approximation:
```

```
lines(delta, exp(-(delta - coef(res))^2 /
                 (2 * vcov(res))), lty = 2)
## Add confidence limits:
level <- c(0.95, 0.99)
lim <- sapply(level, function(x)
              exp(-qchisq(x, df=1)/2) )
abline(h = lim, col = "grey")
points(confint(res), rep(lim[1], 2), pch = 4)
```

`findcr` *Find the critical value of a one-tailed binomial test*

Description

Finds the critical value in a one-tailed binomial test

Usage

```
findcr(sample.size, alpha = .05, p0 = .5, pd0 = 0,
               test = c("difference", "similarity"))
```

Arguments

`sample.size`	the sample size of the binomial test (must be a positve integer)
`alpha`	the test I error-level of the test (must be between zero and one)
`p0`	the guessing probability under the null-hypothesis (must be between zero and one); 1/2 for the duotrio and twoAFC tests and 1/3 for the triangle, tetrad and threeAFC tests
`pd0`	the proportion of discriminators in the population of interest
`test`	the type of test

Details

The critical value of the standard one-tailed difference test of "no difference" is obtained with `pd0 = 0`.

The probability of a correct answer under the null hypothesis is given by `pd0 + p0 * (1 - pd0)`.

Value

The critical value in a one-tailed binomial test, that is, the smallest integer such that the null hypothesis binomial probability of being larger (smaller for similarity hypotheses) than or equal to this number is smaller than or equal to the type I error-level of the test.

Author(s)

Rune Haubo B Christensen and Per Bruun Brockhoff

See Also

triangle, twoAFC, threeAFC, duotrio, tetrad, discrim, discrimPwr, discrimSim, AnotA discrimSS, samediff

Examples

```
## Find the critical value for a triangle test for the level 0.05 test
## with 25 subjects:
findcr(sample.size = 25, , p0 = 1/3)

## Similarity example:
findcr(sample.size = 25, p0 = 1/3, pd0 = .2, test = "simil")
```

---

hexad *Create hexad binomial family*

Description

Creates af binomial family object with the inverse link function equal to the psychometric function for the unspecified Hexad test.

Usage

```
hexad()
```

Value

A binomial family object for models. Among other things it inludes the psychometric function as `linkinv` and the inverse psychometric function (for direct d-prime computation) as `linkfun`.

Note

Several functions in this package makes use of functions in the hexad family object, but it may also be used on its own—see the example below.

Author(s)

Karolina Stachlewska

References

Eberhardt, K., Aubry, V., & Robinson, K. (2008). A thurstonian model for the unspecified hexad test. In 2008 Sensometrics Meeting 'Discover a New World of Data' (E-5). Kraft Foods.

See Also

duotrio, triangle, twoAFC, threeAFC, tetrad, twofive, twofiveF, discrim, discrimPwr, discrimSim, AnotA, discrimSS, samediff, findcr

Examples

```
## Estimating d-prime using glm for an unspecified Hexad test:
xt <- matrix(c(10, 5), ncol = 2) ## data: 10 correct answers, 5 incorrect
res <- glm(xt ~ 1, family = hexad)
summary(res)
## Equivalent to (Estimate and Std. Error):
discrim(10, 15, method="hexad")


## Extended example plotting the profile likelihood
## data: 10 correct answers, 9 incorrect
xt <- matrix(c(10, 9), ncol = 2)
summary(res <- glm(xt ~ 1, family = hexad))
N <- 100
dev <- double(N)
delta <- seq(1e-4, 3, length = N)
for(i in 1:N)
  dev[i] <- glm(xt ~ -1 + offset(delta[i]),
                family = hexad)$deviance
plot(delta, exp(-dev/2), type = "l",
     xlab = expression(delta),
     ylab = "Normalized Profile Likelihood")
## Add Normal approximation:
lines(delta, exp(-(delta - coef(res))^2 /
                 (2 * vcov(res))), lty = 2)
## Add confidence limits:
level <- c(0.95, 0.99)
lim <- sapply(level, function(x) exp(-qchisq(x, df=1)/2) )
abline(h = lim, col = "grey")
```

`plot.discrim` *Plot function for discrim objects*

Description

This function plots the latent distributions of sensory intensity corresponding to the items or products tested in the discrimination test.

Usage

```
## S3 method for class 'discrim'
plot(x, main = TRUE, length = 1000, ...)
```

Arguments

`x`	The `discrim` object whose latent distributions are to be plotted
`main`	include an automatically generated title on the plot? Default is `TRUE`
`length`	the length of the vectors to be plotted. Longer vectors gives more smooth curves.
`...`	additional arguments to `plot` and `lines`

Value

The function produces a plot and does not return any value.

Author(s)

Rune Haubo B Christensen

Examples

```
## Generate discrim objects to be plotted:
fm1 <- discrim(10, 15, method = "threeAFC")
fm2 <- discrim(10, 15, method = "triangle")
old <- par(mfrow=c(2,1)) ## Split plotting window in two
## Plot the distributions of sensory intensity for the two objects
## and increase the line width
plot(fm1, lwd=2)
plot(fm2, lwd=2)
par(old)
```

---

plot.samediff *Plot function for samediff objects*

Description

This function plots the latent distributions of sensory intensity corresponding to the items or products tested in the discrimination test.

Usage

```
## S3 method for class 'samediff'
plot(x, main = TRUE, length = 1000,
           limits, fig = TRUE, ...)
```

Arguments

x	The samediff object whose latent distributions are to be plotted
main	include an automatically generated title on the plot? Default is TRUE
length	the length of the vectors to be plotted. Longer vectors gives more smooth curves, but can take a little time.
limits	optional limits on the x-axis; vector of length two.
fig	logical: Should the function create the plot? Defaults to TRUE.
...	additional arguments to plot and lines

Value

If `fig = TRUE`, the function will produce the plot. The function invisibly returns a data.frame with elements

`z`	values for the x-axis of lenght `length`.
`base.dist`	y-values for the base distribution of same-samples, ie. a standard normal distribution
`delta.dist`	y-values for the distribution of different-samples, ie. a normal distribution centred at `delta` with unit variance.

This facilitates later plotting and changing the appearance of the plot.

Author(s)

Rune Haubo B Christensen

Examples

```
## Make same-diff object:
sadi <- samediff(8, 5, 4, 9)
## Plot distributions of sensory intensity:
plot(sadi)
```

`posthoc` *Post-hoc estimates and tests for multiple discrimination experiments.*

Description

This function provides estimates and p-values for post-hoc tests such as pairwise comparisons. p-values are (by default) adjusted for multiplicity.

Usage

```
posthoc(x, ...)

## S3 method for class 'dprime_compare'
posthoc(x, alpha = 0.05,
    test = c("pairwise", "common", "base", "zero"), base = 1,
    alternative = c("two.sided", "less", "greater"),
    statistic = c("likelihood", "Wald"),
    padj.method = c("holm", "bonferroni", "none"), ...)

## S3 method for class 'dprime_test'
posthoc(x, alpha = 0.05,
    test = c("pairwise", "common", "base", "zero"), base = 1,
    alternative = c("two.sided", "less", "greater"),
    statistic = c("likelihood", "Wald"),
    padj.method = c("holm", "bonferroni", "none"), ...)
```

Arguments

x	an object of class dprime_compare or dprime_test.
alpha	the significance level for tests and confidence intervals.
test	the type of post-hoc tests performed. Se the details section for further details.
base	when test = "base", the experiment against which to provide pairwise comparisons.
alternative	direction of the hypothesis test.
statistic	The test statistic used - currently there is only partial support for statistic = "likelihood".
padj.method	controls the method by which p-values are adjusted for multiplicity. Any one of the values in p.adjust.methods (currently "holm" "hochberg" "hommel" "bonferroni" "BH" "BY" "fdr" "none") may be specified, cf. p.adjust.
...	currently not used.

Details

The test argument specifies the type of test performed. "pairwise" performs all pairwise comparisons and produces a compact letter display indicating groups of experiments that different/not-different. "common" tests, for each experiment in turn, if the by-experiment d-prime is different from a common d-prime computed from the remaining experiments. "base" provides pairwise comparisons to a single experiment indicated by the separate argument base. If test = "zero" all d-primes are tested versus zero. As a final option a numeric value can be supplied, e.g. test = 1 in which case all d-primes are tested versus one. Note that test = 0 gives the same test as test = "zero".

When test = "pairwise" a compact letter display is provided and it is determined from the p-values *after* adjustment of these for multiplicity.

The dprime_compare and dprime_test methods a have (common) print method.

Value

an object of class c(paste0("posthoc.", class(x)), class(x)) with the following elements from the original object, x and :

posthoc	coefficient table for the post-hoc tests.
test	the value of the test argument.
alternative	the value of the alternative argument.
padj.method	the method used to adjust p-values with.
base	the value of the base argument.
posthoc.stat	name of the statistic for the post-hoc tests.
Letters	if test = "pairwise" the compact letter display, otherwise NULL.
dprime0	unless test = "pairwise" or "common" the value of d-prime under the null hypothesis.

Author(s)

Rune Haubo B Christensen

See Also

dprime_test, dprime_table, dprime_compare.

Examples

```
## Make some fake data:
n <- rep(40, 4)
x <- c(25, 25, 30, 35)
protocol <- c("triangle", "duotrio", "threeAFC", "twoAFC")
## Look at the data table with d-primes etc.:
dprime_table(x, n, protocol)

## 'any differences' test:
## ML estimation and test with likelihood statistic:
(dpc <- dprime_compare(x, n, protocol))

posthoc(dpc, alpha=.1) ## test="pairwise"

## Test if each d' is different from the common d' estimated from the
## remaining experiments:
posthoc(dpc, test="common")

## Test if d' from experiment 2 is different from the others (with
## adjustment for multiplicity):
posthoc(dpc, test="base", base=2)

## Test if each d' is different from 2 (with Bonferroni adjustment for
## multiplicity) using the Wald statistic:
posthoc(dpc, test=2, stat="Wald", padj.method="bonferroni")
```

---

profile.discrim *Profile likelihood and confidence interval methods for discrim objects*

Description

Computes the (normalized or relative) profile likelihood for the parameters of a discrimination test, plots the normalized profile likelihood.

Usage

```
## S3 method for class 'discrim'
profile(fitted, ...)

## S3 method for class 'profile.discrim'
```

```
plot(x, level = c(0.99, 0.95), fig = TRUE,
            method = "natural", n = 1e3, ...)

## S3 method for class 'discrim'
confint(object, parm, level = 0.95, ...)
```

Arguments

fitted	a discrim object
x	a profile.discrim object
object	a discrim object
parm	currently not used
method	the type of spline to be used in approximating the profile likelihood curve (trace)—se spline for details
n	the number of spline interpolations to use in plotting the profile likelihood curve (trace)
level	for plot: At which levels to include horizontal lines to indicate confidence levels in plots of the normalized profile likelihoods. For confint: at which level to compute the confidence interval
fig	logical: should the normalized profile likelihoods be plotted?
...	For plot: additional arguments to plot. Otherwise not used.

Details

confint returns the confidence interval computed in discrim possibly at another level. The statistic used to compute the confidence interval is therefore determined in the discrim call and may not be the likelihood root.

The likelihood profile is extracted from the discrim object fitted with statistic = "likelihood".

Value

For profile: An object of class "profile.discrim", "data.frame"—a data.frame with two columns giving the value of the parameter and the corresponding value of the profile likelihood.

For plot: The profile object is returned invisibly.

For confint:

A 3x2 matrix with columns named "lower", "upper" giving the lower and upper (100 * level)% confidence interval for the parameters named in the rows.

Author(s)

Rune Haubo B Christensen and Per Bruun Brockhoff

References

Brockhoff, P.B. and Christensen R.H.B. (2010). Thurstonian models for sensory discrimination tests as generalized linear models. Food Quality and Preference, 21, pp. 330-338.

See Also

discrim

Examples

```
## 7 success out of 10 samples in a duo-trio experiment:
(dd <- discrim(7, 10, method = "duotrio", statistic = "likelihood"))
confint(dd)
plot(profile(dd))
points(confint(dd)[3,], rep(.1465, 2), pch = 3, cex = 2, lwd=2)
```

---

profile.samediff *Profile likelihood methods for samediff objects.*

Description

Computes the (normalized or relative) profile likelihood for the parameters of a same-different test, plots the normalized profile likelihood and computes profile likelihood confidence intervals.

Usage

```
## S3 method for class 'samediff'
profile(fitted, which = 1:2, max = 2, numpts = 100,
           max.delta = 10, max.tau = 10, ...)
## S3 method for class 'profile.samediff'
plot(x, which = 1:nc, level = c(0.99, 0.95),
           fig = TRUE, ...)
## S3 method for class 'samediff'
confint(object, parm = c("tau", "delta"), level = 0.95, max = c(10, 10)
           , ...)
```

Arguments

fitted	a samediff object
x	a profile.samediff object
object	a samediff object
which	numeric: which parameters to profile or plot; either "1" or "2" or "1:2" to mean "tau", "delta" or both respectively.
parm	the parameter(s) to compute the confidence interval for
max	for profile: control parameter to specify how many units beyond the MLE, the profiling should proceed. For confint: control parameter, that can control the convergence for especially very large delta
numpts	control parameter: At how many points should the profile likelihood be evaluated?

max.delta	control parameter: The maximum point at which to evaluate the profile likelihood for delta
max.tau	same as max.delta for "tau".
level	for plot: At which levels to include horizontal lines to indicate confidence levels in plots of the normalized profile likelihoods. For confint: at which level to compute the confidence interval.
fig	logical: Should the normalized profile likelihoods be plotted?
...	not currently used.

Value

For profile: An object of class "profile.samediff", "data.frame"—a data.frame with two columns for each parameter profiled giving the value of the parameter and the corresponding value of the profile likelihood.

For plot: An object of class "nProfile.samediff", "data.frame"—the data.frame from the profile-object with extra columns corresponding to the which parameter containing the normalized profile liklelihood.

For confint: A 2x2 matrix with columns named "lower", "upper" giving the lower and upper (1 - alpha)% confidence interval for the parameters named in the rows.

Author(s)

Rune Haubo B Christensen

See Also

summary.samediff

Examples

```
# data: 8 of the same samples were judged to be same
#       5 of the same samples were judged to be different
#       4 of the different samples were judged to be same
#       9 of the different samples were judged to be different

sadi <- samediff(8, 5, 4, 9)
confint(sadi)
plot(profile(sadi))
```

`rescale` *Transform or rescale between pc, pd and d-prime for sensory discrimination protocols*

Description

Transforms or rescales estimates and optionally standard errors between the three levels at which a sensory difference is measured: pc (proportion of correct answers), pd (proportion of discriminators) and d-prime. `rescale` is the main function and only one of pc, pd or d-prime should be given as argument — values for the remaining two scales will be computed.

A number of auxiliary functions are also provided:

`psyfun` implements the psychometric functions and maps from d-prime to pc

`psyinv` implements the inverse psychometric functions and maps from pc to d-prime

`psyderiv` implements the derivative of the psychometric functions

`pc2pd` maps from pc to pd

`pd2pc` maps from pd to pc

Usage

```
rescale(pc, pd, d.prime, std.err,
        method = c("duotrio", "tetrad", "threeAFC", "twoAFC",
        "triangle", "hexad", "twofive", "twofiveF"),
        double = FALSE)

psyfun(d.prime, method = c("duotrio", "tetrad", "threeAFC", "twoAFC",
       "triangle", "hexad", "twofive", "twofiveF"),
        double = FALSE)

psyinv(pc, method = c("duotrio", "tetrad", "threeAFC", "twoAFC",
       "triangle", "hexad", "twofive", "twofiveF"),
        double = FALSE)

psyderiv(d.prime, method = c("duotrio", "tetrad", "threeAFC", "twoAFC",
         "triangle", "hexad", "twofive", "twofiveF"),
        double = FALSE)

pc2pd(pc, Pguess)

pd2pc(pd, Pguess)
```

Arguments

`pc`	the proportion of correct answers; a numerical vector between 0 and 1

pd	the proportion of discriminators; a numerical vector between 0 and 1
d.prime	the sensory difference on the d-prime scale; a non-negative numerical vector.
std.err	optional numerical vector of standard errors of the same length as the either of pc, pd or d.prime. Negative values are not allowed, but values may be NA
method	the sensory discrimination protocol for which the results should apply
double	should the 'double' variant of the discrimination protocol be used? Logical scalar.
Pguess	the guessing probability implied by the protocol; a numeric scalar between 0 and 1

Details

The rescale function is based on the fact that once the protocol and one of pc, pd and d-prime is known, the other two can be computed. The same applies to the standard errors of these parameters.

Standard errors are optional, but if they are supplied, the length of the std.err argument has to match the length of pc, pd or d.prime whichever is given.

A print method is implemented for rescale objects.

Value

For rescale an object of class rescale with elements

coefficients	a data.frame with values of pc, pd and d.prime corresponding to the input
std.err	if standard errors are given trough the std.err argument a data.frame of the same size and shape as coefficients with standard errors. Otherwise missing.
method	the sensory discrimination protocol for which the results apply

For psyfun, psyinv, psyderiv, pc2pd and pd2pc a numerical vector of the same length as the first argument with appropriate contents.

Author(s)

Rune Haubo B Christensen

Examples

```
## suppose 15 out of 20 are observed in a duo-trio experiment, then
## the estimated probability of correct a answer is
(pc <- 15/20)
## The standard error of this estimate is
(se.pc <- sqrt(pc * (1 - pc) / 20))
## The corresponding estimate of proportion of discriminators (pd) and
## d-prime with associated standard errors are:
rescale(pc = pc, std.err = se.pc, method = "duotrio")

## Can also do
rescale(pd = c(.6,.7), std.err = c(.2, NA))
psyfun(2, method = "triangle")
```

```
psyinv(0.8, method = "twoAFC")
psyderiv(2, method = "duotrio")
pc2pd(0.7, 1/2)
pd2pc(0.3, 1/3)
```

ROC *Plot the Receiver Operating Characteristic Curve*

Description

The function computes and plots the empirical ROC (receiver operating characteristic) curve.

Usage

```
ROC(object, ...)

## Default S3 method:
ROC(object, se.d, scale = 1, length = 1000,
fig = TRUE, se.type = c("CI", "SE"), CI.alpha = 0.05, ...)

## S3 method for class 'anota'
ROC(object, length = 1000, fig = TRUE,
se.type = c("CI", "SE"), CI.alpha = 0.05, ...)
```

Arguments

`object`	the class of the object defines, which of the methods is invoked. If obejct is a single element numeric vector it is taken as a d-prime value and the default method is invoked. If the object is of class `anota`, the method for `anota` objects is invoked.
`se.d`	a unit length vector with the standard error of d-prime. If supplied confidence intervals or standard errors are plotted
`scale`	a unit length vector giving the ratio of scale (ie. standard deviation) of the latent distribution for the no-class items relative to that of the yes-class items
`length`	the length of the vectors to be plotted. Longer vectors gives more smooth curves.
`fig`	Should a plot be produced?
`se.type`	The type of band for the ROC curve, `"CI"` for confidence interval and `"SE"` for standard error.
`CI.alpha`	the type I level of the confidence interval of AUC
`...`	additional arguments to `plot` and `lines`

Details

The function currently ignores the variance of the scale in the computation of the uncertainty of the ROC curve.

Value

The function makes a plot of the ROC curve, and if `se.d` is supplied, standard errors or confidence intervals for the curve are added to the plot.

The function also (invisibly) returns a list with the following components

`ROCx`	x-coordinates to the ROC curve
`ROCy`	y-coordinates to the ROC curve

If `se.d` is supplied, the object also contains

`lower`	y-coordinates to the lower limit
`upper`	y-coordinates to the upper limit

Author(s)

Rune Haubo B Christensen

Examples

```
## ROC.default:
(mat <- matrix(c(8, 17, 1, 24), 2, byrow = TRUE))
(d.prime <- SDT(mat, "probit")[3])
ROC(d.prime)
## ROC.anota:
fm1 <- AnotA(8, 25, 1, 25)
ROC(fm1)
```

`samediff` *Computation of tau and dprime for same different test*

Description

Computation of tau and dprime and their uncertainties for the same different test using maximum likelihood.

Usage

```
samediff(nsamesame, ndiffsame, nsamediff, ndiffdiff, VCOV = TRUE)
```

Arguments

`nsamesame`	The number of same-answers on same-samples
`ndiffsame`	The number of different-answers on same-samples
`nsamediff`	The number of same-answers on different-samples
`ndiffdiff`	The number of different-answers on different-samples
`VCOV`	Should the variance-covariance matrix of the parameters be computed. Defaults to `TRUE`.

Details

The function computes the maximum likelihood estimates of `tau` and `delta`.

Value

An object of class `samediff` with elements

`coef`	named vector of coefficients (d-prime and tau)
`vcov`	variance-covariance matrix of the coefficients
`se`	named vector with standard error of the coefficients (standard error of d-prime)
`data`	a named vector with the data supplied to the function
`test`	a string with the name of the test (`same-different`)
`call`	the matched call
`convergence`	convergence indicater. 0 indicates convergence. For error codes see `optim`.
`logLik`	Value of the log-likelihood at the MLE of the parameters.
`case`	A case indicator for internal use

Author(s)

Rune Haubo B Christensen

References

Christensen, R.H.B., Brockhoff, P.B. (2009). Estimation and inference in the same-different test. Food, Quality and Preference, 20 pp. 514–520

Examples

```
# data: 8 of the same samples were judged to be same
#       5 of the same samples were judged to be different
#       4 of the different samples were judged to be same
#       9 of the different samples were judged to be different

samediff(8, 5, 4, 9)
```

`samediffPwr` *Power Analysis for Same-different Experiments*

Description

Computes the power for at same-different discrimination experiment with a no-difference null hypothesis via simulation.

Usage

```
samediffPwr(n = 1000, tau, delta, Ns, Nd, alpha = 0.05)
```

Arguments

n	the number of samples to use in the simulation. More samples means higher precision, but takes longer to compute.
tau	the value of tau
delta	the underlying sensory difference under the *alternative* hypothesis (non-negative)
Ns	the number of same-samples (a positive integer)
Nd	the number of different-samples (a positive integer)
alpha	the type I level of the test (must be between zero and one)

Details

The power is computed using simulations. n datasets is simulated from the Same Different model with specified parameters. The power is the fraction of times the p-value is lower than alpha.

Under some parameter combinations, there is a non-significant probability that data will fall, so that the MLE of delta is not defined and the p-value is not defined. All such undefined p-values are silently ignored.

The estimated power may change between runs and especially if the power is either very large or very small (ie. close to 0 or 1). Using more simulations will provide higher accuracy.

It is often a good idea to run the power simulation a couple of times to ensure that the variation in the result is acceptable.

Value

A single numeric value giving the power of the specified test.

Author(s)

Rune Haubo B Christensen

References

Christensen, R.H.B., Brockhoff, P.B. (2009). Estimation and inference in the same-different test. Food, Quality and Preference, 20 pp. 514–520

See Also

samediff, samediffSim

Examples

```
## Finding the power of a discrimination test with a sensory delta of 2
## (alternative hypothesis) versus a null hypothesis of delta = 0 with
## a sample of size 2 x 10 and a type I level of .05. n should be higher
## for a reasonable precision:

samediffPwr(n = 100, tau = 1, delta = 2, Ns = 10, Nd = 10)
```

samediffSim *Simulates data from a samediff test*

Description

Simulates the outcome of n same-different experiments.

Usage

```
samediffSim(n, tau, delta, Ns, Nd)
```

Arguments

n	the number of experiments to simulate.
tau	the value of "tau".
delta	the value of delta (d-prime).
Ns	number of same-samples
Nd	number of different-samples

Details

The function makes two calls to rbinom.

Value

A matrix of with n rows and four columns named ss, ds, sd, dd with the number of same-answers to same-samples, different-answers to same-samples, same-answers to different-samples and different-answers to different-samples respectively.

Author(s)

Rune Haubo B Christensen

References

Christensen, R.H.B., Brockhoff, P.B. (2009). Estimation and inference in the same-different test. Food, Quality and Preference, 20 pp. 514–520

See Also

discrimSim

Examples

```
## Running simulations:
samediffSim(n = 10, tau = 1, delta = 1, Ns = 10, Nd = 10)
```

SDT *Signal Detection Theory Computation of d-prime*

Description

The function computes d-prime for any 2 x J table where J >= 2 for the "yes–no" or "A-Not A" experiment using the Signal Detection Theory (SDT) algorithm to compute J-1 d-prime's. The algorithm is also called the "empirical probit transform". The function also provides the "logit" counterpart.

Usage

```
SDT(tab, method = c("probit", "logit"))
```

Arguments

tab	A 2 x J table with true class relation in rows (only two true classes) and the J-class response in columns
method	should the empirical probit or logit transform be computed?

Value

A (J-1) x 3 matrix. The first two columns contains the z-transform of the Hit rate and the False Alarm rate respectively—ready to plot along with the empirical ROC curve. The third column contains the estimated d-primes.

Author(s)

Rune Haubo B Christensen

References

MacMillan , A. N. and Creelman, C. D (2005) Detection Theory A User's Guide. Lawrence Elbaum Associates, Inc. 2nd edition.

Examples

```
### Design table:
## 8  "yes"-responses to yes-samples
## 1  "yes"-responses to no-samples
## 17 "no"-response to yes-samples
## 24 "no"-responses to no-samples
## Note that response-class is columnwise and true-class is rowwise:
(mat <- rbind(c(8, 17),
              c(1, 24)))
SDT(mat, "logit")
SDT(mat, "probit")
```

```
## compare to AnotA():
m1 <- AnotA(8, 25, 1, 25)
m1

## Compute d-prime 'by hand':
## Hit rate and False alarm rates:
H <- 8/(8+17)
FA <- 1/(1+24)
zH <- qnorm(H)
zFA <- qnorm(FA)
## d-prime:
zH - zFA  # d'



## Multi-response-class example (odor example from MacMillan and
## Creelman, 2005)
(odor <- matrix(c(112, 112, 72, 53, 22, 4, 7, 38, 50, 117, 101, 62), 2,
                byrow = TRUE))
obj <- SDT(odor)
ROC(obj[3,3])
```

`sensR-deprecated` *Deprecated Functions in sensR Package*

Description

These functions are provided for compatibility with older versions of the **sensR** package only, and may be removed eventually.

Details

The `clls` function is deprecated and users encouraged to use `clm` instead from the **ordinal** package.

`summary.samediff` *Summary method for samediff objects.*

Description

Makes a summary of a `samediff` object with option to use profile likelihood for confidence intervals and p-values or the assymptotic variance-covariance matrix.

Usage

```
## S3 method for class 'samediff'
summary(object, profile = TRUE, ...)
```

Arguments

object	a samediff object
profile	logical: Should the profile likelihood be used for confidence intervals and p-values for the parameters? Defaults to TRUE. If FALSE the assymptotic variance-covariance matrix derived from the observed Fisher information matrix will be used. See Details for more information.
...	can be level, eg 0.95 to specify the confidence level of the intervals.

Details

Note that the variance-covariance matrix does not always exist in contrast to the profile likelihood. profile = FALSE may therefore cause confidence intervals etc. to be NA.

Value

An object of class summary.samediff inheriting elements from the samediff object and with the following additional elements

table	matrix with parameter estimates, standard errors, confidence intervals and p-values.
AIC	the AIC of the object.

Author(s)

Rune Haubo B Christensen

See Also

confint.samediff, profile.samediff

Examples

```
# data: 8 of the same samples were judged to be same
#       5 of the same samples were judged to be different
#       4 of the different samples were judged to be same
#       9 of the different samples were judged to be different

sadi <- samediff(8, 5, 4, 9)
summary(sadi)
summary(sadi, FALSE)
```

tetrad *Create tetrad binomial family*

Description

Creates a binomial family object with the inverse link function equal to the psychometric function for the unspecified method of tetrads.

Usage

```
tetrad()
```

Value

A binomial family object for models. Among other things it inludes the psychometric function as `linkinv` and the inverse psychometric function (for direct d-prime computation) as `linkfun`.

Note

Several functions in this package makes use of functions in the tetrad family object, but it may also be used on its own—see the example below.

Author(s)

Rune Haubo B Christensen

References

Ennis, J. M., Ennis, D. M., Yip, D., & O'Mahony, M. (1998). Thurstonian models for variants of the method of tetrads. British Journal of Mathematical and Statistical Psychology, 51, pp. 205-215.

Ennis, J. M., & Jesionka, V. (2011). The power of sensory discrimination methods revisited. Journal of Sensory Studies, 26, pp. 371-382.

See Also

duotrio, twoAFC, threeAFC, discrim, discrimPwr, discrimSim, AnotA, discrimSS, samediff, findcr

Examples

```
## Estimating d-prime using glm for a Tetrad test:
xt <- matrix(c(10, 5), ncol = 2) ## data: 10 correct answers, 5 incorrect
res <- glm(xt ~ 1, family = tetrad)
summary(res)
## Equivalent to (Estimate and Std. Error):
discrim(10, 15, method="tetrad")
```

```
## Extended example plotting the profile likelihood
## data: 10 correct answers, 9 incorrect
xt <- matrix(c(10, 9), ncol = 2)
summary(res <- glm(xt ~ 1, family = tetrad))
N <- 100
dev <- double(N)
delta <- seq(1e-4, 3, length = N)
for(i in 1:N)
  dev[i] <- glm(xt ~ -1 + offset(delta[i]),
                family = tetrad)$deviance
plot(delta, exp(-dev/2), type = "l",
     xlab = expression(delta),
     ylab = "Normalized Profile Likelihood")
## Add Normal approximation:
lines(delta, exp(-(delta - coef(res))^2 /
                 (2 * vcov(res))), lty = 2)
## Add confidence limits:
level <- c(0.95, 0.99)
lim <- sapply(level, function(x) exp(-qchisq(x, df=1)/2) )
abline(h = lim, col = "grey")
```

---

threeAFC *Create 3-AFC binomial family*

Description

Creates a copy of the binomial family with the inverse link function changed to equal the 3-AFC psychometric function and correspondingly changed link function and derivative of the inverse link function.

Usage

```
threeAFC()
```

Value

A binomial family object for models. Among other things it inludes the psychometric function as `linkinv` and the inverse psychometric function (for direct dprime computation) as `linkfun`.

Note

Several functions in this package makes use of the function, but it may also be used on its own—see the example below.

Author(s)

Rune Haubo B Christensen and Per Bruun Brockhoff

References

Brockhoff, P.B. and Christensen, R.H.B. (2010). Thurstonian models for sensory discrimination tests as generalized linear models. Food Quality and Preference, 21, pp. 330-338.

See Also

triangle, twoAFC, tetrad, duotrio, discrim, discrimPwr, discrimSim, AnotA, discrimSS, samediff, findcr

Examples

```
## Estimating d-prime using glm for a 3-AFC test:
xt <- matrix(c(10, 5), ncol = 2) ## data: 10 correct answers, 5 incorrect
res <- glm(xt ~ 1, family = threeAFC)
summary(res)
## Equivalent to (Estimate and Std. Error):
discrim(10, 15, method="threeAFC")


## Extended example plotting the profile likelihood
## data: 10 correct answers, 5 incorrect
xt <- matrix(c(10, 2), ncol = 2)
summary(res <- glm(xt ~ 1, family = threeAFC))#, etastart = etastart))
N <- 100
dev <- double(N)
level <- c(0.95, 0.99)
delta <- seq(1e-4, 5, length = N)
for(i in 1:N)
  dev[i] <- glm(xt ~ -1 + offset(delta[i]),
                family = threeAFC)$deviance
plot(delta, exp(-dev/2), type = "l",
     xlab = expression(delta),
     ylab = "Normalized Profile Likelihood")
## Add Normal approximation:
lines(delta, exp(-(delta - coef(res))^2 /
                 (2 * vcov(res))), lty = 2)
## Add confidence limits:
lim <- sapply(level, function(x)
              exp(-qchisq(x, df=1)/2) )
abline(h = lim, col = "grey")
```

`triangle` *Create triangle binomial family*

Description

Creates a copy of the binomial family with the inverse link function changed to equal the triangle psychometric function and correspondingly changed link function and derivative of the inverse link function.

Usage

```
triangle()
```

Value

A binomial family object for models. Among other things it inludes the psychometric function as `linkinv` and the inverse psychometric function (for direct dprime computation) as `linkfun`.

Note

Several functions in this package makes use of the function, but it may also be used on its own—see the example below.

Author(s)

Rune Haubo B Christensen and Per Bruun Brockhoff

References

Brockhoff, P.B. and Christensen, R.H.B. (2010). Thurstonian models for sensory discrimination tests as generalized linear models. Food Quality and Preference, 21, pp. 330-338.

See Also

duotrio, twoAFC, tetrad, threeAFC, discrim, discrimPwr, discrimSim, AnotA, discrimSS, samediff, findcr

Examples

```
## Estimating d-prime using glm for a Triangle test:
xt <- matrix(c(10, 5), ncol = 2) ## data: 10 correct answers, 5 incorrect
res <- glm(xt ~ 1, family = triangle)
summary(res)
## Equivalent to (Estimate and Std. Error):
discrim(10, 15, method="triangle")


## Extended example plotting the profile likelihood
## data: 10 correct answers, 9 incorrect
xt <- matrix(c(10, 9), ncol = 2)
summary(res <- glm(xt ~ 1, family = triangle))
N <- 100
dev <- double(N)
delta <- seq(1e-4, 3, length = N)
for(i in 1:N)
  dev[i] <- glm(xt ~ -1 + offset(delta[i]),
                family = triangle)$deviance
plot(delta, exp(-dev/2), type = "l",
     xlab = expression(delta),
     ylab = "Normalized Profile Likelihood")
## Add Normal approximation:
```

```
lines(delta, exp(-(delta - coef(res))^2 /
                 (2 * vcov(res))), lty = 2)
## Add confidence limits:
level <- c(0.95, 0.99)
lim <- sapply(level, function(x) exp(-qchisq(x, df=1)/2) )
abline(h = lim, col = "grey")
```

---

twoAC *2-AC Discrimination and Preference Protocol*

Description

Computes estimates and standard errors of d-prime and tau for the two alternative (2-AC) protocol. A confidence interval and significance test for d-prime is also provided. The 2-AC protocol is equivalent to a 2-AFC protocol with a "no-difference" option, and equivalent to a paired preference test with an "no-preference" option.

Usage

```
twoAC(data, d.prime0 = 0, conf.level = 0.95,
      statistic = c("likelihood", "Wald"),
      alternative = c("two.sided", "less", "greater"), ...)
```

Arguments

`data`	a non-negative numeric vector of length 3 with the number of observations in the three response categories in the form ("prefer A", "no-preference", "prefer B"). If the third element is larger than the first element, the estimate of d-prime is positive.
`d.prime0`	the value of d-prime under the null hypothesis for the significance test.
`conf.level`	the confidence level.
`statistic`	the statistic to use for confidence level and significance test.
`alternative`	the type of alternative hypothesis.
`...`	not currently used.

Details

`confint`, `profile`, `logLik`, `vcov`, and `print` methods are implemented for `twoAC` objects.

Power computations for the 2-AC protocol is implemented in `twoACpwr`.

Value

An object of class `twoAC` with elements

`coefficients`	2 by 2 coefficient matrix with estimates and standard errors of d-prime and tau. If the variance-covariance matrix of the parameters is not defined, the standard errors are `NA`.
`vcov`	variance-covariance matrix of the parameter estimates. Only present if defined for the supplied data.
`data`	the data supplied to the function.
`call`	the matched call.
`logLik`	the value of the log-likelihood at the maximum likelihood estimates.
`alternative`	the name of the alternative hypothesis for the significance test.
`statistic`	the name of the test statistic used for the significance test.
`conf.level`	the confidence level for the confidence interval for d-prime.
`d.prime0`	the value of d-prime under the null hypothesis in the significance test.
`p.value`	p-value of the significance test.
`confint`	two-sided condfidence interval for d-prime. This is only available if the standard errors are defined, which may happen in boundary cases. Use `profile` and `confint` methods to get confidence intervals instead; see the examples.

Author(s)

Rune Haubo B Christensen

References

Christensen R.H.B., Lee H-S and Brockhoff P.B. (2012). Estimation of the Thurstonian model for the 2-AC protocol. Food Quality and Preference, 24(1), pp.119-128.

See Also

`clm2twoAC`, `twoACpwr`

Examples

```
## Simple:
fit <- twoAC(c(2,2,6))
fit

## Typical discrimination-difference test:
(fit <- twoAC(data = c(2, 5, 8), d.prime0 = 0, alternative = "greater"))

## Typical discrimination-similarity test:
(fit <- twoAC(data = c(15, 15, 20), d.prime0 = .5, alternative = "less"))

## Typical preference-difference test:
(fit <- twoAC(data = c(3, 5, 12), d.prime0 = 0,
```

```
              alternative = "two.sided"))

## Typical preference (non-)inferiority test:
(fit <- twoAC(data = c(3, 5, 12), d.prime0 = 0,
              alternative = "greater"))

## For preference equivalence tests (two-sided) use CI with alpha/2:
## declare equivalence at the 5% level if 90% CI does not contain,
## e.g, -1 or 1:
(fit <- twoAC(data = c(15, 10, 10), d.prime0 = 0, conf.level = .90))

## The var-cov matrix and standard errors of the parameters are not
## defined in all situations. If standard errors are not
## defined, then confidence intervals are not provided directly:
(fit <- twoAC(c(5, 0, 15)))
## We may use profile and confint methods to get confidence intervals
## never the less:
pr <- profile(fit, range = c(-1, 3))
confint(pr)
plot(pr)
```

---

twoACpwr *Exact Power Computation for the 2-AC Discrimination Protocol*

Description

Computes the exact power for the 2-AC protocol using the (signed) likelihood root statistic. Power is computed for a significance test of d-prime. The `tol` argument specifies the precision with which power should be computed.

Usage

```
twoACpwr(tau, d.prime, size, d.prime0 = 0, alpha = 0.05, tol = 1e-5,
         return.dist = FALSE, statistic = "likelihood",
         alternative = c("two.sided", "less", "greater"))
```

Arguments

`tau`	the value of tau under the alternative hypothesis
`d.prime`	the value of d.prime under the alternative hypothesis
`size`	the sample size
`d.prime0`	the value of d-prime under the null hypothesis in the significance test for which power should be computed
`alpha`	the size of the test

tol	specifies the precision with which power should be computed, e.g., 1e-4 cause power to be computed correctly to three significant digits. Lower values of tau gives higher precision, but also longer computation times.
return.dist	should the p-value distribution be returned rather than the power be computed?
statistic	the statistic used in the significance test for which the power should be computed. Currently only the (signed) likelihood root statistic is available—se the details for more information.
alternative	the type of alternative hypothesis in the significance test for which the power should be computed

Details

The main idea in this function is to compute all possible data outcomes and then compute the p-value for the chosen significance test for each of these outcomes. This gives the exact distribution of p-values from which the exact power can be computed. This is basically what happens if tol = 0.

There is, however, a problem with this approach if size is large, since the the number of possible outcomes increases very fast with the size; the order is O(n^2). The solution to this problem is to ignore those outcomes which will occur with very small probability. Often, a large proportion of the outcomes, say 90% will occur so rarely that they account for, say 1e-4 percent of the probability mass; it is therefore safe to ignore those outcomes without compromising the accuracy of the computed power by any relevant amount. For more information see the referenced paper and the package vignette Statistical Methodology.

The Wald statistic is not available here. The reason is that the Wald statistic is not always defined and the problem is therefore what to do with those cases where it is not defined? On the other hand the likelihood root statistic is defined in all cases, so theres is no problem here, and since the likelihood root statistic is more accurate than the Wald statistic, there is not much reason to use the Wald statistic after all.

For the record; the Wald statistic is not defined, when the standard error of d-prime is not defined. This happens when the variance-covariance matrix of tau and d-prime is not defined, which occurs in a number of boundary cases, i.e., when one or more cells contain zero frequencies. Since these outcomes occur with positive probability, the algorithm used by twoACpwr will always encounter those cases and have to deal with them. This would be cumbersome to implement.

Value

A data.frame with one line and the following entries

power	the computed power
actual.alpha	the actual size of the test (different from the nominal alpha given as argument due to the discreteness of the observations).
samples	the number of possible outcomes for this size
discarded	the number of outcomes for which the p-value is not computed. This number is zero if tol = 0
kept	the number of outcomes for which the p-value is computed in. This number equals samples if tol = 0

p — the probability vector of the multinomial distribution implied by the values of tau and d.prime.

Author(s)

Rune Haubo B Christensen

References

Christensen R.H.B., Lee H-S and Brockhoff P.B. (2012). Estimation of the Thurstonian model for the 2-AC protocol. Food Quality and Preference, 24(1), pp.119-128.

See Also

clm2twoAC, twoACpwr

Examples

```
## Exact power:
twoACpwr(tau = .5, d.prime = .7, size = 50, tol = 0)

## Power exact to a reasonable number of digits
twoACpwr(tau = .5, d.prime = .7, size = 50, tol = 1e-5)

## Power for a similarity test in a discrimination setting where the
## true parameter values are expected to be tau = 0.4 and true d.prime
## = .5, while we want to show that d.prime < 1, i.e., under the null
## hypothesis d.prime = 1:
twoACpwr(tau = .4, d.prime = .5, size = 100, d.prime0 = 1, tol = 1e-5,
         alternative = "less")

## Power for a difference test in a preference setting where the true
## parameter values are expected to be tau = 0.4 and d.prime = -0.5,
## while we want to show that d.prime is different from zero:
twoACpwr(tau = 0.4, d.prime = -0.5, size = 100, d.prime0 = 0, tol = 1e-5,
         alternative = "two.sided")
```

---

twoAFC *Create 2-AFC binomial family*

Description

Creates a copy of the binomial family with the inverse link function changed to equal the 2-AFC psychometric function and correspondingly changed link function and derivative of the inverse link function.

Usage

```
twoAFC()
```

Value

A binomial family object for models. Among other things it inludes the psychometric function as `linkinv` and the inverse psychometric function (for direct dprime computation) as `linkfun`.

Note

Several functions in this package makes use of the function, but it may also be used on its own—see the example below.

Author(s)

Rune Haubo B Christensen and Per Bruun Brockhoff

References

Brockhoff, P.B. and Christensen, R.H.B. (2010). Thurstonian models for sensory discrimination tests as generalized linear models. Food Quality and Preference, 21, pp. 330-338.

See Also

triangle, threeAFC, tetrad, duotrio, discrim, discrimPwr, discrimSim, AnotA, discrimSS, samediff, findcr

Examples

```
## Estimating d-prime using glm for a 2-AFC test:
xt <- matrix(c(10, 5), ncol = 2) ## data: 10 correct answers, 5 incorrect
res <- glm(xt ~ 1, family = twoAFC)
summary(res)
## Equivalent to (Estimate and Std. Error):
discrim(10, 15, method="twoAFC")


## Extended example plotting the profile likelihood
## data: 10 correct and 8 incorrect:
xt <- matrix(c(10, 8), ncol = 2)
summary(res <- glm(xt ~ 1, family = twoAFC))
N <- 100
dev <- double(N)
level <- c(0.95, 0.99)
delta <- seq(1e-4, 3, length = N)
for(i in 1:N)
  dev[i] <- glm(xt ~ -1 + offset(delta[i]),
                family = twoAFC)$deviance
plot(delta, exp(-dev/2), type = "l",
     xlab = expression(delta),
     ylab = "Normalized Profile Likelihood")
## Add Normal approximation:
lines(delta, exp(-(delta - coef(res))^2 /
                 (2 * vcov(res))), lty = 2)
## Add confidence limits:
```

```
lim <- sapply(level, function(x)
              exp(-qchisq(x, df=1)/2) )
abline(h = lim, col = "grey")
```

`twofive` *Create twofive binomial family*

Description

Creates af binomial family object with the inverse link function equal to the psychometric function for the Two-Out-of-Five test.

Usage

```
twofive()
```

Value

A binomial family object for models. Among other things it inludes the psychometric function as `linkinv` and the inverse psychometric function (for direct d-prime computation) as `linkfun`.

Note

Several functions in this package makes use of functions in the twofive family object, but it may also be used on its own—see the example below.

Author(s)

Karolina Stachlewska

References

Ennis, J. M. (2013). A thurstonian analysis of the Two-Out-of-Five test. Journal of Sensory Studies, 28(4), pp. 297-310.

See Also

`duotrio`, `triangle`, `twoAFC`, `threeAFC`, `tetrad`, `twofiveF`, `hexad`, `discrim`, `discrimPwr`, `discrimSim`, `AnotA`, `discrimSS`, `samediff`, `findcr`

Examples

```
## Estimating d-prime using glm for a Two-Out-of-Five test:
xt <- matrix(c(10, 5), ncol = 2) ## data: 10 correct answers, 5 incorrect
res <- glm(xt ~ 1, family = twofive)
summary(res)
## Equivalent to (Estimate and Std. Error):
discrim(10, 15, method="twofive")


## Extended example plotting the profile likelihood
## data: 10 correct answers, 9 incorrect
xt <- matrix(c(10, 9), ncol = 2)
summary(res <- glm(xt ~ 1, family = twofive))
N <- 100
dev <- double(N)
delta <- seq(1e-4, 3, length = N)
for(i in 1:N)
  dev[i] <- glm(xt ~ -1 + offset(delta[i]),
                family = twofive)$deviance
plot(delta, exp(-dev/2), type = "l",
     xlab = expression(delta),
     ylab = "Normalized Profile Likelihood")
## Add Normal approximation:
lines(delta, exp(-(delta - coef(res))^2 /
                 (2 * vcov(res))), lty = 2)
## Add confidence limits:
level <- c(0.95, 0.99)
lim <- sapply(level, function(x) exp(-qchisq(x, df=1)/2) )
abline(h = lim, col = "grey")
```

`twofiveF` *Create twofiveF binomial family*

Description

Creates af binomial family object with the inverse link function equal to the psychometric function for the Two-Out-of-Five with forgiveness test.

Usage

```
twofiveF()
```

Value

A binomial family object for models. Among other things it inludes the psychometric function as `linkinv` and the inverse psychometric function (for direct d-prime computation) as `linkfun`.

Note

Several functions in this package makes use of functions in the twofiveF family object, but it may also be used on its own—see the example below.

Author(s)

Karolina Stachlewska

References

Ennis, J. M. (2013). A thurstonian analysis of the Two-Out-of-Five test. Journal of Sensory Studies, 28(4), pp. 297-310.

See Also

duotrio, triangle, twoAFC, threeAFC, tetrad, twofive, hexad, discrim, discrimPwr, discrimSim, AnotA, discrimSS, samediff, findcr

Examples

```
## Estimating d-prime using glm for a Two-Out-of-Five with forgiveness test:
xt <- matrix(c(10, 5), ncol = 2) ## data: 10 correct answers, 5 incorrect
res <- glm(xt ~ 1, family = twofiveF)
summary(res)
## Equivalent to (Estimate and Std. Error):
discrim(10, 15, method="twofiveF")


## Extended example plotting the profile likelihood
## data: 10 correct answers, 9 incorrect
xt <- matrix(c(10, 9), ncol = 2)
summary(res <- glm(xt ~ 1, family = twofiveF))
N <- 100
dev <- double(N)
delta <- seq(1e-4, 3, length = N)
for(i in 1:N)
  dev[i] <- glm(xt ~ -1 + offset(delta[i]),
                family = twofiveF)$deviance
plot(delta, exp(-dev/2), type = "l",
     xlab = expression(delta),
     ylab = "Normalized Profile Likelihood")
## Add Normal approximation:
lines(delta, exp(-(delta - coef(res))^2 /
                 (2 * vcov(res))), lty = 2)
## Add confidence limits:
level <- c(0.95, 0.99)
lim <- sapply(level, function(x) exp(-qchisq(x, df=1)/2) )
abline(h = lim, col = "grey")
```

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