Package ‘abtest’

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Methods defined for objects returned from the `ab_test` function.

Usage

```r
## S3 method for class 'ab'
summary(object, digits = 3, raw = FALSE, ...)

## S3 method for class 'summary.ab'
print(x, ...)

## S3 method for class 'ab'
print(x, ...)

## S3 method for class 'ab'
plot(x, ...)
```

Arguments

- `object, x` object of class `ab` as returned from `ab_test`.
- `digits` number of digits to print for the summary.
- `raw` if `TRUE`, the raw posterior samples are used to estimate the mean, sd, and quantiles for the summary of the posterior. If `FALSE`, parametric fits to the marginal posteriors are used to obtain the mean, sd, and quantiles. Specifically, a normal distribution is fitted for `psi` (logor) and `beta`; a log-normal distribution is fitted for `or` and `rrisk`; beta distributions are fitted for `p1` and `p2`; a scaled beta distribution is fitted for `arisk`. These distributional fits are also used in `plot_posterior`.
- `...` further arguments, currently ignored.
ab_test

Value

The print methods prints the Bayes factors, prior probabilities of the hypotheses, and posterior probabilities of the hypotheses (and returns nothing).

The plot method visualizes the prior probabilities of the hypotheses and posterior probabilities of the hypotheses (the next plots is obtained by hitting Return) using the prob_wheel function.

The summary methods returns the ab object that is guaranteed to contain posterior samples (i.e., it adds posterior samples if they were not included already). Additionally, it adds to the object a posterior summary matrix (i.e., ab$post$post_summary) for the posterior under H1 and the arguments digits (used for printing) and raw (added to ab$input).

---

ab_test

Bayesian A/B Test

---

Description

Function for conducting a Bayesian A/B test (i.e., test between two proportions).

Usage

ab_test(
  data = NULL,
  prior_par = list(mu_psi = 0, sigma_psi = 1, mu_beta = 0, sigma_beta = 1),
  prior_prob = NULL,
  nsamples = 10000,
  is_df = 5,
  posterior = FALSE,
  y = NULL,
  n = NULL
)

Arguments

data

list or data frame with the data. This list (data frame) needs to contain the following elements: y1 (number of "successes" in the control condition), n1 (number of trials in the control condition), y2 (number of "successes" in the experimental condition), n2 (number of trials in the experimental condition). Each of these elements needs to be an integer. Alternatively, the user can provide for each of the elements a vector with a cumulative sequence of "successes"/trials. This allows the user to produce a sequential plot of the posterior probabilities for each hypothesis by passing the result object of class "ab" to the plot_sequential function. Sequential data can also be provided in form of a data frame or matrix that has the columns "outcome" (containing only 0 and 1 to indicate the binary outcome) and "group" (containing only 1 and 2 to indicate the group membership). Note that the data can also be provided by specifying the arguments y and n instead (not possible for sequential data).
prior_par  list with prior parameters. This list needs to contain the following elements:
mu_psi (prior mean for the normal prior on the test-relevant log odds ratio),  
sigma_psi (prior standard deviation for the normal prior on the test-relevant log odds ratio), mu_beta (prior mean for the normal prior on the grand mean of the log odds), sigma_beta (prior standard deviation for the normal prior on the grand mean of the log odds). Each of the elements needs to be a real number (the standard deviations need to be positive). The default are standard normal priors for both the log odds ratio parameter and the grand mean of the log odds parameter.

prior_prob  named vector with prior probabilities for the four hypotheses "H1", "H+", "H-", and "H0". "H1" states that the "success" probability differs between the control and the experimental condition but does not specify which one is higher. "H+" states that the "success" probability in the experimental condition is higher than in the control condition, "H-" states that the "success" probability in the experimental condition is lower than in the control condition. "H0" states that the "success" probability is identical (i.e., there is no effect). The one-sided hypotheses "H+" and "H-" are obtained by truncating the normal prior on the log odds ratio so that it assigns prior mass only to the allowed log odds ratio values (e.g., for "H+" a normal prior that is truncated from below at 0). If NULL (default) the prior probabilities are set to c(0, 1/4, 1/4, 1/2). That is, the default assigns prior probability .5 to the hypothesis that there is no effect (i.e., "H0"). The remaining prior probability (i.e., also .5) is split evenly across the hypothesis that there is a positive effect (i.e., "H+") and the hypothesis that there is a negative effect (i.e., "H-").

nsamples  determines the number of importance samples for obtaining the log marginal likelihood for "H+" and "H-" and the number of posterior samples in case posterior = TRUE. The default is 10000.

is_df  degrees of freedom of the multivariate t importance sampling proposal density. The default is 5.

posterior  Boolean which indicates whether posterior samples should be returned. The default is FALSE.

y  integer vector of length 2 containing the number of "successes" in the control and experimental condition

n  integer vector of length 2 containing the number of trials in the control and experimental condition

Details

The implemented Bayesian A/B test is based on the following model by Kass and Vaidyanathan (1992, section 3):

\[
\log\left(\frac{p_1}{1-p_1}\right) = \beta - \psi/2 \\
\log\left(\frac{p_2}{1-p_2}\right) = \beta + \psi/2 \\
y_1 \text{ Binomial}(n_1, p_1) \\
y_2 \text{ Binomial}(n_2, p_2).
\]

"H0" states that \( \psi = 0 \), "H1" states that \( \psi = 0 \), "H+" states that \( \psi > 0 \), and "H-" states that \( \psi < 0 \). Normal priors are assigned to the two parameters \( \psi \) (i.e., the test-relevant log odds ratio) and \( \beta \).
(i.e., the grand mean of the log odds which is a nuisance parameter). Log marginal likelihoods for "H0" and "H1" are obtained via Laplace approximations (see Kass & Vaidyanathan, 1992) which work well even for very small sample sizes. For the one-sided hypotheses "H+" and "H-" the log marginal likelihoods are obtained based on importance sampling which uses as a proposal a multivariate t distribution with location and scale matrix obtained via a Laplace approximation to the (log-transformed) posterior. If posterior = TRUE, posterior samples are obtained using importance sampling.

**Value**

returns an object of class "ab" with components:

- **input**: a list with the input arguments.
- **post**: a list with parameter posterior samples for the three hypotheses "H1", "H+" (in the output called "Hplus"), and "H-" (in the output called "Hminus"). Only contains samples if posterior = TRUE.
- **laplace**: a list with the approximate parameter posterior mode and variance/covariance matrix for each hypothesis obtained via a Laplace approximation.
- **method**: character that indicates the method that has been used to obtain the results. The default is "log-is" (importance sampling with multivariate t proposal based on a Laplace approximation to the log transformed posterior). If this method fails (for the one-sided hypotheses), method "is-sn" is used (i.e., importance sampling is used to obtain unconstrained samples, then a skew-normal distribution is fitted to the samples to obtain the results for the one-sided hypotheses). If method = "is-sn", posterior samples can only be obtained for "H1".
- **logml**: a list with the estimated log marginal likelihoods for the hypotheses "H0" (i.e., "logml0"), "H1" (i.e., "logml1"), "H+" (i.e., "logmlplus"), and "H-" (i.e., "logmlminus").
- **post_prob**: a named vector with the posterior probabilities of the four hypotheses "H1", "H+", "H-", and "H0".
- **logbf**: a list with the log Bayes factor in favor of "H1" over "H0", the log Bayes factor in favor of "H+" over "H0", and the log Bayes factor in favor of "H-" over "H0".
- **bf**: a list with the Bayes factor in favor of "H1" over "H0" (i.e., "bf10"), the Bayes factor in favor of "H+" over "H0" (i.e., "bfplus0"), and the Bayes factor in favor of "H-" over "H0" (i.e., "bfminus0").

**Author(s)**

Quentin F. Gronau

**References**


See Also

elicit_prior allows the user to elicit a prior based on providing quantiles for either the log odds ratio, the odds ratio, the relative risk, or the absolute risk. The resulting prior is always translated to the corresponding normal prior on the log odds ratio. The plot_prior function allows the user to visualize the prior distribution. The simulate_priors function produces samples from the prior distribution. The prior and posterior probabilities of the hypotheses can be visualized using the prob_wheel function. Parameter posteriors can be visualized using the plot_posterior function. The plot_sequential function allows the user to sequentially plot the posterior probabilities of the hypotheses (only possible if the data object contains vectors with the cumulative "successes"/trials).

Examples

# synthetic data
data <- list(y1 = 10, n1 = 28, y2 = 14, n2 = 26)

# Bayesian A/B test with default settings
ab <- ab_test(data = data)
print(ab)

# different prior parameter settings
prior_par <- list(mu_psi = 0.2, sigma_psi = 0.8,
                 mu_beta = 0, sigma_beta = 0.7)
ab2 <- ab_test(data = data, prior_par = prior_par)
print(ab2)

# different prior probabilities
prior_prob <- c(.1, .3, .2, .4)
names(prior_prob) <- c("H1", "H+", "H-", "H0")
ab3 <- ab_test(data = data, prior_prob = prior_prob)
print(ab3)

# also possible to obtain posterior samples
ab4 <- ab_test(data = data, posterior = TRUE)

# plot parameter posterior
plot_posterior(x = ab4, what = "logor")

dprior

Prior Density

Description

Function for evaluating the prior density.

Usage

dprior(
  x1,
  x2 = NULL,
)
prior_par = list(mu_psi = 0, sigma_psi = 1, mu_beta = 0, sigma_beta = 1),
what = "logor",
hypothesis = "H1"
)

Arguments

x1 numeric vector with values at which the prior density should be evaluated.

x2 if what = "p1p2", value of p2 (i.e., the latent "success" probability in the experimental condition) at which the joint prior density should be evaluated. If what = "p2givenp1", the given value of p1 (i.e., the latent "success" probability in the control condition).

prior_par list with prior parameters. This list needs to contain the following elements: mu_psi (prior mean for the normal prior on the test-relevant log odds ratio), sigma_psi (prior standard deviation for the normal prior on the test-relevant log odds ratio), mu_beta (prior mean for the normal prior on the grand mean of the log odds), sigma_beta (prior standard deviation for the normal prior on the grand mean of the log odds). Each of the elements needs to be a real number (the standard deviations need to be positive). The default are standard normal priors for both the log odds ratio parameter and the grand mean of the log odds parameter.

what character specifying for which quantity the prior density should be evaluated. Either "logor" (i.e., log odds ratio), "or" (i.e., odds ratio), "p1p2" (i.e., the joint density of the latent "success" probability in the experimental and control condition), "p1" (i.e., latent "success" probability in the control condition), "p2" (i.e., latent "success" probability in the experimental condition), "p2givenp1" (i.e., conditional distribution of the latent "success" probability in the experimental condition given a "success" probability of p1 in the control condition), "rrisk" (i.e., relative risk, the ratio of the "success" probability in the experimental and control condition), or "arisk" (i.e., absolute risk, the difference of the "success" probability in the experimental and control condition).

hypothesis character specifying whether to evaluate the two-sided prior density (i.e., "H1"), the one-sided prior density with lower truncation point (i.e., "H+"), or the one-sided prior density with upper truncation point (i.e., "H-").

Value

numeric vector with the values of the prior density.

Note

Internally, the test-relevant prior is always a normal prior on the log odds ratio, consequently, if what is not "logor", the implied prior density for the quantity is returned.

Author(s)

Quentin F. Gronau
Examples

# prior parameters
prior_par <- list(mu_psi = 0, sigma_psi = 1,
                mu_beta = 0, sigma_beta = 1)

# prior density
dprior(x1 = 0.1, prior_par = prior_par, what = "logor")
dprior(x1 = 1.1, prior_par = prior_par, what = "or")
dprior(x1 = 0.49, x2 = 0.51, prior_par = prior_par, what = "p1p2")
dprior(x1 = 0.45, prior_par = prior_par, what = "p1")
dprior(x1 = 0.45, prior_par = prior_par, what = "p2")
dprior(x1 = 0.49, x2 = 0.51, prior_par = prior_par, what = "p2givenp1")
dprior(x1 = 1.05, prior_par = prior_par, what = "rrisk")
dprior(x1 = 0.02, prior_par = prior_par, what = "arisk")

# also works for vectors
dprior(x1 = c(-0.1, 0, 0.1, 0.2), prior_par = prior_par, what = "logor")

elicit_prior

Elicit Prior

Description

Function for eliciting a prior distribution.

Usage

elicit_prior(
  q,
  prob,
  what = "logor",
  hypothesis = "H1",
  mu_beta = 0,
  sigma_beta = 1
)

Arguments

q vector with quantiles for the quantity of interest.
prob vector with probabilities corresponding to the quantiles (e.g., for the median the corresponding element of prob would need to be .5).
what character specifying for which quantity a prior should be elicited. Either "logor" (i.e., log odds ratio), "or" (i.e., odds ratio), "rrisk" (i.e., relative risk, the ratio of the "success" probability in the experimental and the control condition), or "arisk" (i.e., absolute risk, the difference of the "success" probability in the experimental and control condition).
elicit_prior

- **hypothesis**: character specifying whether the provided quantiles correspond to a two-sided prior (i.e., "H1"), a one-sided prior with lower truncation point (i.e., "H+"), or a one-sided prior with upper truncation point (i.e., "H-").

- **mu_beta**: prior mean of the nuisance parameter $\beta$ (i.e., the grand mean of the log odds). The default is 0.

- **sigma_beta**: prior standard deviation of the nuisance parameter $\beta$ (i.e., the grand mean of the log odds). The default is 1.

**Details**

It is assumed that the prior on the grand mean of the log odds (i.e., $\beta$) is not the primary target of prior elicitation and is fixed (e.g., to a standard normal prior). The reason is that the grand mean nuisance parameter $\beta$ is not the primary target of inference and changes in the prior on this nuisance parameter do not affect the results much in most cases (see Kass & Vaidyanathan, 1992). Nevertheless, it should be emphasized that the implemented approach allows users to set the prior parameters `mu_beta` and `sigma_beta` flexibly; the only constraint is that this takes place before the prior on the test-relevant log odds ratio parameter $\psi$ is elicited. The `elicit_prior` function allows the user to elicit a prior not only in terms of the log odds ratio parameter $\psi$, but also in terms of the odds ratio, the relative risk (i.e., the ratio of the "success" probability in the experimental and the control condition), or the absolute risk (i.e., the difference of the "success" probability in the experimental and control condition). In case the prior is not elicited for the log odds ratio directly, the elicited prior is always translated to the closest corresponding normal prior on the log odds ratio. The prior parameters `mu_psi` and `sigma_psi` are obtained using least squares minimization.

**Value**

- `mu_psi` (prior mean for the normal prior on the test-relevant log odds ratio).
- `sigma_psi` (prior standard deviation for the normal prior on the test-relevant log odds ratio).
- `mu_beta` (prior mean for the normal prior on the grand mean of the log odds).
- `sigma_beta` (prior standard deviation for the normal prior on the grand mean of the log odds).

Note that the prior on the grand mean of the log odds is not part of the elicitation and is assumed to be fixed by the user (using the arguments `mu_beta` and `sigma_beta`). Consequently, the returned values for `mu_beta` and `sigma_beta` simply correspond to the input values.

**Author(s)**

Quentin F. Gronau

**References**


See Also

The `plot_prior` function allows the user to visualize the elicited prior distribution.

Examples

```r
# elicit prior
prior_par <- elicit_prior(q = c(0.1, 0.3, 0.5),
                           prob = c(.025, .5, .975),
                           what = "arisk")
print(prior_par)

# plot elicited prior (absolute risk)
plot_prior(prior_par = prior_par, what = "arisk")

# plot corresponding normal prior on log odds ratio
plot_prior(prior_par = prior_par, what = "logor")
```

extractors  

**Extraction functions for ab objects**

Description

Extraction functions for objects returned from the `ab_test` function.

Usage

```r
get_bf(x, log = FALSE)
get_prior_prob(x)
get_post_prob(x)
get_post_samples(x, hypothesis = "H1")
```

Arguments

- `x`  
  object of class "ab" as returned from `ab_test`.
- `log`  
  determines whether the log Bayes factors are returned.
- `hypothesis`  
  determines for which hypothesis posterior samples are returned. Needs to be either "H1", "H+", or "H-" (the default is "H1").

Value

- `get_bf` returns the Bayes factors in favor of "H1", "H+", and "H-" (compared to H0).
- `get_prior_prob` returns the prior probabilities of the hypotheses.
- `get_post_prob` returns the posterior probabilities of the hypotheses.
- `get_post_samples` returns posterior samples for the specified hypothesis.
plot_posterior

Examples

# synthetic data
data <- list(y1 = 10, n1 = 28, y2 = 14, n2 = 26)

# Bayesian A/B test with default settings
ab <- ab_test(data = data, posterior = TRUE)

# extract Bayes factors
get_bf(ab)

# extract prior probabilities
get_prior_prob(ab)

# extract posterior probabilities
get_post_prob(ab)

# extract posterior samples for H1
s <- get_post_samples(ab, hypothesis = "H1")

plot_posterior

Plot Posterior

Description

Function for plotting the posterior distribution.

Usage

plot_posterior(
  x,
  what = "logor",
  hypothesis = "H1",
  ci = 0.95,
  p1lab = "p1",
  p2lab = "p2",
  p1adj = 0.44,
  p2adj = 0.56,
  ...
)

Arguments

x
  object of class "ab".

what
  character specifying for which quantity the posterior should be plotted. Either
  "logor" (i.e., log odds ratio), "or" (i.e., odds ratio), "p1p2" (i.e., the marginal
  posteriors of the latent "success" probabilities in the experimental and control
  condition), "rrisk" (i.e., relative risk, the ratio of the "success" probability in
  the experimental and the control condition), or "arisk" (i.e., absolute risk, the
difference of the "success" probability in the experimental and control condition).

**hypothesis**
- character specifying whether to plot the two-sided posterior distribution (i.e., "H1"), the one-sided posterior distribution with lower truncation point (i.e., "H+"), or the one-sided posterior distribution with upper truncation point (i.e., "H-").

**ci**
- numeric value specifying the ci\% central credible interval. The default is 0.95 which yields a 95\% central credible interval.

**p1lab**
- determines p1 x-axis label. Only relevant for what = "p1p2".

**p2lab**
- determines p2 x-axis label. Only relevant for what = "p1p2".

**p1adj**
- determines p1 x-axis label adjustment. Only relevant for what = "p1p2".

**p2adj**
- determines p2 x-axis label adjustment. Only relevant for what = "p1p2".

**...**
- further arguments

**Details**

The resulting plot displays the posterior density for the quantity of interest and also displays the corresponding prior density. The values of the posterior median and a ci\% central credible interval are displayed on top of the plot.

**Author(s)**

Quentin F. Gronau

**Examples**

```r
# synthetic data
data <- list(y1 = 10, n1 = 28, y2 = 14, n2 = 26)

# Bayesian A/B test with default settings
ab <- ab_test(data = data, posterior = TRUE)

# plot parameter posterior
plot_posterior(x = ab, what = "logor")
plot_posterior(x = ab, what = "or")
plot_posterior(x = ab, what = "p1p2")
plot_posterior(x = ab, what = "rrisk")
plot_posterior(x = ab, what = "arisk")

# example of good width and height values for saving to file
cairo_pdf(file.path(tempdir(), "test_plot.pdf"),
          width = 530 / 72, height = 400 / 72)
plot_posterior(ab, what = "p1p2")
dev.off()
```
Description

Function for plotting parameter prior distributions.

Usage

```r
plot_prior(
  prior_par = list(mu_psi = 0, sigma_psi = 1, mu_beta = 0, sigma_beta = 1),
  what = "logor",
  hypothesis = "H1",
  p1 = 0.5,
  ...
)
```

Arguments

- `prior_par` list with prior parameters. This list needs to contain the following elements:
  - `mu_psi` (prior mean for the normal prior on the test-relevant log odds ratio),
  - `sigma_psi` (prior standard deviation for the normal prior on the test-relevant log odds ratio),
  - `mu_beta` (prior mean for the normal prior on the grand mean of the log odds),
  - `sigma_beta` (prior standard deviation for the normal prior on the grand mean of the log odds). Each of the elements needs to be a real number (the standard deviations need to be positive). The default are standard normal priors for both the log odds ratio parameter and the grand mean of the log odds parameter.

- `what` character specifying for which quantity the prior should be plotted. Either "logor" (i.e., log odds ratio), "or" (i.e., odds ratio), "p1p2" (i.e., plots the joint distribution of the latent "success" probability in the experimental and control condition), "p1" (i.e., latent "success" probability in the control condition), "p2" (i.e., latent "success" probability in the experimental condition), "p2givenp1" (i.e., plots the conditional distribution of the latent "success" probability in the experimental condition given a "success" probability of p1 in the control condition), "rrisk" (i.e., relative risk, the ratio of the "success" probability in the experimental and the control condition), or "arisk" (i.e., absolute risk, the difference of the "success" probability in the experimental and control condition).

- `hypothesis` character specifying whether to plot a two-sided prior (i.e., "H1"), a one-sided prior with lower truncation point (i.e., "H+"), or a one-sided prior with upper truncation point (i.e., "H-").

- `p1` value of the "success" probability in the control condition. Only used when `what` = "p2givenp1".

- `...` further arguments.
Note

Internally, the test-relevant prior is always a normal prior on the log odds ratio, however, the plot_prior function also allows one to plot the implied prior on different quantities.

Author(s)

Quentin F. Gronau

Examples

```r
# prior parameters
prior_par <- list(mu_psi = 0, sigma_psi = 1,
                  mu_beta = 0, sigma_beta = 1)

# plot prior
plot_prior(prior_par = prior_par, what = "logor")
plot_prior(prior_par = prior_par, what = "or")
plot_prior(prior_par = prior_par, what = "p1p2")
plot_prior(prior_par = prior_par, what = "p1")
plot_prior(prior_par = prior_par, what = "p2")
plot_prior(prior_par = prior_par, what = "p2givenp1", p1 = 0.3)
plot_prior(prior_par = prior_par, what = "rrisk")
plot_prior(prior_par = prior_par, what = "arisk")
```

Description

Function for plotting Bayes factor robustness check results (i.e., prior sensitivity analysis).

Usage

```r
plot_robustness(
  x,
  bftype = "BF10",
  log = FALSE,
  mu_range = c(0, 0.3),
  sigma_range = c(0.25, 1),
  mu_steps = 40,
  sigma_steps = 40,
  cores = 1,
  ...
)
```
Arguments

- **x**
  - object of class "ab".
- **bftype**
  - character that specifies which Bayes factor is plotted. Either "BF10", "BF01", "BF+0", "BF0+", "BF-0", or "BF0-".
- **log**
  - Boolean that specifies whether the log Bayes factor is plotted.
- **mu_range**
  - numeric vector of length two that specifies the range of mu_psi values to consider.
- **sigma_range**
  - numeric vector of length two that specifies the range of sigma_psi values to consider.
- **mu_steps**
  - numeric value that specifies in how many discrete steps the interval mu_range is partitioned.
- **sigma_steps**
  - numeric value that specifies in how many discrete steps the interval sigma_range is partitioned.
- **cores**
  - number of cores used for the computations.
- **...**
  - further arguments passed to `filled.contour`.

Details

The plot shows how the Bayes factor changes as a function of the normal prior location parameter mu_psi and the normal prior scale parameter sigma_psi (i.e., a prior sensitivity analysis with respect to the normal prior on the test-relevant log odds ratio).

Value

Returns a data.frame with the mu_psi values, sigma_psi values, and corresponding (log) Bayes factors.

Author(s)

Quentin F. Gronau

Examples

```R
## Not run:
# synthetic data
data <- list(y1 = 10, n1 = 28, y2 = 14, n2 = 26)

# Bayesian A/B test with default settings
ab <- ab_test(data = data)

# plot robustness check (i.e., prior sensitivity analysis)
p <- plot_robustness(ab)

# returned object contains the Bayes factors for the different prior settings
head(p)

## End(Not run)
```
plot_sequential  

**Plot Sequential Analysis**

### Description

Function for plotting the posterior probabilities of the hypotheses sequentially.

### Usage

```r
plot_sequential(x, thin = 1, cores = 1, ...)
```

### Arguments

- **x**: object of class "ab". Note that the "ab" object needs to contain sequential data.
- **thin**: allows the user to skip every kth data point for plotting, where the number k is specified via thin. For instance, in case thin = 2, only every second element of the data is displayed.
- **cores**: number of cores used for the computations.
- **...**: further arguments

### Details

The plot shows the posterior probabilities of the hypotheses as a function of the total number of observations across the experimental and control group. On top of the plot, probability wheels (see also `prob_wheel`) visualize the prior probabilities of the hypotheses and the posterior probabilities of the hypotheses after taking into account all available data.

**N.B.**: This plot has been designed to look good in the following format: In inches, 530 / 72 (width) by 400 / 72 (height); in pixels, 530 (width) by 400 (height).

### Author(s)

Quentin F. Gronau

### Examples

```r
### 1.

# synthetic sequential data (observations alternate between the groups)
# note that the cumulative number of successes and trials need to be provided
data <- list(y1 = c(1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 2, 2, 3, 3, 4, 4),
           n1 = c(1, 1, 2, 2, 3, 3, 4, 4, 5, 5, 6, 6, 7, 7, 8, 8, 9, 9, 10, 10),
           y2 = c(0, 1, 1, 2, 2, 3, 3, 4, 4, 5, 5, 6, 6, 7, 7, 8, 8, 9, 9, 9),
           n2 = c(0, 1, 1, 2, 2, 3, 3, 4, 4, 5, 5, 6, 6, 7, 7, 8, 8, 9, 9, 9, 10))

# conduct Bayesian A/B test with default settings
ab <- ab_test(data = data)
print(ab)
```
# produce sequential plot of posterior probabilities of the hypotheses
# (using recommended width and height values for saving to file)
cairo_pdf(file.path(tempdir(), "test_plot.pdf"),
  width = 530 / 72, height = 400 / 72)
plot_sequential(ab)
dev.off()

### 2.

# synthetic sequential data (observations alternate between the groups)
# this time provided in the alternative format
data2 <- data.frame(outcome = c(1, 1, 0, 1, 0, 1, 0, 1, 0, 1,
  0, 1, 0, 1, 1, 1, 1, 1, 1, 0),
  group = rep(c(1, 2), 10))

# conduct Bayesian A/B test with default settings
ab2 <- ab_test(data = data2)
print(ab2)

# produce sequential plot of posterior probabilities of the hypotheses
# (using recommended width and height values for saving to file)
cairo_pdf(file.path(tempdir(), "test_plot2.pdf"),
  width = 530 / 72, height = 400 / 72)
plot_sequential(ab2)
dev.off()

## Not run:
### 3.
data(seqdata)

# conduct Bayesian A/B test with default settings
ab3 <- ab_test(data = seqdata)
print(ab3)

# produce sequential plot of posterior probabilities of the hypotheses
# (using recommended width and height values for saving to file)
cairo_pdf(file.path(tempdir(), "test_plot3.pdf"),
  width = 530 / 72, height = 400 / 72)
plot_sequential(ab3, thin = 4)
dev.off()

## End(Not run)
Description

Function for evaluating the prior cumulative distribution function (CDF).

Usage

```r
pprior(
  q,
  prior_par = list(mu_psi = 0, sigma_psi = 1, mu_beta = 0, sigma_beta = 1),
  what = "logor",
  hypothesis = "H1"
)
```

Arguments

- **q**: numeric vector with quantiles.
- **prior_par**: list with prior parameters. This list needs to contain the following elements: `mu_psi` (prior mean for the normal prior on the test-relevant log odds ratio), `sigma_psi` (prior standard deviation for the normal prior on the test-relevant log odds ratio), `mu_beta` (prior mean for the normal prior on the grand mean of the log odds), `sigma_beta` (prior standard deviation for the normal prior on the grand mean of the log odds). Each of the elements needs to be a real number (the standard deviations need to be positive). The default are standard normal priors for both the log odds ratio parameter and the grand mean of the log odds parameter.
- **what**: character specifying for which quantity the prior CDF should be evaluated. Either "logor" (i.e., log odds ratio), "or" (i.e., odds ratio), "rrisk" (i.e., relative risk, the ratio of the "success" probability in the experimental and the control condition), or "arisk" (i.e., absolute risk, the difference of the "success" probability in the experimental and control condition).
- **hypothesis**: character specifying whether to evaluate the CDF for a two-sided prior (i.e., "H1"), a one-sided prior with lower truncation point (i.e., "H+"), or a one-sided prior with upper truncation point (i.e., "H-").

Value

numeric vector with the values of the prior CDF.

Note

Internally, the test-relevant prior is always a normal prior on the log odds ratio, consequently, if what is not "logor", the implied prior CDF for the quantity is returned.

Author(s)

Quentin F. Gronau
Examples

```r
# prior parameters
prior_par <- list(mu.psi = 0, sigma.psi = 1, 
                 mu.beta = 0, sigma.beta = 1)

# evaluate prior CDF
pprior(q = 0.1, prior_par = prior_par, what = "logor")
pprior(q = 1.1, prior_par = prior_par, what = "or")
pprior(q = 1.05, prior_par = prior_par, what = "rrisk")
pprior(q = 0.02, prior_par = prior_par, what = "arisk")

# also works for vectors
pprior(q = c(-0.1, 0, 0.1, 0.2), prior_par = prior_par, what = "logor")
```

---

**prob_wheel**

*Plot Probability Wheel*

**Description**

Function for visualizing prior and posterior probabilities of the hypotheses as a probability wheel.

**Usage**

```r
prob_wheel(x, type = "posterior")
```

**Arguments**

- `x` object of class "ab".
- `type` character indicating whether to plot a probability wheel visualizing the prior probabilities of the hypotheses (i.e., `type = "prior"`) or the posterior probabilities of the hypotheses (i.e., `type = "posterior"`). The default is "posterior".

**Author(s)**

Quentin F. Gronau

**Examples**

```r
# synthetic data
data <- list(y1 = 10, n1 = 28, y2 = 14, n2 = 26)

# Bayesian A/B test with default settings
ab <- ab_test(data = data)
print(ab)

# visualize prior probabilities of the hypotheses
prob_wheel(ab, type = "prior")

# visualize posterior probabilities of the hypotheses
prob_wheel(ab, type = "posterior")
```
Prior Quantile Function

Description

Function for evaluating the prior quantile function.

Usage

```r
qprior(
  p,
  prior_par = list(mu_psi = 0, sigma_psi = 1, mu_beta = 0, sigma_beta = 1),
  what = "logor",
  hypothesis = "H1"
)
```

Arguments

- `p` numeric vector with probabilities.
- `prior_par` list with prior parameters. This list needs to contain the following elements: `mu_psi` (prior mean for the normal prior on the test-relevant log odds ratio), `sigma_psi` (prior standard deviation for the normal prior on the test-relevant log odds ratio), `mu_beta` (prior mean for the normal prior on the grand mean of the log odds), `sigma_beta` (prior standard deviation for the normal prior on the grand mean of the log odds). Each of the elements needs to be a real number (the standard deviations need to be positive). The default are standard normal priors for both the log odds ratio parameter and the grand mean of the log odds parameter.
- `what` character specifying for which quantity the prior quantile function should be evaluated. Either "logor" (i.e., log odds ratio), "or" (i.e., odds ratio), "rrisk" (i.e., relative risk, the ratio of the "success" probability in the experimental and the control condition), or "arisk" (i.e., absolute risk, the difference of the "success" probability in the experimental and control condition).
- `hypothesis` character specifying whether to evaluate the quantile function for a two-sided prior (i.e., "H1"), a one-sided prior with lower truncation point (i.e., "H+"), or a one-sided prior with upper truncation point (i.e., "H-").

Value

numeric vector with the values of the prior quantile function.

Author(s)

Quentin F. Gronau
Examples

# prior parameters
prior_par <- list(mu_psi = 0, sigma_psi = 1,
                  mu_beta = 0, sigma_beta = 1)

# evaluate prior quantile function
qprior(p = .1, prior_par = prior_par, what = "logor")
qprior(p = .7, prior_par = prior_par, what = "or")
qprior(p = .9, prior_par = prior_par, what = "rrisk")
qprior(p = .7, prior_par = prior_par, what = "arisk")

# also works for vectors
qprior(p = c(.1, .2, .5, .7, .9), prior_par = prior_par, what = "logor")

seqdata  

Synthetic Sequential Data

Description

This data set contains synthetic sequential A/B data (500 observations in each of the two groups, where the observations are alternating between groups). y1 denotes the number of successes for the first group, n1 denotes the corresponding total number of observations for the first group. Similarly, y2 denotes the number of successes for the second group and n2 denotes the corresponding total number of observations for the second group.

Usage

seqdata

Format

A list with 4 elements.

Examples

data(seqdata)

# conduct Bayesian A/B test with default settings
ab <- ab_test(data = seqdata)
print(ab)

# produce sequential plot of posterior probabilities of the hypotheses
plot_sequential(ab, thin = 4)

# example of good width and height values for saving to file
cairo_pdf(file.path(tempdir(), "test_plot.pdf"),
          width = 530 / 72, height = 400 / 72)
plot_sequential(ab)
simulate_priors

Simulate from Parameter Priors

Description
Function for simulating from the parameter prior distributions.

Usage

simulate_priors(
  nsamples,
  prior_par = list(mu_psi = 0, sigma_psi = 1, mu_beta = 0, sigma_beta = 1),
  hypothesis = "H1"
)

Arguments

- **nsamples**: number of samples.
- **prior_par**: list with prior parameters. This list needs to contain the following elements: `mu_psi` (prior mean for the normal prior on the test-relevant log odds ratio), `sigma_psi` (prior standard deviation for the normal prior on the test-relevant log odds ratio), `mu_beta` (prior mean for the normal prior on the grand mean of the log odds), `sigma_beta` (prior standard deviation for the normal prior on the grand mean of the log odds). Each of the elements needs to be a real number (the standard deviations need to be positive). The default are standard normal priors for both the log odds ratio parameter and the grand mean of the log odds parameter.
- **hypothesis**: character specifying whether to sample from a two-sided prior (i.e., "H1"), a one-sided prior with lower truncation point (i.e., "H+"), or a one-sided prior with upper truncation point (i.e., "H-").

Value

A data frame with prior samples for the following quantities (see ?ab_test for a description of the underlying model):

- **beta**: prior samples for the grand mean of the log odds.
- **psi**: prior samples for the log odds ratio.
- **p1**: prior samples for the latent "success" probability in the control group.
- **p2**: prior samples for the latent "success" probability in the experimental group.
- **logor**: prior samples for the log odds ratio (identical to psi, only included for easier reference).
- **or**: prior samples for the odds ratio.
· \textit{rrisk}: prior samples for the relative risk (i.e., the ratio of the "success" probability in the experimental and the control condition).
· \textit{arisk}: prior samples for the absolute risk (i.e., the difference of the "success" probability in the experimental and control condition)

\textbf{Examples}

```r
# prior parameters
prior_par <- list(mu_psi = 0, sigma_psi = 1,
                  mu_beta = 0, sigma_beta = 1)

# obtain prior samples
samples <- simulate_priors(nsamples = 1000, prior_par = prior_par)

# plot, e.g., prior samples for absolute risk
hist(samples$arisk)
```

\textbf{Author(s)}

Quentin F. Gronau
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