Package ‘NAP’

January 6, 2022

Type Package

Title Non-Local Alternative Priors in Psychology

Version 1.1

Date 2022-1-6

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Description
Conducts Bayesian Hypothesis tests of a point null hypothesis against a two-sided alternative using Non-local Alternative Prior (NAP) for one- and two-sample z- and t-tests (Pramanik and Johnson, 2022). Under the alternative, the NAP is assumed on the standardized effects size in one-sample tests and on their differences in two-sample tests. The package considers two types of NAP densities: (1) the normal moment prior, and (2) the composite alternative.
In fixed design tests, the functions calculate the Bayes factors and the expected weight of evidence for varied effect size and sample size. The package also provides a sequential testing framework using the
Sequential Bayes Factor (SBF) design. The functions calculate the operating characteristics (OC) and the average sample number (ASN), and also conducts sequential tests for a sequentially observed data.

Imports foreach, stats, utils, parallel, doParallel, graphics

License GPL (>= 2)

NeedsCompilation no

Repository CRAN

Date/Publication 2022-01-06 12:30:02 UTC

R topics documented:

NAP-package *Non-Local Alternative Priors in Psychology*

Description

Conducts Bayesian Hypothesis tests of a point null hypothesis against a two-sided alternative using Non-local Alternative Prior (NAP) for one- and two-sample z- and t-tests (Pramanik and Johnson, 2022). Under the alternative, the NAP is assumed on the standardized effects size in one-sample tests and on their differences in two-sample tests. The package considers two types of NAP densities: (1) the normal moment prior, and (2) the composite alternative. In fixed design tests, the functions calculate the Bayes factors and the expected weight of evidence for varied effect size and sample size. The package also provides a sequential testing framework using the Sequential Bayes Factor (SBF) design. The functions calculate the operating characteristics (OC) and the average sample number (ASN), and also conducts sequential tests for a sequentially observed data.

Details

Package:	NAP
Type:	Package
Version:	1.1
Date:	2022-1-6
License: GPL (>= 2)	

Author(s)

Sandipan Pramanik [aut, cre], Valen E. Johnson [aut]

Maintainer: Sandipan Pramanik <sandy@stat.tamu.edu>

References

Pramanik, S. and Johnson, V. (2022). *Efficient Alternatives for Bayesian Hypothesis Tests in Psychology. Psychological Methods. Just accepted.*

Johnson, V. and Rossell, R. (2010). *On the use of non-local prior densities in Bayesian hypothesis tests. Journal of the Royal Statistical Society: Series B, 72:143-170.* [Article]

fixedHajnal.onet_es *Fixed-design one-sample t-tests using Hajnal's ratio for varied sample sizes*

Description

In two-sided fixed design one-sample t-tests with *composite alternative prior* assumed on the standardized effect size μ/σ under the alternative, this function calculates the expected log(Hajnal's ratio) at a prefixed standardized effect size for a varied range of sample sizes.

Usage

```
fixedHajnal.onet_es(es = 0, es1 = 0.3, nmin = 20, nmax = 5000,
                    batch.size.increment, nReplicate = 50000)
```

Arguments

`es`	Numeric. Standardized effect size where the expected weights of evidence is desired. **Default:** `0`.
`es1`	Positive numeric. **Default:** 0.3. For this, the composite alternative prior on the standardized effect size μ/σ takes values 0.3 and -0.3 each with equal probability 1/2.
`nmin`	Positive integer. Minimum sample size to be considered. **Default:** 20.
`nmax`	Positive integer. Maximum sample size to be considered. **Default:** 5000.
`batch.size.increment`	Positive numeric. Increment in sample size. The sequence of sample size thus considered for the fixed design test is from `nmin` to `nmax` with an increment of `batch.size.increment`. **Default:** `function(narg){20}`. This means an increment of 20 samples at each step.
`nReplicate`	Positve integer. Number of replicated studies based on which the expected weights of evidence is calculated. **Default:** 50,000.

Value

A list with two components named `summary` and `BF`.

`$summary` is a data frame with columns `n` containing the values of sample sizes and `avg.logBF` containing the expected log(Hajnal's ratios) at those values.

`$BF` is a matrix of dimension `number of sample sizes considered` by `nReplicate`. Each row contains the Hajnal's ratios at the corresponding sample size in `nReplicate` replicated studies.

Author(s)

Sandipan Pramanik and Valen E. Johnson

References

Hajnal, J. (1961). *A two-sample sequential t-test.Biometrika, 48:65-75*, [Article].

Schnuerch, M. and Erdfelder, E. (2020). *A two-sample sequential t-test.Biometrika, 48:65-75*, [Article].

Examples

```
out = fixedHajnal.onet_es(nmax = 100)
```

`fixedHajnal.onet_n` *Fixed-design one-sample t-tests using Hajnal's ratio and a pre-fixed sample size*

Description

In two-sided fixed design one-sample t-tests with *composite alternative prior* assumed on the standardized effect size μ/σ under the alternative and a prefixed sample size, this function calculates the expected log(Hajnal's ratio) at a varied range of standardized effect sizes.

Usage

```
fixedHajnal.onet_n(es1 = 0.3, es = c(0, 0.2, 0.3, 0.5),
                   n.fixed = 20,
                   nReplicate = 50000, nCore)
```

Arguments

`es1`	Positive numeric. **Default:** 0.3. For this, the composite alternative prior on the standardized effect size μ/σ takes values 0.3 and -0.3 each with equal probability 1/2.
`es`	Numeric vector. Standardized effect sizes μ/σ where the expected weights of evidence is desired. **Default:** `c(0,0.2,0.3,0.5)`.
`n.fixed`	Positive integer. Prefixed sample size. **Default:** 20.
`nReplicate`	Positve integer. Number of replicated studies based on which the expected weights of evidence is calculated. **Default:** 50,000.
`nCore`	Positive integer. **Default:** One less than the total number of available cores.

Value

A list with two components named `summary` and `BF`.

`$summary` is a data frame with columns `effect.size` containing the values in `es` and `avg.logBF` containing the expected log(Hajnal's ratios) at those values.

`$BF` is a matrix of dimension `length(es)` by `nReplicate`. Each row contains the Hajnal's ratios at the corresponding standardized effec size in `nReplicate` replicated studies.

Author(s)

Sandipan Pramanik and Valen E. Johnson

References

Hajnal, J. (1961). *A two-sample sequential t-test.Biometrika, 48:65-75*, [Article].

Schnuerch, M. and Erdfelder, E. (2020). *A two-sample sequential t-test.Biometrika, 48:65-75*, [Article].

Examples

```
out = fixedHajnal.onet_n(n.fixed = 20, es = c(0, 0.3), nCore = 1)
```

---

fixedHajnal.onez_es *Fixed-design one-sample z-tests using Hajnal's ratio for varied sample sizes*

Description

In two-sided fixed design one-sample z-tests with *composite alternative prior* assumed on the standardized effect size μ/σ_0 under the alternative, this function calculates the expected log(Hajnal's ratio) at a prefixed standardized effect size for a varied range of sample sizes.

Usage

```
fixedHajnal.onez_es(es = 0, es1 = 0.3, nmin = 20, nmax = 5000,
                    sigma0 = 1, batch.size.increment, nReplicate = 50000)
```

Arguments

es	Numeric. Standardized effect size where the expected weights of evidence is desired. **Default:** `0`.
es1	Positive numeric. **Default:** 0.3. For this, the composite alternative prior on the standardized effect size μ/σ_0 takes values 0.3 and -0.3 each with equal probability 1/2.
nmin	Positive integer. Minimum sample size to be considered. **Default:** 20.
nmax	Positive integer. Maximum sample size to be considered. **Default:** 5000.
sigma0	Positive numeric. Known standard deviation in the population. **Default:** 1.
batch.size.increment	function. Increment in sample size. The sequence of sample size thus considered for the fixed design test is from `nmin` to `nmax` with an increment of `batch.size.increment`. **Default:** `function(narg){20}`. This means an increment of 20 samples at each step.
nReplicate	Positve integer. Number of replicated studies based on which the expected weights of evidence is calculated. **Default:** 50,000.

Value

A list with two components named `summary` and `BF`.

`$summary` is a data frame with columns `n` containing the values of sample sizes and `avg.logBF` containing the expected log(Hajnal's ratios) at those values.

`$BF` is a matrix of dimension `number of sample sizes considered` by `nReplicate`. Each row contains the Hajnal's ratios at the corresponding sample size in `nReplicate` replicated studies.

Author(s)

Sandipan Pramanik and Valen E. Johnson

References

Hajnal, J. (1961). *A two-sample sequential t-test.Biometrika, 48:65-75*, [Article].

Schnuerch, M. and Erdfelder, E. (2020). *A two-sample sequential t-test.Biometrika, 48:65-75*, [Article].

Examples

```
out = fixedHajnal.onez_es(nmax = 100)
```

---

fixedHajnal.onez_n — *Fixed-design one-sample z-tests using Hajnal's ratio and a pre-fixed sample size*

Description

In two-sided fixed design one-sample z-tests with *composite alternative prior* assumed on the standardized effect size μ/σ_0 under the alternative and a prefixed sample size, this function calculates the expected log(Hajnal's ratio) at a varied range of standardized effect sizes.

Usage

```
fixedHajnal.onez_n(es1 = 0.3, es = c(0, 0.2, 0.3, 0.5),
                   n.fixed = 20, sigma0 = 1,
                   nReplicate = 50000, nCore)
```

Arguments

`es1`	Positive numeric. **Default:** 0.3. For this, the composite alternative prior on the standardized effect size μ/σ_0 takes values 0.3 and -0.3 each with equal probability 1/2.
`es`	Numeric vector. Standardized effect sizes μ/σ_0 where the expected weights of evidence is desired. **Default:** `c(0,0.2,0.3,0.5)`.
`n.fixed`	Positive integer. Prefixed sample size. **Default:** 20.
`sigma0`	Positive numeric. Known standard deviation in the population. **Default:** 1.
`nReplicate`	Positve integer. Number of replicated studies based on which the expected weights of evidence is calculated. **Default:** 50,000.
`nCore`	Positive integer. **Default:** One less than the total number of available cores.

Value

A list with two components named `summary` and `BF`.

`$summary` is a data frame with columns `effect.size` containing the values in `es` and `avg.logBF` containing the expected log(Hajnal's ratios) at those values.

`$BF` is a matrix of dimension `length(es)` by `nReplicate`. Each row contains the Hajnal's ratios at the corresponding standardized effec size in `nReplicate` replicated studies.

Author(s)

Sandipan Pramanik and Valen E. Johnson

References

Hajnal, J. (1961). *A two-sample sequential t-test.Biometrika, 48:65-75*, [Article].

Schnuerch, M. and Erdfelder, E. (2020). *A two-sample sequential t-test.Biometrika, 48:65-75*, [Article].

Examples

```
out = fixedHajnal.onez_n(n.fixed = 20, es = c(0, 0.3), nCore = 1)
```

`fixedHajnal.twot_es` *Fixed-design two-sample t-tests with NAP for varied sample sizes*

Description

In two-sided fixed design two-sample t-tests with *composite alternative prior* assumed on the difference between standardized effect sizes $(\mu_2 - \mu_1)/\sigma$ under the alternative, this function calculates the expected log(Hajnal's ratio) at a prefixed standardized effect size for a varied range of sample sizes.

Usage

```
fixedHajnal.twot_es(es = 0, es1 = 0.3, n1min = 20, n2min = 20,
                    n1max = 5000, n2max = 5000,
                    batch1.size.increment, batch2.size.increment,
                    nReplicate = 50000)
```

Arguments

`es`	Numeric. Difference between standardized effect sizes where the expected weights of evidence is desired. **Default:** `0`.
`es1`	Positive numeric. δ as above. **Default:** 0.3. For this, the prior on $(\mu_2 - \mu_1)/\sigma$ takes values 0.3 and -0.3 each with equal probability 1/2.

`n1min` Positive integer. Minimum sample size from Grpup-1 to be considered. **Default:** 20.

`n2min` Positive integer. Minimum sample size from Grpup-2 to be considered. **Default:** 20.

`n1max` Positive integer. Maximum sample size from Grpup-1 to be considered. **Default:** 5000.

`n2max` Positive integer. Maximum sample size from Grpup-2 to be considered. **Default:** 5000.

`batch1.size.increment`
Positive numeric. Increment in sample size from Group-1. The sequence of sample size thus considered from Group-1 for the fixed design test is from `n1min` to `n1max` with an increment of `batch1.size.increment`. **Default:** `function(narg){20}`. This means an increment of 20 samples from Group-1 at each step.

`batch2.size.increment`
Positive numeric. Increment in sample size from Group-2. The sequence of sample size thus considered from Group-2 for the fixed design test is from `n2min` to `n2max` with an increment of `batch2.size.increment`. **Default:** `function(narg){20}`. This means an increment of 20 samples from Group-2 at each step.

`nReplicate` Positve integer. Number of replicated studies based on which the expected weights of evidence is calculated. **Default:** 50,000.

Value

A list with two components named `summary` and `BF`.

`$summary` is a data frame with columns `n` containing the values of sample sizes and `avg.logBF` containing the expected log(Hajnal's ratios) at those values.

`$BF` is a matrix of dimension `number of sample sizes considered` by `nReplicate`. Each row contains the Hajnal's ratios at the corresponding sample size in `nReplicate` replicated studies.

Author(s)

Sandipan Pramanik and Valen E. Johnson

References

Hajnal, J. (1961). *A two-sample sequential t-test.Biometrika, 48:65-75*, [Article].

Schnuerch, M. and Erdfelder, E. (2020). *A two-sample sequential t-test.Biometrika, 48:65-75*, [Article].

Examples

```
out = fixedHajnal.twot_es(n1max = 100, n2max = 100)
```

`fixedHajnal.twot_n` *Fixed-design two-sample t-tests using Hajnal's ratio and a pre-fixed sample size*

Description

In two-sided fixed design two-sample t-tests with *composite alternative prior* assumed on the standardized effect size $(\mu_2 - \mu_1)/\sigma$ under the alternative and a prefixed sample size, this function calculates the expected log(Hajnal's ratio) at a varied range of differences between standardized effect sizes.

Usage

```
fixedHajnal.twot_n(es1 = 0.3, es = c(0, 0.2, 0.3, 0.5),
                   n1.fixed = 20, n2.fixed = 20,
                   nReplicate = 50000, nCore)
```

Arguments

`es1`	Positive numeric. δ as above. **Default:** 0.3. For this, the prior on $(\mu_2 - \mu_1)/\sigma$ takes values 0.3 and -0.3 each with equal probability 1/2.
`es`	Numeric vector. Standardized effect size differences $(\mu_2 - \mu_1)/\sigma$ where the expected weights of evidence is desired. **Default:** `c(0,0.2,0.3,0.5)`.
`n1.fixed`	Positive integer. Prefixed sample size from Group-1. **Default:** 20.
`n2.fixed`	Positive integer. Prefixed sample size from Group-2. **Default:** 20.
`nReplicate`	Positve integer. Number of replicated studies based on which the expected weights of evidence is calculated. **Default:** 50,000.
`nCore`	Positive integer. **Default:** One less than the total number of available cores.

Value

A list with two components named `summary` and `BF`.

`$summary` is a data frame with columns `effect.size` containing the values in `es` and `avg.logBF` containing the expected log(Hajnal's ratios) at those values.

`$BF` is a matrix of dimension `length(es)` by `nReplicate`. Each row contains the Hajnal's ratios at the corresponding standardized effec size in `nReplicate` replicated studies.

Author(s)

Sandipan Pramanik and Valen E. Johnson

References

Hajnal, J. (1961). *A two-sample sequential t-test.Biometrika, 48:65-75*, [Article].

Schnuerch, M. and Erdfelder, E. (2020). *A two-sample sequential t-test.Biometrika, 48:65-75*, [Article].

Examples

```
out = fixedHajnal.twot_n(n1.fixed = 20, n2.fixed = 20, es = c(0, 0.3), nCore = 1)
```

`fixedHajnal.twoz_es` *Fixed-design two-sample z-tests with NAP for varied sample sizes*

Description

In two-sided fixed design two-sample z-tests with *composite alternative prior* assumed on the difference between standardized effect sizes $(\mu_2 - \mu_1)/\sigma_0$ under the alternative, this function calculates the expected log(Hajnal's ratio) at a prefixed standardized effect size for a varied range of sample sizes.

Usage

```
fixedHajnal.twoz_es(es = 0, es1 = 0.3, n1min = 20, n2min = 20,
                    n1max = 5000, n2max = 5000, sigma0 = 1,
                    batch1.size.increment, batch2.size.increment,
                    nReplicate = 50000)
```

Arguments

`es` Numeric. Difference between standardized effect sizes where the expected weights of evidence is desired. **Default:** `0`.

`es1` Positive numeric. δ as above. **Default:** 0.3. For this, the prior on $(\mu_2 - \mu_1)/\sigma_0$ takes values 0.3 and -0.3 each with equal probability 1/2.

`n1min` Positive integer. Minimum sample size from Grpup-1 to be considered. **Default:** 20.

`n2min` Positive integer. Minimum sample size from Grpup-2 to be considered. **Default:** 20.

`n1max` Positive integer. Maximum sample size from Grpup-1 to be considered. **Default:** 5000.

`n2max` Positive integer. Maximum sample size from Grpup-2 to be considered. **Default:** 5000.

`sigma0` Positive numeric. Known common standard deviation of the populations. **Default:** 1.

`batch1.size.increment`
Positive numeric. Increment in sample size from Group-1. The sequence of sample size thus considered from Group-1 for the fixed design test is from `n1min` to `n1max` with an increment of `batch1.size.increment`. **Default:** `function(narg){20}`. This means an increment of 20 samples from Group-1 at each step.

`batch2.size.increment`
: Positive numeric. Increment in sample size from Group-2. The sequence of sample size thus considered from Group-2 for the fixed design test is from `n2min` to `n2max` with an increment of `batch2.size.increment`. **Default:** `function(narg){20}`. This means an increment of 20 samples from Group-2 at each step.

`nReplicate`
: Positve integer. Number of replicated studies based on which the expected weights of evidence is calculated. **Default:** 50,000.

Value

A list with two components named `summary` and `BF`.

`$summary` is a data frame with columns `n` containing the values of sample sizes and `avg.logBF` containing the expected log(Hajnal's ratios) at those values.

`$BF` is a matrix of dimension `number of sample sizes considered` by `nReplicate`. Each row contains the Hajnal's ratios at the corresponding sample size in `nReplicate` replicated studies.

Author(s)

Sandipan Pramanik and Valen E. Johnson

References

Hajnal, J. (1961). *A two-sample sequential t-test.Biometrika, 48:65-75*, [Article].

Schnuerch, M. and Erdfelder, E. (2020). *A two-sample sequential t-test.Biometrika, 48:65-75*, [Article].

Examples

```
out = fixedHajnal.twoz_es(n1max = 100, n2max = 100)
```

`fixedHajnal.twoz_n` *Fixed-design two-sample z-tests using Hajnal's ratio and a pre-fixed sample size*

Description

In two-sided fixed design two-sample z-tests with *composite alternative prior* assumed on the standardized effect size $(\mu_2 - \mu_1)/\sigma_0$ under the alternative and a prefixed sample size, this function calculates the expected log(Hajnal's ratio) at a varied range of differences between standardized effect sizes.

Usage

```
fixedHajnal.twoz_n(es1 = 0.3, es = c(0, 0.2, 0.3, 0.5),
                   n1.fixed = 20, n2.fixed = 20, sigma0 = 1,
                   nReplicate = 50000, nCore)
```

Arguments

es1	Positive numeric. **Default:** 0.3. For this, the prior on $(\mu_2 - \mu_1)/\sigma_0$ takes values 0.3 and -0.3 each with equal probability 1/2.
es	Numeric vector. Standardized effect size differences $(\mu_2 - \mu_1)/\sigma_0$ where the expected weights of evidence is desired. **Default:** `c(0,0.2,0.3,0.5)`.
n1.fixed	Positive integer. Prefixed sample size from Group-1. **Default:** 20.
n2.fixed	Positive integer. Prefixed sample size from Group-2. **Default:** 20.
sigma0	Positive numeric. Known common standard deviation of the populations. **Default:** 1.
nReplicate	Positve integer. Number of replicated studies based on which the expected weights of evidence is calculated. **Default:** 50,000.
nCore	Positive integer. **Default:** One less than the total number of available cores.

Value

A list with two components named `summary` and `BF`.

`$summary` is a data frame with columns `effect.size` containing the values in `es` and `avg.logBF` containing the expected log(Hajnal's ratios) at those values.

`$BF` is a matrix of dimension `length(es)` by `nReplicate`. Each row contains the Hajnal's ratios at the corresponding standardized effec size in `nReplicate` replicated studies.

Author(s)

Sandipan Pramanik and Valen E. Johnson

References

Hajnal, J. (1961). *A two-sample sequential t-test.Biometrika, 48:65-75*, [Article].

Schnuerch, M. and Erdfelder, E. (2020). *A two-sample sequential t-test.Biometrika, 48:65-75*, [Article].

Examples

```
out = fixedHajnal.twoz_n(n1.fixed = 20, n2.fixed = 20, es = c(0, 0.3), nCore = 1)
```

fixedNAP.onet_es *Fixed-design one-sample t-tests with NAP for varied sample sizes*

Description

In two-sided fixed design one-sample t-tests with *normal moment prior* assumed on the standardized effect size μ/σ under the alternative, this function calculates the expected weights of evidence (that is, expected log(Bayes Factor)) of the test at a prefixed standardized effect size for a varied range of sample sizes.

Usage

```
fixedNAP.onet_es(es = 0, nmin = 20, nmax = 5000,
                 tau.NAP = 0.3/sqrt(2),
                 batch.size.increment, nReplicate = 50000)
```

Arguments

- `es` — Numeric. Standardized effect size where the expected weights of evidence is desired. **Default:** `0`.
- `nmin` — Positive integer. Minimum sample size to be considered. **Default:** 20.
- `nmax` — Positive integer. Maximum sample size to be considered. **Default:** 5000.
- `tau.NAP` — Positive numeric. Parameter in the moment prior. **Default:** $0.3/\sqrt{2}$. This places the prior modes of the standardized effect size μ/σ at 0.3 and -0.3.
- `batch.size.increment` — Positive numeric. Increment in sample size. The sequence of sample size thus considered for the fixed design test is from `nmin` to `nmax` with an increment of `batch.size.increment`. **Default:** `function(narg){20}`. This means an increment of 20 samples at each step.
- `nReplicate` — Positve integer. Number of replicated studies based on which the expected weights of evidence is calculated. **Default:** 50,000.

Value

A list with two components named `summary` and `BF`.

`$summary` is a data frame with columns `n` containing the values of sample sizes and `avg.logBF` containing the expected weight of evidence values at those values.

`$BF` is a matrix of dimension `number of sample sizes considered` by `nReplicate`. Each row contains the Bayes factor values at the corresponding sample size in `nReplicate` replicated studies.

Author(s)

Sandipan Pramanik and Valen E. Johnson

References

Pramanik, S. and Johnson, V. (2022). *Efficient Alternatives for Bayesian Hypothesis Tests in Psychology. Psychological Methods. Just accepted.*

Johnson, V. and Rossell, R. (2010). *On the use of non-local prior densities in Bayesian hypothesis tests. Journal of the Royal Statistical Society: Series B, 72:143-170.* [Article]

Examples

```
out = fixedNAP.onet_es(nmax = 100)
```

---

fixedNAP.onet_n — *Fixed-design one-sample t-tests with NAP and a pre-fixed sample size*

Description

In two-sided fixed design one-sample t-tests with *normal moment prior* assumed on the standardized effect size μ/σ under the alternative and a prefixed sample size, this function calculates the expected weights of evidence (that is, expected log(Bayes Factor)) of the test at a varied range of standardized effect sizes.

Usage

```
fixedNAP.onet_n(es = c(0, 0.2, 0.3, 0.5), n.fixed = 20,
                tau.NAP = 0.3/sqrt(2),
                nReplicate = 50000, nCore)
```

Arguments

`es`	Numeric vector. Standardized effect sizes μ/σ where the expected weights of evidence is desired. **Default:** `c(0,0.2,0.3,0.5)`.
`n.fixed`	Positive integer. Prefixed sample size. **Default:** 20.
`tau.NAP`	Positive numeric. Parameter in the moment prior. **Default:** $0.3/\sqrt{2}$. This places the prior modes of the standardized effect size μ/σ at 0.3 and -0.3.
`nReplicate`	Positve integer. Number of replicated studies based on which the expected weights of evidence is calculated. **Default:** 50,000.
`nCore`	Positive integer. **Default:** One less than the total number of available cores.

Value

A list with two components named `summary` and `BF`.

`$summary` is a data frame with columns `effect.size` containing the values in `es` and `avg.logBF` containing the expected weight of evidence values at those values.

`$BF` is a matrix of dimension `length(es)` by `nReplicate`. Each row contains the Bayes factor values at the corresponding standardized effec size in `nReplicate` replicated studies.

Author(s)

Sandipan Pramanik and Valen E. Johnson

References

Pramanik, S. and Johnson, V. (2022). *Efficient Alternatives for Bayesian Hypothesis Tests in Psychology. Psychological Methods. Just accepted.*

Johnson, V. and Rossell, R. (2010). *On the use of non-local prior densities in Bayesian hypothesis tests. Journal of the Royal Statistical Society: Series B, 72:143-170.* [Article]

Examples

```
out = fixedNAP.onet_n(n.fixed = 20, es = c(0, 0.3), nCore = 1)
```

`fixedNAP.onez_es` *Fixed-design one-sample z-tests with NAP for varied sample sizes*

Description

In two-sided fixed design one-sample z-tests with *normal moment prior* assumed on the standardized effect size μ/σ_0 under the alternative, this function calculates the expected weights of evidence (that is, expected log(Bayes Factor)) of the test at a prefixed standardized effect size for a varied range of sample sizes.

Usage

```
fixedNAP.onez_es(es = 0, nmin = 20, nmax = 5000,
                 tau.NAP = 0.3/sqrt(2), sigma0 = 1,
                 batch.size.increment, nReplicate = 50000)
```

Arguments

`es` Numeric. Standardized effect size where the expected weights of evidence is desired. **Default:** `0`.

`nmin` Positive integer. Minimum sample size to be considered. **Default:** 20.

`nmax` Positive integer. Maximum sample size to be considered. **Default:** 5000.

`tau.NAP` Positive numeric. Parameter in the moment prior. **Default:** $0.3/\sqrt{2}$. This places the prior modes of the standardized effect size μ/σ_0 at 0.3 and -0.3.

`sigma0` Positive numeric. Known standard deviation in the population. **Default:** 1.

`batch.size.increment` function. Increment in sample size. The sequence of sample size thus considered for the fixed design test is from `nmin` to `nmax` with an increment of `batch.size.increment`. **Default:** `function(narg){20}`. This means an increment of 20 samples at each step.

`nReplicate` Positve integer. Number of replicated studies based on which the expected weights of evidence is calculated. **Default:** 50,000.

Value

A list with two components named `summary` and `BF`.

`$summary` is a data frame with columns `n` containing the values of sample sizes and `avg.logBF` containing the expected weight of evidence values at those values.

`$BF` is a matrix of dimension `number of sample sizes considered` by `nReplicate`. Each row contains the Bayes factor values at the corresponding sample size in `nReplicate` replicated studies.

Author(s)

Sandipan Pramanik and Valen E. Johnson

References

Pramanik, S. and Johnson, V. (2022). *Efficient Alternatives for Bayesian Hypothesis Tests in Psychology. Psychological Methods. Just accepted.*

Johnson, V. and Rossell, R. (2010). *On the use of non-local prior densities in Bayesian hypothesis tests. Journal of the Royal Statistical Society: Series B, 72:143-170.* [Article]

Examples

```
out = fixedNAP.onez_es(nmax = 100)
```

`fixedNAP.onez_n` *Fixed-design one-sample z-tests with NAP and a pre-fixed sample size*

Description

In two-sided fixed design one-sample z-tests with *normal moment prior* assumed on the standardized effect size μ/σ_0 under the alternative and a prefixed sample size, this function calculates the expected weights of evidence (that is, expected log(Bayes Factor)) of the test at a varied range of standardized effect sizes.

Usage

```
fixedNAP.onez_n(es = c(0, 0.2, 0.3, 0.5), n.fixed = 20,
                tau.NAP = 0.3/sqrt(2), sigma0 = 1,
                nReplicate = 50000, nCore)
```

Arguments

`es`	Numeric vector. Standardized effect sizes μ/σ_0 where the expected weights of evidence is desired. **Default:** `c(0,0.2,0.3,0.5)`.
`n.fixed`	Positive integer. Prefixed sample size. **Default:** 20.
`tau.NAP`	Positive numeric. Parameter in the moment prior. **Default:** $0.3/\sqrt{2}$. This places the prior modes of the standardized effect size μ/σ_0 at 0.3 and -0.3.

sigma0	Positive numeric. Known standard deviation in the population. **Default:** 1.
nReplicate	Positve integer. Number of replicated studies based on which the expected weights of evidence is calculated. **Default:** 50,000.
nCore	Positive integer. **Default:** One less than the total number of available cores.

Value

A list with two components named `summary` and `BF`.

`$summary` is a data frame with columns `effect.size` containing the values in `es` and `avg.logBF` containing the expected weight of evidence values at those values.

`$BF` is a matrix of dimension `length(es)` by `nReplicate`. Each row contains the Bayes factor values at the corresponding standardized effec size in `nReplicate` replicated studies.

Author(s)

Sandipan Pramanik and Valen E. Johnson

References

Pramanik, S. and Johnson, V. (2022). *Efficient Alternatives for Bayesian Hypothesis Tests in Psychology. Psychological Methods. Just accepted.*

Johnson, V. and Rossell, R. (2010). *On the use of non-local prior densities in Bayesian hypothesis tests. Journal of the Royal Statistical Society: Series B, 72:143-170.* [Article]

Examples

```
out = fixedNAP.onez_n(n.fixed = 20, es = c(0, 0.3), nCore = 1)
```

---

fixedNAP.twot_es   *Fixed-design two-sample t-tests with NAP for varied sample sizes*

Description

In two-sided fixed design two-sample t-tests with *normal moment prior* assumed on the difference between standardized effect sizes $(\mu_2 - \mu_1)/\sigma$ under the alternative, this function calculates the expected weights of evidence (that is, expected log(Bayes Factor)) of the test at a prefixed differences between standardized effect size for a varied range of sample sizes.

Usage

```
fixedNAP.twot_es(es = 0, n1min = 20, n2min = 20,
                 n1max = 5000, n2max = 5000,
                 tau.NAP = 0.3/sqrt(2),
                 batch1.size.increment, batch2.size.increment,
                 nReplicate = 50000)
```

Arguments

- `es` — Numeric. Difference between standardized effect sizes where the expected weights of evidence is desired. **Default:** `0`.
- `n1min` — Positive integer. Minimum sample size from Grpup-1 to be considered. **Default:** 20.
- `n2min` — Positive integer. Minimum sample size from Grpup-2 to be considered. **Default:** 20.
- `n1max` — Positive integer. Maximum sample size from Grpup-1 to be considered. **Default:** 5000.
- `n2max` — Positive integer. Maximum sample size from Grpup-2 to be considered. **Default:** 5000.
- `tau.NAP` — Positive numeric. Parameter in the moment prior. **Default:** $0.3/\sqrt{2}$. This places the prior modes of $(\mu_2 - \mu_1)/\sigma$ at 0.3 and -0.3.
- `batch1.size.increment` — Positive numeric. Increment in sample size from Group-1. The sequence of sample size thus considered from Group-1 for the fixed design test is from `n1min` to `n1max` with an increment of `batch1.size.increment`. **Default:** `function(narg){20}`. This means an increment of 20 samples from Group-1 at each step.
- `batch2.size.increment` — Positive numeric. Increment in sample size from Group-2. The sequence of sample size thus considered from Group-2 for the fixed design test is from `n2min` to `n2max` with an increment of `batch2.size.increment`. **Default:** `function(narg){20}`. This means an increment of 20 samples from Group-2 at each step.
- `nReplicate` — Positve integer. Number of replicated studies based on which the expected weights of evidence is calculated. **Default:** 50,000.

Details

`n1min`, `n1max`, `batch1.size.increment`, and `n2min`, `n2max`, `batch2.size.increment` should be chosen such that the length of sample sizes considered from Group 1 and 2 are equal.

Value

A list with two components named `summary` and `BF`.

`$summary` is a data frame with columns `n1` containing the sample sizes from Group-1, `n2` containing the sample sizes from Group-2, and `avg.logBF` containing the expected weight of evidence values at those values.

`$BF` is a matrix of dimension `number of sample sizes considered` by `nReplicate`. Each row contains the Bayes factor values at the corresponding sample size in `nReplicate` replicated studies.

Author(s)

Sandipan Pramanik and Valen E. Johnson

References

Pramanik, S. and Johnson, V. (2022). *Efficient Alternatives for Bayesian Hypothesis Tests in Psychology. Psychological Methods. Just accepted.*

Johnson, V. and Rossell, R. (2010). *On the use of non-local prior densities in Bayesian hypothesis tests. Journal of the Royal Statistical Society: Series B, 72:143-170.* [Article]

Examples

```
out = fixedNAP.twot_es(n1max = 100, n2max = 100)
```

`fixedNAP.twot_n` *Fixed-design two-sample t-tests with NAP and a pre-fixed sample size*

Description

In two-sided fixed design two-sample t-tests with *normal moment prior* assumed on the difference between standardized effect sizes $(\mu_2 - \mu_1)/\sigma$ under the alternative and a prefixed sample size, this function calculates the expected weights of evidence (that is, expected log(Bayes Factor)) of the test at a varied range of differences between standardized effect sizes.

Usage

```
fixedNAP.twot_n(es = c(0, 0.2, 0.3, 0.5), n1.fixed = 20, n2.fixed = 20,
                tau.NAP = 0.3/sqrt(2), nReplicate = 50000, nCore)
```

Arguments

`es`	Numeric vector. Standardized effect size differences $(\mu_2 - \mu_1)/\sigma$ where the expected weights of evidence is desired. **Default:** `c(0,0.2,0.3,0.5)`.
`n1.fixed`	Positive integer. Prefixed sample size from Group-1. **Default:** 20.
`n2.fixed`	Positive integer. Prefixed sample size from Group-2. **Default:** 20.
`tau.NAP`	Positive numeric. Parameter in the moment prior. **Default:** $0.3/\sqrt{2}$. This places the prior modes of $(\mu_2 - \mu_1)/\sigma$ at 0.3 and -0.3.
`nReplicate`	Positve integer. Number of replicated studies based on which the expected weights of evidence is calculated. **Default:** 50,000.
`nCore`	Positive integer. **Default:** One less than the total number of available cores.

Value

A list with two components named `summary` and `BF`.

`$summary` is a data frame with columns `effect.size` containing the values in `es` and `avg.logBF` containing the expected weight of evidence values at those values.

`$BF` is a matrix of dimension `length(es)` by `nReplicate`. Each row contains the Bayes factor values at the corresponding standardized effec size differences in `nReplicate` replicated studies.

Author(s)

Sandipan Pramanik and Valen E. Johnson

References

Pramanik, S. and Johnson, V. (2022). *Efficient Alternatives for Bayesian Hypothesis Tests in Psychology. Psychological Methods. Just accepted.*

Johnson, V. and Rossell, R. (2010). *On the use of non-local prior densities in Bayesian hypothesis tests. Journal of the Royal Statistical Society: Series B, 72:143-170.* [Article]

Examples

```
out = fixedNAP.twot_n(n1.fixed = 20, n2.fixed = 20, es = c(0, 0.3), nCore = 1)
```

---

fixedNAP.twoz_es *Fixed-design two-sample z-tests with NAP for varied sample sizes*

Description

In two-sided fixed design two-sample z-tests with *normal moment prior* assumed on the difference between standardized effect sizes $(\mu_2 - \mu_1)/\sigma_0$ under the alternative, this function calculates the expected weights of evidence (that is, expected log(Bayes Factor)) of the test at a prefixed differences between standardized effect size for a varied range of sample sizes.

Usage

```
fixedNAP.twoz_es(es = 0, n1min = 20, n2min = 20,
                 n1max = 5000, n2max = 5000,
                 tau.NAP = 0.3/sqrt(2), sigma0 = 1,
                 batch1.size.increment, batch2.size.increment,
                 nReplicate = 50000)
```

Arguments

`es`	Numeric. Difference between standardized effect sizes where the expected weights of evidence is desired. **Default:** `0`.
`n1min`	Positive integer. Minimum sample size from Grpup-1 to be considered. **Default:** 20.
`n2min`	Positive integer. Minimum sample size from Grpup-2 to be considered. **Default:** 20.
`n1max`	Positive integer. Maximum sample size from Grpup-1 to be considered. **Default:** 5000.
`n2max`	Positive integer. Maximum sample size from Grpup-2 to be considered. **Default:** 5000.

- `tau.NAP` Positive numeric. Parameter in the moment prior. **Default:** $0.3/\sqrt{2}$. This places the prior modes of $(\mu_2 - \mu_1)/\sigma_0$ at 0.3 and -0.3.
- `sigma0` Positive numeric. Known common standard deviation of the populations. **Default:** 1.
- `batch1.size.increment` Positive numeric. Increment in sample size from Group-1. The sequence of sample size thus considered from Group-1 for the fixed design test is from `n1min` to `n1max` with an increment of `batch1.size.increment`. **Default:** `function(narg){20}`. This means an increment of 20 samples from Group-1 at each step.
- `batch2.size.increment` Positive numeric. Increment in sample size from Group-2. The sequence of sample size thus considered from Group-2 for the fixed design test is from `n2min` to `n2max` with an increment of `batch2.size.increment`. **Default:** `function(narg){20}`. This means an increment of 20 samples from Group-2 at each step.
- `nReplicate` Positve integer. Number of replicated studies based on which the expected weights of evidence is calculated. **Default:** 50,000.

Details

`n1min`, `n1max`, `batch1.size.increment`, and `n2min`, `n2max`, `batch2.size.increment` should be chosen such that the length of sample sizes considered from Group 1 and 2 are equal.

Value

A list with two components named `summary` and `BF`.

`$summary` is a data frame with columns `n1` containing the sample sizes from Group-1, `n2` containing the sample sizes from Group-2, and `avg.logBF` containing the expected weight of evidence values at those values.

`$BF` is a matrix of dimension `number of sample sizes considered` by `nReplicate`. Each row contains the Bayes factor values at the corresponding sample size in `nReplicate` replicated studies.

Author(s)

Sandipan Pramanik and Valen E. Johnson

References

Pramanik, S. and Johnson, V. (2022). *Efficient Alternatives for Bayesian Hypothesis Tests in Psychology. Psychological Methods. Just accepted.*

Johnson, V. and Rossell, R. (2010). *On the use of non-local prior densities in Bayesian hypothesis tests. Journal of the Royal Statistical Society: Series B, 72:143-170.* [Article]

Examples

```
out = fixedNAP.twoz_es(n1max = 100, n2max = 100)
```

fixedNAP.twoz_n *Fixed-design two-sample z-tests with NAP and a pre-fixed sample size*

Description

In two-sided fixed design two-sample z-tests with *normal moment prior* assumed on the difference between standardized effect sizes $(\mu_2 - \mu_1)/\sigma_0$ under the alternative and a prefixed sample size, this function calculates the expected weights of evidence (that is, expected log(Bayes Factor)) of the test at a varied range of differences between standardized effect sizes.

Usage

```
fixedNAP.twoz_n(es = c(0, 0.2, 0.3, 0.5), n1.fixed = 20, n2.fixed = 20,
                tau.NAP = 0.3/sqrt(2), sigma0 = 1,
                nReplicate = 50000, nCore)
```

Arguments

`es`	Numeric vector. Standardized effect size differences $(\mu_2 - \mu_1)/\sigma_0$ where the expected weights of evidence is desired. **Default:** `c(0,0.2,0.3,0.5)`.
`n1.fixed`	Positive integer. Prefixed sample size from Group-1. **Default:** 20.
`n2.fixed`	Positive integer. Prefixed sample size from Group-2. **Default:** 20.
`tau.NAP`	Positive numeric. Parameter in the moment prior. **Default:** $0.3/\sqrt{2}$. This places the prior modes of $(\mu_2 - \mu_1)/\sigma_0$ at 0.3 and -0.3.
`sigma0`	Positive numeric. Known common standard deviation of the populations. **Default:** 1.
`nReplicate`	Positve integer. Number of replicated studies based on which the expected weights of evidence is calculated. **Default:** 50,000.
`nCore`	Positive integer. **Default:** One less than the total number of available cores.

Value

A list with two components named `summary` and `BF`.

`$summary` is a data frame with columns `effect.size` containing the values in `es` and `avg.logBF` containing the expected weight of evidence values at those values.

`$BF` is a matrix of dimension `length(es)` by `nReplicate`. Each row contains the Bayes factor values at the corresponding standardized effec size differences in `nReplicate` replicated studies.

Author(s)

Sandipan Pramanik and Valen E. Johnson

References

Pramanik, S. and Johnson, V. (2022). *Efficient Alternatives for Bayesian Hypothesis Tests in Psychology. Psychological Methods. Just accepted.*

Johnson, V. and Rossell, R. (2010). *On the use of non-local prior densities in Bayesian hypothesis tests. Journal of the Royal Statistical Society: Series B, 72:143-170.* [Article]

Examples

```
out = fixedNAP.twoz_n(n1.fixed = 20, n2.fixed = 20, es = c(0, 0.3), nCore = 1)
```

HajnalBF_onet *Hajnal's ratio in one-sample t tests*

Description

In a $N(\mu, \sigma^2)$ population with unknown variance σ^2, consider the two-sided one-sample z-test for testing the point null hypothesis $H_0 : \mu = 0$ against $H_1 : \mu \neq 0$. Based on an observed data, this function calculates the Hajnal's ratio in favor of H_1 when the prior assumed on the standardized effect size μ/σ under the alternative places equal probability at $+\delta$ and $-\delta$ ($\delta > 0$ prefixed).

Usage

```
HajnalBF_onet(obs, nObs, mean.obs, sd.obs, test.statistic, es1 = 0.3)
```

Arguments

`obs`	Numeric vector. Observed vector of data.
`nObs`	Numeric or numeric vector. Sample size(s). Same as `length(obs)` when numeric.
`mean.obs`	Numeric or numeric vector. Sample mean(s). Same as `mean(obs)` when numeric.
`sd.obs`	Positive numeric or numeric vector. Sample standard deviation(s). Same as `sd(obs)` when numeric.
`test.statistic`	Numeric or numeric vector. Test-statistic value(s).
`es1`	Positive numeric. δ as above. **Default:** 0.3. For this, the prior on the standardized effect size μ/σ takes values 0.3 and -0.3 each with equal probability 1/2.

Details

- Users can either specify `obs`, or `nObs`, `mean.obs` and `sd.obs`, or `nObs` and `test.statistic`.
- If `obs` is provided, it returns the corresponding Bayes factor value.
- If `nObs`, `mean.obs` and `sd.obs` are provided, the function is vectorized over the arguments. Bayes factor values corresponding to the values therein are returned.
- If `nObs` and `test.statistic` are provided, the function is vectorized over the arguments. Bayes factor values corresponding to the values therein are returned.

Value

Positive numeric or numeric vector. The Hajnal's ratio(s).

Author(s)

Sandipan Pramanik and Valen E. Johnson

References

Hajnal, J. (1961). *A two-sample sequential t-test.Biometrika, 48:65-75*, [Article].

Schnuerch, M. and Erdfelder, E. (2020). *A two-sample sequential t-test.Biometrika, 48:65-75*, [Article].

Examples

```
HajnalBF_onet(obs = rnorm(100))
```

`HajnalBF_onez` *Hajnal's ratio in one-sample z tests*

Description

In a $N(\mu, \sigma_0^2)$ population with known variance σ_0^2, consider the two-sided one-sample z-test for testing the point null hypothesis $H_0 : \mu = 0$ against $H_1 : \mu \neq 0$. Based on an observed data, this function calculates the Hajnal's ratio in favor of H_1 when the prior assumed on the standardized effect size μ/σ_0 under the alternative places equal probability at $+\delta$ and $-\delta$ ($\delta > 0$ prefixed).

Usage

```
HajnalBF_onez(obs, nObs, mean.obs, test.statistic,
              es1 = 0.3, sigma0 = 1)
```

Arguments

obs	Numeric vector. Observed vector of data.
nObs	Numeric or numeric vector. Sample size(s). Same as length(obs) when numeric.
mean.obs	Numeric or numeric vector. Sample mean(s). Same as mean(obs) when numeric.
test.statistic	Numeric or numeric vector. Test-statistic value(s).
es1	Positive numeric. δ as above. **Default:** 0.3. For this, the prior on the standardized effect size μ/σ_0 takes values 0.3 and -0.3 each with equal probability 1/2.
sigma0	Positive numeric. Known standard deviation in the population. **Default:** 1.

Details

- Users can either specify obs, or nObs and mean.obs, or nObs and test.statistic.
- If obs is provided, it returns the corresponding Bayes factor value.
- If nObs and mean.obs are provided, the function is vectorized over both arguments. Bayes factor values corresponding to the values therein are returned.
- If nObs and test.statistic are provided, the function is vectorized over both arguments. Bayes factor values corresponding to the values therein are returned.

Value

Positive numeric or numeric vector. The Hajnal's ratio(s).

Author(s)

Sandipan Pramanik and Valen E. Johnson

References

Hajnal, J. (1961). *A two-sample sequential t-test.Biometrika, 48:65-75*, [Article].

Schnuerch, M. and Erdfelder, E. (2020). *A two-sample sequential t-test.Biometrika, 48:65-75*, [Article].

Examples

```
HajnalBF_onez(obs = rnorm(100))
```

HajnalBF_twot *Hajnal's ratio in two-sample t tests*

Description

In case of two independent populations $N(\mu_1, \sigma^2)$ and $N(\mu_2, \sigma^2)$ with unknown common variance σ^2, consider the two-sample t-test for testing the point null hypothesis of difference in their means $H_0 : \mu_2 - \mu_1 = 0$ against $H_1 : \mu_2 - \mu_1 \neq 0$. Based on an observed data, this function calculates the Hajnal's ratio in favor of H_1 when the prior assumed under the alternative on the difference between standardized effect sizes $(\mu_2 - \mu_1)/\sigma$ places equal probability at $+\delta$ and $-\delta$ ($\delta > 0$ prefixed).

Usage

```
HajnalBF_twot(obs1, obs2, n1Obs, n2Obs, mean.obs1, mean.obs2,
              sd.obs1, sd.obs2, test.statistic, es1 = 0.3)
```

Arguments

`obs1`	Numeric vector. Observed vector of data from Group-1.
`obs2`	Numeric vector. Observed vector of data from Group-2.
`n1Obs`	Numeric or numeric vector. Sample size(s) from Group-1. Same as `length(obs1)` when numeric.
`n2Obs`	Numeric or numeric vector. Sample size(s) from Group-2. Same as `length(obs2)` when numeric.
`mean.obs1`	Numeric or numeric vector. Sample mean(s) from Group-1. Same as `mean(obs1)` when numeric.
`mean.obs2`	Numeric or numeric vector. Sample mean(s) from Group-2. Same as `mean(obs2)` when numeric.
`sd.obs1`	Numeric or numeric vector. Sample standard deviations(s) from Group-1. Same as `sd(obs1)` when numeric.
`sd.obs2`	Numeric or numeric vector. Sample standard deviations(s) from Group-2. Same as `sd(obs2)` when numeric.
`test.statistic`	Numeric or numeric vector. Test-statistic value(s).
`es1`	Positive numeric. δ as above. **Default:** 0.3. For this, the prior on $(\mu_2 - \mu_1)/\sigma$ takes values 0.3 and -0.3 each with equal probability 1/2.

Details

- A user can either specify `obs1` and `obs2`, or `n1Obs`, `n2Obs`, `mean.obs1`, `mean.obs2`, `sd.obs1` and `sd.obs2`, or `n1Obs`, `n2Obs`, and `test.statistic`.
- If `obs1` and `obs2` are provided, it returns the corresponding Bayes factor value.
- If `n1Obs`, `n2Obs`, `mean.obs1`, `mean.obs2`, `sd.obs1` and `sd.obs2` are provided, the function is vectorized over the arguments. Bayes factor values corresponding to the values therein are returned.
- If `n1Obs`, `n2Obs`, and `test.statistic` are provided, the function is vectorized over each of the arguments. Bayes factor values corresponding to the values therein are returned.

Value

Positive numeric or numeric vector. The Hajnal's ratio(s).

Author(s)

Sandipan Pramanik and Valen E. Johnson

References

Hajnal, J. (1961). *A two-sample sequential t-test.Biometrika, 48:65-75*, [Article].

Schnuerch, M. and Erdfelder, E. (2020). *A two-sample sequential t-test.Biometrika, 48:65-75*, [Article].

Examples

```
HajnalBF_twot(obs1 = rnorm(100), obs2 = rnorm(100))
```

`HajnalBF_twoz` *Hajnal's ratio in two-sample z tests*

Description

In case of two independent populations $N(\mu_1, \sigma_0^2)$ and $N(\mu_2, \sigma_0^2)$ with known common variance σ_0^2, consider the two-sample z-test for testing the point null hypothesis of difference in their means $H_0 : \mu_2 - \mu_1 = 0$ against $H_1 : \mu_2 - \mu_1 \neq 0$. Based on an observed data, this function calculates the Hajnal's ratio in favor of H_1 when the prior assumed under the alternative on the difference between standardized effect sizes $(\mu_2 - \mu_1)/\sigma_0$ places equal probability at $+\delta$ and $-\delta$ ($\delta > 0$ prefixed).

Usage

```
HajnalBF_twoz(obs1, obs2, n1Obs, n2Obs, mean.obs1, mean.obs2,
              test.statistic, es1 = 0.3, sigma0 = 1)
```

Arguments

`obs1`	Numeric vector. Observed vector of data from Group-1.
`obs2`	Numeric vector. Observed vector of data from Group-2.
`n1Obs`	Numeric or numeric vector. Sample size(s) from Group-1. Same as `length(obs1)` when numeric.
`n2Obs`	Numeric or numeric vector. Sample size(s) from Group-2. Same as `length(obs2)` when numeric.
`mean.obs1`	Numeric or numeric vector. Sample mean(s) from Group-1. Same as `mean(obs1)` when numeric.
`mean.obs2`	Numeric or numeric vector. Sample mean(s) from Group-2. Same as `mean(obs2)` when numeric.

`test.statistic`	Numeric or numeric vector. Test-statistic value(s).
`es1`	Positive numeric. δ as above. **Default:** 0.3. For this, the prior on $(\mu_2 - \mu_1)/\sigma_0$ takes values 0.3 and -0.3 each with equal probability 1/2.
`sigma0`	Positive numeric. Known common standard deviation of the populations. **Default:** 1.

Details

- A user can either specify `obs1` and `obs2`, or `n1Obs`, `n2Obs`, `mean.obs1` and `mean.obs2`, or `n1Obs`, `n2Obs`, and `test.statistic`.
- If `obs1` and `obs2` are provided, it returns the corresponding Bayes factor value.
- If `n1Obs`, `n2Obs`, `mean.obs1` and `mean.obs2` are provided, the function is vectorized over the arguments. Bayes factor values corresponding to the values therein are returned.
- If `n1Obs`, `n2Obs`, and `test.statistic` are provided, the function is vectorized over each of the arguments. Bayes factor values corresponding to the values therein are returned.

Value

Positive numeric or numeric vector. The Hajnal's ratio(s).

Author(s)

Sandipan Pramanik and Valen E. Johnson

References

Hajnal, J. (1961). *A two-sample sequential t-test.Biometrika, 48:65-75*, [Article].

Schnuerch, M. and Erdfelder, E. (2020). *A two-sample sequential t-test.Biometrika, 48:65-75*, [Article].

Examples

```
HajnalBF_twoz(obs1 = rnorm(100), obs2 = rnorm(100))
```

`implement.SBFHajnal_onet` *Implement Sequential Bayes Factor using the Hajnal's ratio for one-sample t-tests*

Description

In a $N(\mu, \sigma^2)$ population with unknown variance σ^2, consider the two-sided one-sample t-test for testing the point null hypothesis $H_0 : \mu = 0$ against $H_1 : \mu \neq 0$. For a sequentially observed data, this function implements the Sequential Bayes Factor design when the prior assumed on the standardized effect size μ/σ under the alternative places equal probability at $+\delta$ and $-\delta$ ($\delta > 0$ prefixed).

Usage

```
implement.SBFHajnal_onet(obs, es1 = 0.3,
                         RejectH1.threshold = exp(-3), RejectH0.threshold = exp(3),
                      batch.size, return.plot = TRUE, until.decision.reached = TRUE)
```

Arguments

`obs`	Numeric vector. The vector of sequentially observed data.
`es1`	Positive numeric. δ as above. **Default:** 0.3. For this, the prior on the standardized effect size μ/σ takes values 0.3 and -0.3 each with equal probability 1/2.
`RejectH1.threshold`	Positive numeric. H_0 is accepted if BF ≤`RejectH1.threshold`. **Default:** `exp(-3)`.
`RejectH0.threshold`	Positive numeric. H_0 is rejected if BF ≥`RejectH0.threshold`. **Default:** `exp(3)`.
`batch.size`	Integer vector. The vector of batch sizes at each sequential comparison. **Default:** `c(2,rep(1,length(obs)-2))`.
`return.plot`	Logical. Whether a sequential comparison plot to be returned. **Default:** `TRUE`.
`until.decision.reached`	Logical. Whether the sequential comparison is performed until a decision is reached or until the data is observed. **Default:** `TRUE`. This means the comparison is performed until a decision is reached.

Value

A list with three components named `N`, `BF`, and `decision`.

`$N` contains the number of sample size used.

`$BF` contains the Bayes factor values at each sequential comparison.

`$decision` contains the decision reached. `'A'` indicates acceptance of H_0, `'R'` indicates rejection of H_0, and `'I'` indicates inconclusive.

Author(s)

Sandipan Pramanik and Valen E. Johnson

References

Hajnal, J. (1961). *A two-sample sequential t-test.Biometrika, 48:65-75*, [Article].

Schnuerch, M. and Erdfelder, E. (2020). *A two-sample sequential t-test.Biometrika, 48:65-75*, [Article].

Examples

```
out = implement.SBFHajnal_onet(obs = rnorm(100))
```

implement.SBFHajnal_onez

Implement Sequential Bayes Factor using the Hajnal's ratio for one-sample z-tests

Description

In a $N(\mu, \sigma_0^2)$ population with known variance σ_0^2, consider the two-sided one-sample z-test for testing the point null hypothesis $H_0 : \mu = 0$ against $H_1 : \mu \neq 0$. For a sequentially observed data, this function implements the Sequential Bayes Factor design when the prior assumed on the standardized effect size μ/σ_0 under the alternative places equal probability at $+\delta$ and $-\delta$ ($\delta > 0$ prefixed).

Usage

```
implement.SBFHajnal_onez(obs, es1 = 0.3, sigma0 = 1,
                         RejectH1.threshold = exp(-3), RejectH0.threshold = exp(3),
                      batch.size, return.plot = TRUE, until.decision.reached = TRUE)
```

Arguments

- `obs` — Numeric vector. The vector of sequentially observed data.
- `es1` — Positive numeric. δ as above. **Default:** 0.3. For this, the prior on the standardized effect size μ/σ_0 takes values 0.3 and -0.3 each with equal probability 1/2.
- `sigma0` — Positive numeric. Known standard deviation in the population. **Default:** 1.
- `RejectH1.threshold` — Positive numeric. H_0 is accepted if BF $\leq$`RejectH1.threshold`. **Default:** `exp(-3)`.
- `RejectH0.threshold` — Positive numeric. H_0 is rejected if BF $\geq$`RejectH0.threshold`. **Default:** `exp(3)`.
- `batch.size` — Integer vector. The vector of batch sizes at each sequential comparison. **Default:** `rep(1,length(obs))`.
- `return.plot` — Logical. Whether a sequential comparison plot to be returned. **Default:** `TRUE`.
- `until.decision.reached` — Logical. Whether the sequential comparison is performed until a decision is reached or until the data is observed. **Default:** `TRUE`. This means the comparison is performed until a decision is reached.

Value

A list with three components named `N`, `BF`, and `decision`.

`$N` contains the number of sample size used.

`$BF` contains the Bayes factor values at each sequential comparison.

`$decision` contains the decision reached. `'A'` indicates acceptance of H_0, `'R'` indicates rejection of H_0, and `'I'` indicates inconclusive.

Author(s)

Sandipan Pramanik and Valen E. Johnson

References

Hajnal, J. (1961). *A two-sample sequential t-test.Biometrika, 48:65-75*, [Article].

Schnuerch, M. and Erdfelder, E. (2020). *A two-sample sequential t-test.Biometrika, 48:65-75*, [Article].

Examples

```
out = implement.SBFHajnal_onez(obs = rnorm(100))
```

`implement.SBFHajnal_twot` *Implement Sequential Bayes Factor using the NAP for two-sample t-tests*

Description

In case of two independent populations $N(\mu_1, \sigma^2)$ and $N(\mu_2, \sigma^2)$ with unknown common variance σ^2, consider the two-sample t-test for testing the point null hypothesis of difference in their means $H_0 : \mu_2 - \mu_1 = 0$ against $H_1 : \mu_2 - \mu_1 \neq 0$. For a sequentially observed data, this function implements the Sequential Bayes Factor design when a *normal moment prior* is assumed on the difference between standardized effect sizes $(\mu_2 - \mu_1)/\sigma$ under the alternative.

Usage

```
implement.SBFHajnal_twot(obs1, obs2, es1 = 0.3,
                         RejectH1.threshold = exp(-3), RejectH0.threshold = exp(3),
                            batch1.size, batch2.size, return.plot = TRUE,
                            until.decision.reached = TRUE)
```

Arguments

`obs1` Numeric vector. The vector of sequentially observed data from Group-1.

`obs2` Numeric vector. The vector of sequentially observed data from Group-2.

`es1` Positive numeric. δ as above. **Default:** 0.3. For this, the prior on $(\mu_2 - \mu_1)/\sigma$ takes values 0.3 and -0.3 each with equal probability 1/2.

`RejectH1.threshold`
: Positive numeric. H_0 is accepted if $BF \leq$`RejectH1.threshold`. **Default:** `exp(-3)`.

`RejectH0.threshold`
: Positive numeric. H_0 is rejected if BF $\geq$`RejectH0.threshold`. **Default:** `exp(3)`.

`batch1.size`
: Integer vector. The vector of batch sizes from Group-1 at each sequential comparison. The first element (the first batch size) needs to be at least 2. **Default:** `c(2,rep(1,length(obs1)-2))`.

`batch2.size`
: Integer vector. The vector of batch sizes from Group-2 at each sequential comparison. The first element (the first batch size) needs to be at least 2. **Default:** `c(2,rep(1,length(obs2)-2))`.

`return.plot`
: Logical. Whether a sequential comparison plot to be returned. **Default:** `TRUE`.

`until.decision.reached`
: Logical. Whether the sequential comparison is performed until a decision is reached or until the data is observed. **Default:** `TRUE`. This means the comparison is performed until a decision is reached.

Value

A list with three components named `N1`, `N2`, `BF`, and `decision`.

`$N1` and `$N2` contains the number of sample size used from Group-1 and 2.

`$BF` contains the Bayes factor values at each sequential comparison.

`$decision` contains the decision reached. `'A'` indicates acceptance of H_0, `'R'` indicates rejection of H_0, and `'I'` indicates inconclusive.

Author(s)

Sandipan Pramanik and Valen E. Johnson

References

Hajnal, J. (1961). *A two-sample sequential t-test.Biometrika, 48:65-75*, [Article].

Schnuerch, M. and Erdfelder, E. (2020). *A two-sample sequential t-test.Biometrika, 48:65-75*, [Article].

Examples

```
out = implement.SBFHajnal_twot(obs1 = rnorm(100), obs2 = rnorm(100))
```

`implement.SBFHajnal_twoz`
Implement Sequential Bayes Factor using the NAP for two-sample z-tests

---

Description

In case of two independent populations $N(\mu_1, \sigma_0^2)$ and $N(\mu_2, \sigma_0^2)$ with known common variance σ_0^2, consider the two-sample z-test for testing the point null hypothesis of difference in their means $H_0 : \mu_2 - \mu_1 = 0$ against $H_1 : \mu_2 - \mu_1 \neq 0$. For a sequentially observed data, this function implements the Sequential Bayes Factor design when a *normal moment prior* is assumed on the difference between standardized effect sizes $(\mu_2 - \mu_1)/\sigma_0$ under the alternative.

Usage

```
implement.SBFHajnal_twoz(obs1, obs2, es1 = 0.3, sigma0 = 1,
                         RejectH1.threshold = exp(-3), RejectH0.threshold = exp(3),
                            batch1.size, batch2.size, return.plot = TRUE,
                            until.decision.reached = TRUE)
```

Arguments

`obs1` Numeric vector. The vector of sequentially observed data from Group-1.

`obs2` Numeric vector. The vector of sequentially observed data from Group-2.

`es1` Positive numeric. δ as above. **Default:** 0.3. For this, the prior on $(\mu_2 - \mu_1)/\sigma_0$ takes values 0.3 and -0.3 each with equal probability 1/2.

`sigma0` Positive numeric. Known standard deviation in the population. **Default:** 1.

`RejectH1.threshold` Positive numeric. H_0 is accepted if BF ≤`RejectH1.threshold`. **Default:** `exp(-3)`.

`RejectH0.threshold` Positive numeric. H_0 is rejected if BF ≥`RejectH0.threshold`. **Default:** `exp(3)`.

`batch1.size` Integer vector. The vector of batch sizes from Group-1 at each sequential comparison. **Default:** `rep(1,length(obs1))`.

`batch2.size` Integer vector. The vector of batch sizes from Group-2 at each sequential comparison. **Default:** `rep(1,length(obs2))`.

`return.plot` Logical. Whether a sequential comparison plot to be returned. **Default:** `TRUE`.

`until.decision.reached` Logical. Whether the sequential comparison is performed until a decision is reached or until the data is observed. **Default:** `TRUE`. This means the comparison is performed until a decision is reached.

Value

A list with three components named `N1`, `N2`, `BF`, and `decision`.

`$N1` and `$N2` contains the number of sample size used from Group-1 and 2.

`$BF` contains the Bayes factor values at each sequential comparison.

`$decision` contains the decision reached. `'A'` indicates acceptance of H_0, `'R'` indicates rejection of H_0, and `'I'` indicates inconclusive.

Author(s)

Sandipan Pramanik and Valen E. Johnson

References

Hajnal, J. (1961). *A two-sample sequential t-test.Biometrika, 48:65-75*, [Article].

Schnuerch, M. and Erdfelder, E. (2020). *A two-sample sequential t-test.Biometrika, 48:65-75*, [Article].

Examples

```
out = implement.SBFHajnal_twoz(obs1 = rnorm(100), obs2 = rnorm(100))
```

`implement.SBFNAP_onet` *Implement Sequential Bayes Factor using the NAP for one-sample t-tests*

Description

In a $N(\mu, \sigma^2)$ population with unknown variance σ^2, consider the two-sided one-sample t-test for testing the point null hypothesis $H_0 : \mu = 0$ against $H_1 : \mu \neq 0$. For a sequentially observed data, this function implements the Sequential Bayes Factor design when a *normal moment prior* is assumed on the standardized effect size μ/σ under the alternative.

Usage

```
implement.SBFNAP_onet(obs, tau.NAP = 0.3/sqrt(2),
                      RejectH1.threshold = exp(-3), RejectH0.threshold = exp(3),
                   batch.size, return.plot = TRUE, until.decision.reached = TRUE)
```

Arguments

`obs` Numeric vector. The vector of sequentially observed data.

`tau.NAP` Positive numeric. Parameter in the moment prior. **Default:** $0.3/\sqrt{2}$. This places the prior modes of the standardized effect size μ/σ at 0.3 and -0.3.

`RejectH1.threshold`
Positive numeric. H_0 is accepted if BF ≤`RejectH1.threshold`. **Default:** `exp(-3)`.

`RejectH0.threshold`
Positive numeric. H_0 is rejected if BF ≥`RejectH0.threshold`. **Default:** `exp(3)`.

`batch.size` Integer vector. The vector of batch sizes at each sequential comparison. The first element (the first batch size) needs to be at least 2. **Default:** `c(2,rep(1,length(obs)-2))`.

`return.plot` Logical. Whether a sequential comparison plot to be returned. **Default:** `TRUE`.

`until.decision.reached`
Logical. Whether the sequential comparison is performed until a decision is reached or until the data is observed. **Default:** `TRUE`. This means the comparison is performed until a decision is reached.

Value

A list with three components named N, BF, and decision.

$N contains the number of sample size used.

$BF contains the Bayes factor values at each sequential comparison.

$decision contains the decision reached. 'A' indicates acceptance of H_0, 'R' indicates rejection of H_0, and 'I' indicates inconclusive.

Author(s)

Sandipan Pramanik and Valen E. Johnson

References

Pramanik, S. and Johnson, V. (2022). *Efficient Alternatives for Bayesian Hypothesis Tests in Psychology. Psychological Methods. Just accepted.*

Johnson, V. and Rossell, R. (2010). *On the use of non-local prior densities in Bayesian hypothesis tests. Journal of the Royal Statistical Society: Series B, 72:143-170.* [Article]

Examples

```
out = implement.SBFNAP_onet(obs = rnorm(100))
```

---

implement.SBFNAP_onez *Implement Sequential Bayes Factor using the NAP for one-sample z-tests*

Description

In a $N(\mu, \sigma_0^2)$ population with known variance σ_0^2, consider the two-sided one-sample z-test for testing the point null hypothesis $H_0 : \mu = 0$ against $H_1 : \mu \neq 0$. For a sequentially observed data, this function implements the Sequential Bayes Factor design when a *normal moment prior* is assumed on the standardized effect size μ/σ_0 under the alternative.

Usage

```
implement.SBFNAP_onez(obs, sigma0 = 1, tau.NAP = 0.3/sqrt(2),
                       RejectH1.threshold = exp(-3), RejectH0.threshold = exp(3),
                    batch.size, return.plot = TRUE, until.decision.reached = TRUE)
```

Arguments

obs	Numeric vector. The vector of sequentially observed data.
tau.NAP	Positive numeric. Parameter in the moment prior. **Default:** $0.3/\sqrt{2}$. This places the prior modes of the standardized effect size μ/σ_0 at 0.3 and -0.3.
sigma0	Positive numeric. Known standard deviation in the population. **Default:** 1.

`RejectH1.threshold`
: Positive numeric. H_0 is accepted if BF $\leq$`RejectH1.threshold`. **Default:** `exp(-3)`.

`RejectH0.threshold`
: Positive numeric. H_0 is rejected if BF $\geq$`RejectH0.threshold`. **Default:** `exp(3)`.

`batch.size`
: Integer vector. The vector of batch sizes at each sequential comparison. **Default:** `rep(1,length(obs))`.

`return.plot`
: Logical. Whether a sequential comparison plot to be returned. **Default:** `TRUE`.

`until.decision.reached`
: Logical. Whether the sequential comparison is performed until a decision is reached or until the data is observed. **Default:** `TRUE`. This means the comparison is performed until a decision is reached.

Value

A list with three components named `N`, `BF`, and `decision`.

`$N` contains the number of sample size used.

`$BF` contains the Bayes factor values at each sequential comparison.

`$decision` contains the decision reached. `'A'` indicates acceptance of H_0, `'R'` indicates rejection of H_0, and `'I'` indicates inconclusive.

Author(s)

Sandipan Pramanik and Valen E. Johnson

References

Pramanik, S. and Johnson, V. (2022). *Efficient Alternatives for Bayesian Hypothesis Tests in Psychology. Psychological Methods. Just accepted.*

Johnson, V. and Rossell, R. (2010). *On the use of non-local prior densities in Bayesian hypothesis tests. Journal of the Royal Statistical Society: Series B, 72:143-170.* [Article]

Examples

```
out = implement.SBFNAP_onez(obs = rnorm(100))
```

`implement.SBFNAP_twot` *Implement Sequential Bayes Factor using the NAP for two-sample t-tests*

Description

In case of two independent populations $N(\mu_1, \sigma^2)$ and $N(\mu_2, \sigma^2)$ with unknown common variance σ^2, consider the two-sample t-test for testing the point null hypothesis of difference in their means $H_0 : \mu_2 - \mu_1 = 0$ against $H_1 : \mu_2 - \mu_1 \neq 0$. For a sequentially observed data, this function implements the Sequential Bayes Factor design when a *normal moment prior* is assumed on the difference between standardized effect sizes $(\mu_2 - \mu_1)/\sigma$ under the alternative.

Usage

```
implement.SBFNAP_twot(obs1, obs2, tau.NAP = 0.3/sqrt(2),
                      RejectH1.threshold = exp(-3), RejectH0.threshold = exp(3),
                       batch1.size, batch2.size, return.plot = TRUE,
                       until.decision.reached = TRUE)
```

Arguments

obs1 — Numeric vector. The vector of sequentially observed data from Group-1.

obs2 — Numeric vector. The vector of sequentially observed data from Group-2.

tau.NAP — Positive numeric. Parameter in the moment prior. **Default:** $0.3/\sqrt{2}$. This places the prior modes of the difference between standardized effect sizes $(\mu_2 - \mu_1)/\sigma$ at 0.3 and -0.3.

RejectH1.threshold — Positive numeric. H_0 is accepted if BF ≤`RejectH1.threshold`. **Default:** `exp(-3)`.

RejectH0.threshold — Positive numeric. H_0 is rejected if BF ≥`RejectH0.threshold`. **Default:** `exp(3)`.

batch1.size — Integer vector. The vector of batch sizes from Group-1 at each sequential comparison. The first element (the first batch size) needs to be at least 2. **Default:** `c(2,rep(1,length(obs1)-2))`.

batch2.size — Integer vector. The vector of batch sizes from Group-2 at each sequential comparison. The first element (the first batch size) needs to be at least 2. **Default:** `c(2,rep(1,length(obs2)-2))`.

return.plot — Logical. Whether a sequential comparison plot to be returned. **Default:** `TRUE`.

until.decision.reached — Logical. Whether the sequential comparison is performed until a decision is reached or until the data is observed. **Default:** `TRUE`. This means the comparison is performed until a decision is reached.

Value

A list with three components named `N1`, `N2`, `BF`, and `decision`.

`$N1` and `$N2` contains the number of sample size used from Group-1 and 2.

`$BF` contains the Bayes factor values at each sequential comparison.

`$decision` contains the decision reached. `'A'` indicates acceptance of H_0, `'R'` indicates rejection of H_0, and `'I'` indicates inconclusive.

Author(s)

Sandipan Pramanik and Valen E. Johnson

References

Pramanik, S. and Johnson, V. (2022). *Efficient Alternatives for Bayesian Hypothesis Tests in Psychology. Psychological Methods. Just accepted.*

Johnson, V. and Rossell, R. (2010). *On the use of non-local prior densities in Bayesian hypothesis tests. Journal of the Royal Statistical Society: Series B, 72:143-170.* [Article]

Examples

```
out = implement.SBFNAP_twot(obs1 = rnorm(100), obs2 = rnorm(100))
```

---

implement.SBFNAP_twoz *Implement Sequential Bayes Factor using the NAP for two-sample z-tests*

Description

In case of two independent populations $N(\mu_1, \sigma_0^2)$ and $N(\mu_2, \sigma_0^2)$ with known common variance σ_0^2, consider the two-sample z-test for testing the point null hypothesis of difference in their means $H_0 : \mu_2 - \mu_1 = 0$ against $H_1 : \mu_2 - \mu_1 \neq 0$. For a sequentially observed data, this function implements the Sequential Bayes Factor design when a *normal moment prior* is assumed on the difference between standardized effect sizes $(\mu_2 - \mu_1)/\sigma_0$ under the alternative.

Usage

```
implement.SBFNAP_twoz(obs1, obs2, sigma0 = 1, tau.NAP = 0.3/sqrt(2),
                          RejectH1.threshold = exp(-3), RejectH0.threshold = exp(3),
                           batch1.size, batch2.size, return.plot = TRUE,
                           until.decision.reached = TRUE)
```

Arguments

`obs1`	Numeric vector. The vector of sequentially observed data from Group-1.
`obs2`	Numeric vector. The vector of sequentially observed data from Group-2.
`tau.NAP`	Positive numeric. Parameter in the moment prior. **Default:** $0.3/\sqrt{2}$. This places the prior modes of the difference between standardized effect sizes $(\mu_2 - \mu_1)/\sigma_0$ at 0.3 and -0.3.
`sigma0`	Positive numeric. Known standard deviation in the population. **Default:** 1.
`RejectH1.threshold`	Positive numeric. H_0 is accepted if BF ≤`RejectH1.threshold`. **Default:** `exp(-3)`.
`RejectH0.threshold`	Positive numeric. H_0 is rejected if BF ≥`RejectH0.threshold`. **Default:** `exp(3)`.
`batch1.size`	Integer vector. The vector of batch sizes from Group-1 at each sequential comparison. **Default:** `rep(1,length(obs1))`.

batch2.size	Integer vector. The vector of batch sizes from Group-2 at each sequential comparison. **Default:** `rep(1,length(obs2))`.
return.plot	Logical. Whether a sequential comparison plot to be returned. **Default:** `TRUE`.
until.decision.reached	Logical. Whether the sequential comparison is performed until a decision is reached or until the data is observed. **Default:** `TRUE`. This means the comparison is performed until a decision is reached.

Value

A list with three components named `N1`, `N2`, `BF`, and `decision`.

`$N1` and `$N2` contains the number of sample size used from Group-1 and 2.

`$BF` contains the Bayes factor values at each sequential comparison.

`$decision` contains the decision reached. `'A'` indicates acceptance of H_0, `'R'` indicates rejection of H_0, and `'I'` indicates inconclusive.

Author(s)

Sandipan Pramanik and Valen E. Johnson

References

Pramanik, S. and Johnson, V. (2022). *Efficient Alternatives for Bayesian Hypothesis Tests in Psychology. Psychological Methods. Just accepted.*

Johnson, V. and Rossell, R. (2010). *On the use of non-local prior densities in Bayesian hypothesis tests. Journal of the Royal Statistical Society: Series B, 72:143-170.* [Article]

Examples

```
out = implement.SBFNAP_twoz(obs1 = rnorm(100), obs2 = rnorm(100))
```

`mycombine.fixed` *Helper function*

Description

Helper function for combining outputs from replicated studies in fixed design tests.

Usage

```
mycombine.fixed(...)
```

Arguments

...	Lists. Outputs from different replicated studies.

Value

A list with two components combining the outputs from replicated studies.

Author(s)

Sandipan Pramanik and Valen E. Johnson

`mycombine.seq.onesample` *Helper function*

Description

Helper function for combining outputs from replicated studies in one-sample tests using Sequential Bayes Factor.

Usage

```
mycombine.seq.onesample(...)
```

Arguments

`...`	Lists. Outputs from different replicated studies.

Value

A list with three components combining the outputs from replicated studies.

Author(s)

Sandipan Pramanik and Valen E. Johnson

`mycombine.seq.twosample` *Helper function*

Description

Helper function for combining results in two-sample tests using Sequential Bayes Factor.

Usage

```
mycombine.seq.twosample(...)
```

Arguments

`...`	Lists. Outputs from different replicated studies.

Value

A list with four components combining the outputs from replicated studies.

Author(s)

Sandipan Pramanik and Valen E. Johnson

`NAPBF_onet` *Bayes factor in favor of the NAP in one-sample t tests*

Description

In a $N(\mu, \sigma^2)$ population with unknown variance σ^2, consider the two-sided one-sample t-test for testing the point null hypothesis $H_0 : \mu = 0$ against $H_1 : \mu \neq 0$. Based on an observed data, this function calculates the Bayes factor in favor of H_1 when a *normal moment prior* is assumed on the standardized effect size μ/σ under the alternative. Under both hypotheses, the Jeffrey's prior $\pi(\sigma^2) \propto 1/\sigma^2$ is assumed on σ^2.

Usage

```
NAPBF_onet(obs, nObs, mean.obs, sd.obs,
           test.statistic, tau.NAP = 0.3/sqrt(2))
```

Arguments

`obs`	Numeric vector. Observed vector of data.
`nObs`	Numeric or numeric vector. Sample size(s). Same as `length(obs)` when numeric.
`mean.obs`	Numeric or numeric vector. Sample mean(s). Same as `mean(obs)` when numeric.
`sd.obs`	Positive numeric or numeric vector. Sample standard deviation(s). Same as `sd(obs)` when numeric.
`test.statistic`	Numeric or numeric vector. Test-statistic value(s).
`tau.NAP`	Positive numeric. Parameter in the moment prior. **Default:** $0.3/\sqrt{2}$. This places the prior modes of the standardized effect size μ/σ at 0.3 and -0.3.

Details

- Users can either specify obs, or nObs, mean.obs and sd.obs, or nObs and test.statistic.
- If obs is provided, it returns the corresponding Bayes factor value.
- If nObs, mean.obs and sd.obs are provided, the function is vectorized over the arguments. Bayes factor values corresponding to the values therein are returned.
- If nObs and test.statistic are provided, the function is vectorized over the arguments. Bayes factor values corresponding to the values therein are returned.

Value

Positive numeric or numeric vector. The Bayes factor value(s).

Author(s)

Sandipan Pramanik and Valen E. Johnson

References

Pramanik, S. and Johnson, V. (2022). *Efficient Alternatives for Bayesian Hypothesis Tests in Psychology. Psychological Methods. Just accepted.*

Johnson, V. and Rossell, R. (2010). *On the use of non-local prior densities in Bayesian hypothesis tests. Journal of the Royal Statistical Society: Series B, 72:143-170.* [Article]

Examples

```
NAPBF_onet(obs = rnorm(100))
```

NAPBF_onez *Bayes factor in favor of the NAP in one-sample z tests*

Description

In a $N(\mu, \sigma_0^2)$ population with known variance σ_0^2, consider the two-sided one-sample z-test for testing the point null hypothesis $H_0 : \mu = 0$ against $H_1 : \mu \neq 0$. Based on an observed data, this function calculates the Bayes factor in favor of H_1 when a *normal moment prior* is assumed on the standardized effect size μ/σ_0 under the alternative.

Usage

```
NAPBF_onez(obs, nObs, mean.obs, test.statistic,
           tau.NAP = 0.3/sqrt(2), sigma0 = 1)
```

Arguments

obs	Numeric vector. Observed vector of data.
nObs	Numeric or numeric vector. Sample size(s). Same as length(obs) when numeric.
mean.obs	Numeric or numeric vector. Sample mean(s). Same as mean(obs) when numeric.
test.statistic	Numeric or numeric vector. Test-statistic value(s).
tau.NAP	Positive numeric. Parameter in the moment prior. **Default:** $0.3/\sqrt{2}$. This places the prior modes of the standardized effect size μ/σ_0 at 0.3 and -0.3.
sigma0	Positive numeric. Known standard deviation in the population. **Default:** 1.

Details

- Users can either specify obs, or nObs and mean.obs, or nObs and test.statistic.
- If obs is provided, it returns the corresponding Bayes factor value.
- If nObs and mean.obs are provided, the function is vectorized over both arguments. Bayes factor values corresponding to the values therein are returned.
- If nObs and test.statistic are provided, the function is vectorized over both arguments. Bayes factor values corresponding to the values therein are returned.

Value

Positive numeric or numeric vector. The Bayes factor value(s).

Author(s)

Sandipan Pramanik and Valen E. Johnson

References

Pramanik, S. and Johnson, V. (2022). *Efficient Alternatives for Bayesian Hypothesis Tests in Psychology. Psychological Methods. Just accepted.*

Johnson, V. and Rossell, R. (2010). *On the use of non-local prior densities in Bayesian hypothesis tests. Journal of the Royal Statistical Society: Series B, 72:143-170.* [Article]

Examples

```
NAPBF_onez(obs = rnorm(100))
```

`NAPBF_twot` *Bayes factor in favor of the NAP in two-sample t tests*

Description

In case of two independent populations $N(\mu_1, \sigma^2)$ and $N(\mu_2, \sigma^2)$ with unknown common variance σ^2, consider the two-sample t-test for testing the point null hypothesis of difference in their means $H_0 : \mu_2 - \mu_1 = 0$ against $H_1 : \mu_2 - \mu_1 \neq 0$. Based on an observed data, this function calculates the Bayes factor in favor of H_1 when a *normal moment prior* is assumed on the difference between standardized effect sizes $(\mu_2 - \mu_1)/\sigma$ under the alternative. Under both hypotheses, the Jeffrey's prior $\pi(\sigma^2) \propto 1/\sigma^2$ is assumed on σ^2.

Usage

```
NAPBF_twot(obs1, obs2, n1Obs, n2Obs,
           mean.obs1, mean.obs2, sd.obs1, sd.obs2,
           test.statistic, tau.NAP = 0.3/sqrt(2))
```

Arguments

`obs1`	Numeric vector. Observed vector of data from Group-1.
`obs2`	Numeric vector. Observed vector of data from Group-2.
`n1Obs`	Numeric or numeric vector. Sample size(s) from Group-1. Same as `length(obs1)` when numeric.
`n2Obs`	Numeric or numeric vector. Sample size(s) from Group-2. Same as `length(obs2)` when numeric.
`mean.obs1`	Numeric or numeric vector. Sample mean(s) from Group-1. Same as `mean(obs1)` when numeric.
`mean.obs2`	Numeric or numeric vector. Sample mean(s) from Group-2. Same as `mean(obs2)` when numeric.
`sd.obs1`	Numeric or numeric vector. Sample standard deviations(s) from Group-1. Same as `sd(obs1)` when numeric.
`sd.obs2`	Numeric or numeric vector. Sample standard deviations(s) from Group-2. Same as `sd(obs2)` when numeric.
`test.statistic`	Numeric or numeric vector. Test-statistic value(s).
`tau.NAP`	Positive numeric. Parameter in the moment prior. **Default:** $0.3/\sqrt{2}$. This places the prior modes of $(\mu_2 - \mu_1)/\sigma$ at 0.3 and -0.3.

Details

- A user can either specify `obs1` and `obs2`, or `n1Obs`, `n2Obs`, `mean.obs1`, `mean.obs2`, `sd.obs1` and `sd.obs2`, or `n1Obs`, `n2Obs`, and `test.statistic`.
- If `obs1` and `obs2` are provided, it returns the corresponding Bayes factor value.

- If `n1Obs`, `n2Obs`, `mean.obs1`, `mean.obs2`, `sd.obs1` and `sd.obs2` are provided, the function is vectorized over the arguments. Bayes factor values corresponding to the values therein are returned.
- If `n1Obs`, `n2Obs`, and `test.statistic` are provided, the function is vectorized over each of the arguments. Bayes factor values corresponding to the values therein are returned.

Value

Positive numeric or numeric vector. The Bayes factor value(s).

Author(s)

Sandipan Pramanik and Valen E. Johnson

References

Pramanik, S. and Johnson, V. (2022). *Efficient Alternatives for Bayesian Hypothesis Tests in Psychology. Psychological Methods. Just accepted.*

Johnson, V. and Rossell, R. (2010). *On the use of non-local prior densities in Bayesian hypothesis tests. Journal of the Royal Statistical Society: Series B, 72:143-170.* [Article]

Examples

```
NAPBF_twot(obs1 = rnorm(100), obs2 = rnorm(100))
```

`NAPBF_twoz` *Bayes factor in favor of the NAP in two-sample z tests*

Description

In case of two independent populations $N(\mu_1, \sigma_0^2)$ and $N(\mu_2, \sigma_0^2)$ with known common variance σ_0^2, consider the two-sample z-test for testing the point null hypothesis of difference in their means $H_0 : \mu_2 - \mu_1 = 0$ against $H_1 : \mu_2 - \mu_1 \neq 0$. Based on an observed data, this function calculates the Bayes factor in favor of H_1 when a *normal moment prior* is assumed on the difference between standardized effect sizes $(\mu_2 - \mu_1)/\sigma_0$ under the alternative.

Usage

```
NAPBF_twoz(obs1, obs2, n1Obs, n2Obs,
           mean.obs1, mean.obs2, test.statistic,
           tau.NAP = 0.3/sqrt(2), sigma0 = 1)
```

Arguments

obs1	Numeric vector. Observed vector of data from Group-1.
obs2	Numeric vector. Observed vector of data from Group-2.
n1Obs	Numeric or numeric vector. Sample size(s) from Group-1. Same as `length(obs1)` when numeric.
n2Obs	Numeric or numeric vector. Sample size(s) from Group-2. Same as `length(obs2)` when numeric.
mean.obs1	Numeric or numeric vector. Sample mean(s) from Group-1. Same as `mean(obs1)` when numeric.
mean.obs2	Numeric or numeric vector. Sample mean(s) from Group-2. Same as `mean(obs2)` when numeric.
test.statistic	Numeric or numeric vector. Test-statistic value(s).
tau.NAP	Positive numeric. Parameter in the moment prior. **Default:** $0.3/\sqrt{2}$. This places the prior modes of $(\mu_2 - \mu_1)/\sigma_0$ at 0.3 and -0.3.
sigma0	Positive numeric. Known common standard deviation of the populations. **Default:** 1.

Details

- A user can either specify `obs1` and `obs2`, or `n1Obs`, `n2Obs`, `mean.obs1` and `mean.obs2`, or `n1Obs`, `n2Obs`, and `test.statistic`.
- If `obs1` and `obs2` are provided, it returns the corresponding Bayes factor value.
- If `n1Obs`, `n2Obs`, `mean.obs1` and `mean.obs2` are provided, the function is vectorized over the arguments. Bayes factor values corresponding to the values therein are returned.
- If `n1Obs`, `n2Obs`, and `test.statistic` are provided, the function is vectorized over each of the arguments. Bayes factor values corresponding to the values therein are returned.

Value

Positive numeric or numeric vector. The Bayes factor value(s).

Author(s)

Sandipan Pramanik and Valen E. Johnson

References

Pramanik, S. and Johnson, V. (2022). *Efficient Alternatives for Bayesian Hypothesis Tests in Psychology. Psychological Methods. Just accepted.*

Johnson, V. and Rossell, R. (2010). *On the use of non-local prior densities in Bayesian hypothesis tests. Journal of the Royal Statistical Society: Series B, 72:143-170.* [Article]

Examples

```
NAPBF_twoz(obs1 = rnorm(100), obs2 = rnorm(100))
```

`SBFHajnal_onet` *Sequential Bayes Factor using the Hajnal's ratio for one-sample t-tests*

Description

In a $N(\mu, \sigma^2)$ population with unknown variance σ^2, consider the two-sided one-sample t-test for testing the point null hypothesis $H_0 : \mu = 0$ against $H_1 : \mu \neq 0$. This function calculates the operating characteristics (OC) and average sample number (ASN) of the Sequential Bayes Factor design when the prior assumed on the standardized effect size μ/σ under the alternative places equal probability at $+\delta$ and $-\delta$ ($\delta > 0$ prefixed).

Usage

```
SBFHajnal_onet(es = c(0, 0.2, 0.3, 0.5), es1 = 0.3,
               nmin = 2, nmax = 5000,
               RejectH1.threshold = exp(-3), RejectH0.threshold = exp(3),
               batch.size.increment, nReplicate = 50000, nCore)
```

Arguments

`es` Numeric vector. Standardized effect sizes μ/σ where OC and ASN are desired. **Default:** `c(0,0.2,0.3,0.5)`.

`es1` Positive numeric. δ as above. **Default:** 0.3. For this, the prior on the standardized effect size μ/σ takes values 0.3 and -0.3 each with equal probability 1/2.

`nmin` Positive integer. Minimum sample size in the sequential comparison. Should be at least 2. **Default:** 1.

`nmax` Positive integer. Maximum sample size in the sequential comparison. **Default:** 1.

`RejectH1.threshold` Positive numeric. H_0 is accepted if BF $\leq$`RejectH1.threshold`. **Default:** `exp(-3)`.

`RejectH0.threshold` Positive numeric. H_0 is rejected if BF $\geq$`RejectH0.threshold`. **Default:** `exp(3)`.

`batch.size.increment` function. Increment in sample size at each sequential step. **Default:** `function(narg){20}`. This means an increment of 20 samples at each step.

`nReplicate` Positve integer. Number of replicated studies based on which the OC and ASN are calculated. **Default:** 50,000.

`nCore` Positive integer. **Default:** One less than the total number of available cores.

Value

A list with three components named summary, BF, and N.

$summary is a data frame with columns effect.size containing the values in es. At those values, acceptH0 contains the proportion of times H_0 is accepted, rejectH0 contains the proportion of times H_0 is rejected, inconclusive contains the proportion of times the test is inconclusive, ASN contains the ASN, and avg.logBF contains the expected weight of evidence values.

$BF is a matrix of dimension length(es) by nReplicate. Each row contains the Bayes factor values at the corresponding standardized effec size in nReplicate replicated studies.

$N is a matrix of the same dimension as $BF. Each row contains the sample size required to reach a decision at the corresponding standardized effec size in nReplicate replicated studies.

Author(s)

Sandipan Pramanik and Valen E. Johnson

References

Hajnal, J. (1961). *A two-sample sequential t-test.Biometrika, 48:65-75*, [Article].

Schnuerch, M. and Erdfelder, E. (2020). *A two-sample sequential t-test.Biometrika, 48:65-75*, [Article].

Examples

```
out = SBFHajnal_onet(nmax = 50, es = c(0, 0.3), nCore = 1)
```

SBFHajnal_onez   *Sequential Bayes Factor using the Hajnal's ratio for one-sample z-tests*

Description

In a $N(\mu, \sigma_0^2)$ population with known variance σ_0^2, consider the two-sided one-sample z-test for testing the point null hypothesis $H_0 : \mu = 0$ against $H_1 : \mu \neq 0$. This function calculates the operating characteristics (OC) and average sample number (ASN) of the Sequential Bayes Factor design when the prior assumed on the standardized effect size μ/σ_0 under the alternative places equal probability at $+\delta$ and $-\delta$ ($\delta > 0$ prefixed).

Usage

```
SBFHajnal_onez(es = c(0, 0.2, 0.3, 0.5), es1 = 0.3,
               nmin = 1, nmax = 5000, sigma0 = 1,
               RejectH1.threshold = exp(-3), RejectH0.threshold = exp(3),
               batch.size.increment, nReplicate = 50000, nCore)
```

Arguments

- `es` Numeric vector. Standardized effect sizes μ/σ_0 where OC and ASN are desired. **Default:** `c(0,0.2,0.3,0.5)`.
- `es1` Positive numeric. δ as above. **Default:** 0.3. For this, the prior on the standardized effect size μ/σ_0 takes values 0.3 and -0.3 each with equal probability 1/2.
- `nmin` Positive integer. Minimum sample size in the sequential comparison. **Default:** 1.
- `nmax` Positive integer. Maximum sample size in the sequential comparison. **Default:** 1.
- `sigma0` Positive numeric. Known standard deviation in the population. **Default:** 1.
- `RejectH1.threshold` Positive numeric. H_0 is accepted if BF $\leq$`RejectH1.threshold`. **Default:** `exp(-3)`.
- `RejectH0.threshold` Positive numeric. H_0 is rejected if BF $\geq$`RejectH0.threshold`. **Default:** `exp(3)`.
- `batch.size.increment` function. Increment in sample size at each sequential step. **Default:** `function(narg){20}`. This means an increment of 20 samples at each step.
- `nReplicate` Positve integer. Number of replicated studies based on which the OC and ASN are calculated. **Default:** 50,000.
- `nCore` Positive integer. **Default:** One less than the total number of available cores.

Value

A list with three components named `summary`, `BF`, and `N`.

`$summary` is a data frame with columns `effect.size` containing the values in `es`. At those values, `acceptH0` contains the proportion of times `H_0` is accepted, `rejectH0` contains the proportion of times `H_0` is rejected, `inconclusive` contains the proportion of times the test is inconclusive, `ASN` contains the ASN, and `avg.logBF` contains the expected weight of evidence values.

`$BF` is a matrix of dimension `length(es)` by `nReplicate`. Each row contains the Bayes factor values at the corresponding standardized effec size in `nReplicate` replicated studies.

`$N` is a matrix of the same dimension as `$BF`. Each row contains the sample size required to reach a decision at the corresponding standardized effec size in `nReplicate` replicated studies.

Author(s)

Sandipan Pramanik and Valen E. Johnson

References

Hajnal, J. (1961). *A two-sample sequential t-test.Biometrika, 48:65-75*, [Article].

Schnuerch, M. and Erdfelder, E. (2020). *A two-sample sequential t-test.Biometrika, 48:65-75*, [Article].

Examples

```
out = SBFHajnal_onez(nmax = 100, es = c(0, 0.3), nCore = 1)
```

`SBFHajnal_twot` *Sequential Bayes Factor using the Hajnal's ratio for two-sample t-tests*

Description

In case of two independent populations $N(\mu_1, \sigma^2)$ and $N(\mu_2, \sigma^2)$ with unknown common variance σ^2, consider the two-sample t-test for testing the point null hypothesis of difference in their means $H_0 : \mu_2 - \mu_1 = 0$ against $H_1 : \mu_2 - \mu_1 \neq 0$. This function calculates the operating characteristics (OC) and average sample number (ASN) of the Sequential Bayes Factor design when the prior assumed under the alternative on the difference between standardized effect sizes $(\mu_2 - \mu_1)/\sigma$ places equal probability at $+\delta$ and $-\delta$ ($\delta > 0$ prefixed).

Usage

```
SBFHajnal_twot(es = c(0, 0.2, 0.3, 0.5), es1 = 0.3,
               n1min = 2, n2min = 2, n1max = 5000, n2max = 5000,
               RejectH1.threshold = exp(-3), RejectH0.threshold = exp(3),
               batch1.size.increment, batch2.size.increment,
               nReplicate = 50000, nCore)
```

Arguments

`es` Numeric vector. Standardized effect size differences $(\mu_2 - \mu_1)/\sigma$ where OC and ASN are desired. **Default:** `c(0,0.2,0.3,0.5)`.

`es1` Positive numeric. δ as above. **Default:** 0.3. For this, the prior on $(\mu_2 - \mu_1)/\sigma$ takes values 0.3 and -0.3 each with equal probability 1/2.

`n1min` Positive integer. Minimum sample size from Group-1 in the sequential comparison. Should be at least 2. **Default:** 1.

`n2min` Positive integer. Minimum sample size from Group-2 in the sequential comparison. Should be at least 2. **Default:** 1.

`n1max` Positive integer. Maximum sample size from Group-1 in the sequential comparison. **Default:** 1.

`n2max` Positive integer. Maximum sample size from Group-2 in the sequential comparison. **Default:** 1.

`RejectH1.threshold`
Positive numeric. H_0 is accepted if $BF \leq$`RejectH1.threshold`. **Default:** `exp(-3)`.

`RejectH0.threshold`
Positive numeric. H_0 is rejected if $BF \geq$`RejectH0.threshold`. **Default:** `exp(3)`.

batch1.size.increment
: function. Increment in sample size from Group-1 at each sequential step. **Default:** `function(narg){20}`. This means an increment of 20 samples at each step.

batch2.size.increment
: function. Increment in sample size from Group-2 at each sequential step. **Default:** `function(narg){20}`. This means an increment of 20 samples at each step.

nReplicate
: Positve integer. Number of replicated studies based on which the OC and ASN are calculated. **Default:** 50,000.

nCore
: Positive integer. **Default:** One less than the total number of available cores.

Value

A list with three components named `summary`, `BF`, and `N`.

`$summary` is a data frame with columns `effect.size` containing the values in `es`. At those values, `acceptH0` contains the proportion of times `H_0` is accepted, `rejectH0` contains the proportion of times `H_0` is rejected, `inconclusive` contains the proportion of times the test is inconclusive, `ASN` contains the ASN, and `avg.logBF` contains the expected weight of evidence values.

`$BF` is a matrix of dimension `length(es)` by `nReplicate`. Each row contains the Bayes factor values at the corresponding standardized effec size in `nReplicate` replicated studies.

`$N` is a matrix of the same dimension as `$BF`. Each row contains the sample size required to reach a decision at the corresponding standardized effec size in `nReplicate` replicated studies.

Author(s)

Sandipan Pramanik and Valen E. Johnson

References

Hajnal, J. (1961). *A two-sample sequential t-test.Biometrika, 48:65-75*, [Article].

Schnuerch, M. and Erdfelder, E. (2020). *A two-sample sequential t-test.Biometrika, 48:65-75*, [Article].

Examples

```
out = SBFHajnal_twot(n1max = 100, n2max = 100, es = c(0, 0.3), nCore = 1)
```

SBFHajnal_twoz	*Sequential Bayes Factor using the Hajnal's ratio for two-sample z-tests*

Description

In case of two independent populations $N(\mu_1, \sigma_0^2)$ and $N(\mu_2, \sigma_0^2)$ with known common variance σ_0^2, consider the two-sample z-test for testing the point null hypothesis of difference in their means $H_0 : \mu_2 - \mu_1 = 0$ against $H_1 : \mu_2 - \mu_1 \neq 0$. This function calculates the operating characteristics (OC) and average sample number (ASN) of the Sequential Bayes Factor design when the prior assumed under the alternative on the difference between standardized effect sizes $(\mu_2 - \mu_1)/\sigma_0$ places equal probability at $+\delta$ and $-\delta$ ($\delta > 0$ prefixed).

Usage

```
SBFHajnal_twoz(es = c(0, 0.2, 0.3, 0.5), es1 = 0.3,
               n1min = 1, n2min = 1, n1max = 5000, n2max = 5000, sigma0 = 1,
               RejectH1.threshold = exp(-3), RejectH0.threshold = exp(3),
               batch1.size.increment, batch2.size.increment,
               nReplicate = 50000, nCore)
```

Arguments

es
: Numeric vector. Standardized effect size differences $(\mu_2 - \mu_1)/\sigma_0$ where OC and ASN are desired. **Default:** `c(0,0.2,0.3,0.5)`.

es1
: Positive numeric. δ as above. **Default:** 0.3. For this, the prior on $(\mu_2 - \mu_1)/\sigma_0$ takes values 0.3 and -0.3 each with equal probability 1/2.

n1min
: Positive integer. Minimum sample size from Group-1 in the sequential comparison. **Default:** 1.

n2min
: Positive integer. Minimum sample size from Group-2 in the sequential comparison. **Default:** 1.

n1max
: Positive integer. Maximum sample size from Group-1 in the sequential comparison. **Default:** 1.

n2max
: Positive integer. Maximum sample size from Group-2 in the sequential comparison. **Default:** 1.

sigma0
: Positive numeric. Known common standard deviation of the populations. **Default:** 1.

RejectH1.threshold
: Positive numeric. H_0 is accepted if $BF \leq$`RejectH1.threshold`. **Default:** `exp(-3)`.

RejectH0.threshold
: Positive numeric. H_0 is rejected if $BF \geq$`RejectH0.threshold`. **Default:** `exp(3)`.

batch1.size.increment
: function. Increment in sample size from Group-1 at each sequential step. **Default:** `function(narg){20}`. This means an increment of 20 samples at each step.

batch2.size.increment
: function. Increment in sample size from Group-2 at each sequential step. **Default:** `function(narg){20}`. This means an increment of 20 samples at each step.

nReplicate
: Positve integer. Number of replicated studies based on which the OC and ASN are calculated. **Default:** 50,000.

nCore
: Positive integer. **Default:** One less than the total number of available cores.

Value

A list with three components named `summary`, `BF`, and `N`.

`$summary` is a data frame with columns `effect.size` containing the values in `es`. At those values, `acceptH0` contains the proportion of times `H_0` is accepted, `rejectH0` contains the proportion of times `H_0` is rejected, `inconclusive` contains the proportion of times the test is inconclusive, `ASN` contains the ASN, and `avg.logBF` contains the expected weight of evidence values.

`$BF` is a matrix of dimension `length(es)` by `nReplicate`. Each row contains the Bayes factor values at the corresponding standardized effec size in `nReplicate` replicated studies.

`$N` is a matrix of the same dimension as `$BF`. Each row contains the sample size required to reach a decision at the corresponding standardized effec size in `nReplicate` replicated studies.

Author(s)

Sandipan Pramanik and Valen E. Johnson

References

Hajnal, J. (1961). *A two-sample sequential t-test.Biometrika, 48:65-75*, [Article].

Schnuerch, M. and Erdfelder, E. (2020). *A two-sample sequential t-test.Biometrika, 48:65-75*, [Article].

Examples

```
out = SBFHajnal_twoz(n1max = 100, n2max = 100, es = c(0, 0.3), nCore = 1)
```

SBFNAP_onet *Sequential Bayes Factor using the NAP for one-sample t-tests*

Description

In a $N(\mu, \sigma^2)$ population with unknown variance σ^2, consider the two-sided one-sample t-test for testing the point null hypothesis $H_0 : \mu = 0$ against $H_1 : \mu \neq 0$. This function calculates the operating characteristics (OC) and average sample number (ASN) of the Sequential Bayes Factor design when a *normal moment prior* is assumed on the standardized effect size μ/σ under the alternative.

Usage

```
SBFNAP_onet(es = c(0, 0.2, 0.3, 0.5), nmin = 2, nmax = 5000,
            tau.NAP = 0.3/sqrt(2),
            RejectH1.threshold = exp(-3), RejectH0.threshold = exp(3),
            batch.size.increment, nReplicate = 50000, nCore)
```

Arguments

`es`	Numeric vector. Standardized effect sizes μ/σ where OC and ASN are desired. **Default:** `c(0,0.2,0.3,0.5)`.
`nmin`	Positive integer. Minimum sample size in the sequential comparison. Should be at least 2. **Default:** 1.
`nmax`	Positive integer. Maximum sample size in the sequential comparison. **Default:** 1.
`tau.NAP`	Positive numeric. Parameter in the moment prior. **Default:** $0.3/\sqrt{2}$. This places the prior modes of the standardized effect size μ/σ at 0.3 and -0.3.
`RejectH1.threshold`	Positive numeric. H_0 is accepted if BF ≤`RejectH1.threshold`. **Default:** `exp(-3)`.
`RejectH0.threshold`	Positive numeric. H_0 is rejected if BF ≥`RejectH0.threshold`. **Default:** `exp(3)`.
`batch.size.increment`	function. Increment in sample size at each sequential step. **Default:** `function(narg){20}`. This means an increment of 20 samples at each step.
`nReplicate`	Positve integer. Number of replicated studies based on which the OC and ASN are calculated. **Default:** 50,000.
`nCore`	Positive integer. **Default:** One less than the total number of available cores.

Value

A list with three components named summary, BF, and N.

$summary is a data frame with columns effect.size containing the values in es. At those values, acceptH0 contains the proportion of times H_0 is accepted, rejectH0 contains the proportion of times H_0 is rejected, inconclusive contains the proportion of times the test is inconclusive, ASN contains the ASN, and avg.logBF contains the expected weight of evidence values.

$BF is a matrix of dimension length(es) by nReplicate. Each row contains the Bayes factor values at the corresponding standardized effec size in nReplicate replicated studies.

$N is a matrix of the same dimension as $BF. Each row contains the sample size required to reach a decision at the corresponding standardized effec size in nReplicate replicated studies.

Author(s)

Sandipan Pramanik and Valen E. Johnson

References

Pramanik, S. and Johnson, V. (2022). *Efficient Alternatives for Bayesian Hypothesis Tests in Psychology. Psychological Methods. Just accepted.*

Johnson, V. and Rossell, R. (2010). *On the use of non-local prior densities in Bayesian hypothesis tests. Journal of the Royal Statistical Society: Series B, 72:143-170.* [Article]

Examples

```
out = SBFNAP_onet(nmax = 100, es = c(0, 0.3), nCore = 1)
```

SBFNAP_onez — *Sequential Bayes Factor using the NAP for one-sample z-tests*

Description

In a $N(\mu, \sigma_0^2)$ population with known variance σ_0^2, consider the two-sided one-sample z-test for testing the point null hypothesis $H_0 : \mu = 0$ against $H_1 : \mu \neq 0$. This function calculates the operating characteristics (OC) and average sample number (ASN) of the Sequential Bayes Factor design when a *normal moment prior* is assumed on the standardized effect size μ/σ_0 under the alternative.

Usage

```
SBFNAP_onez(es = c(0, 0.2, 0.3, 0.5), nmin = 1, nmax = 5000,
            tau.NAP = 0.3/sqrt(2), sigma0 = 1,
            RejectH1.threshold = exp(-3), RejectH0.threshold = exp(3),
            batch.size.increment, nReplicate = 50000, nCore)
```

Arguments

- `es` — Numeric vector. Standardized effect sizes μ/σ_0 where OC and ASN are desired. **Default:** `c(0,0.2,0.3,0.5)`.
- `nmin` — Positive integer. Minimum sample size in the sequential comparison. **Default:** 1.
- `nmax` — Positive integer. Maximum sample size in the sequential comparison. **Default:** 1.
- `tau.NAP` — Positive numeric. Parameter in the moment prior. **Default:** $0.3/\sqrt{2}$. This places the prior modes of the standardized effect size μ/σ_0 at 0.3 and -0.3.
- `sigma0` — Positive numeric. Known standard deviation in the population. **Default:** 1.
- `RejectH1.threshold` — Positive numeric. H_0 is accepted if BF ≤`RejectH1.threshold`. **Default:** `exp(-3)`.
- `RejectH0.threshold` — Positive numeric. H_0 is rejected if BF ≥`RejectH0.threshold`. **Default:** `exp(3)`.
- `batch.size.increment` — function. Increment in sample size at each sequential step. **Default:** `function(narg){20}`. This means an increment of 20 samples at each step.
- `nReplicate` — Positve integer. Number of replicated studies based on which the OC and ASN are calculated. **Default:** 50,000.
- `nCore` — Positive integer. **Default:** One less than the total number of available cores.

Value

A list with three components named `summary`, `BF`, and `N`.

`$summary` is a data frame with columns `effect.size` containing the values in `es`. At those values, `acceptH0` contains the proportion of times `H_0` is accepted, `rejectH0` contains the proportion of times `H_0` is rejected, `inconclusive` contains the proportion of times the test is inconclusive, `ASN` contains the ASN, and `avg.logBF` contains the expected weight of evidence values.

`$BF` is a matrix of dimension `length(es)` by `nReplicate`. Each row contains the Bayes factor values at the corresponding standardized effec size in `nReplicate` replicated studies.

`$N` is a matrix of the same dimension as `$BF`. Each row contains the sample size required to reach a decision at the corresponding standardized effec size in `nReplicate` replicated studies.

Author(s)

Sandipan Pramanik and Valen E. Johnson

References

Pramanik, S. and Johnson, V. (2022). *Efficient Alternatives for Bayesian Hypothesis Tests in Psychology. Psychological Methods. Just accepted.*

Johnson, V. and Rossell, R. (2010). *On the use of non-local prior densities in Bayesian hypothesis tests. Journal of the Royal Statistical Society: Series B, 72:143-170.* [Article]

Examples

```
out = SBFNAP_onez(nmax = 100, es = c(0, 0.3), nCore = 1)
```

SBFNAP_twot *Sequential Bayes Factor using the NAP for two-sample t-tests*

Description

In case of two independent populations $N(\mu_1, \sigma^2)$ and $N(\mu_2, \sigma^2)$ with unknown common variance σ^2, consider the two-sample z-test for testing the point null hypothesis of difference in their means $H_0 : \mu_2 - \mu_1 = 0$ against $H_1 : \mu_2 - \mu_1 \neq 0$. This function calculates the operating characteristics (OC) and average sample number (ASN) of the Sequential Bayes Factor design when a *normal moment prior* is assumed on the difference between standardized effect sizes $(\mu_2 - \mu_1)/\sigma$ under the alternative.

Usage

```
SBFNAP_twot(es = c(0, 0.2, 0.3, 0.5), n1min = 2, n2min = 2,
            n1max = 5000, n2max = 5000,
            tau.NAP = 0.3/sqrt(2),
            RejectH1.threshold = exp(-3), RejectH0.threshold = exp(3),
            batch1.size.increment, batch2.size.increment,
            nReplicate = 50000, nCore)
```

Arguments

`es` Numeric vector. Standardized effect size differences $(\mu_2 - \mu_1)/\sigma$ where OC and ASN are desired. **Default:** `c(0,0.2,0.3,0.5)`.

`n1min` Positive integer. Minimum sample size from Group-1 in the sequential comparison. Should be at least 2. **Default:** 1.

`n2min` Positive integer. Minimum sample size from Group-2 in the sequential comparison. Should be at least 2. **Default:** 1.

`n1max` Positive integer. Maximum sample size from Group-1 in the sequential comparison. **Default:** 1.

`n2max` Positive integer. Maximum sample size from Group-2 in the sequential comparison. **Default:** 1.

`tau.NAP` Positive numeric. Parameter in the moment prior. **Default:** $0.3/\sqrt{2}$. This places the prior modes of $(\mu_2 - \mu_1)/\sigma$ at 0.3 and -0.3.

`RejectH1.threshold` Positive numeric. H_0 is accepted if $BF \leq$`RejectH1.threshold`. **Default:** `exp(-3)`.

`RejectH0.threshold` Positive numeric. H_0 is rejected if $BF \geq$`RejectH0.threshold`. **Default:** `exp(3)`.

batch1.size.increment
: function. Increment in sample size from Group-1 at each sequential step. **Default:** `function(narg){20}`. This means an increment of 20 samples at each step.

batch2.size.increment
: function. Increment in sample size from Group-2 at each sequential step. **Default:** `function(narg){20}`. This means an increment of 20 samples at each step.

nReplicate
: Positve integer. Number of replicated studies based on which the OC and ASN are calculated. **Default:** 50,000.

nCore
: Positive integer. **Default:** One less than the total number of available cores.

Value

A list with three components named `summary`, `BF`, and `N`.

`$summary` is a data frame with columns `effect.size` containing the values in `es`. At those values, `acceptH0` contains the proportion of times `H_0` is accepted, `rejectH0` contains the proportion of times `H_0` is rejected, `inconclusive` contains the proportion of times the test is inconclusive, `ASN` contains the ASN, and `avg.logBF` contains the expected weight of evidence values.

`$BF` is a matrix of dimension `length(es)` by `nReplicate`. Each row contains the Bayes factor values at the corresponding standardized effec size in `nReplicate` replicated studies.

`$N` is a matrix of the same dimension as `$BF`. Each row contains the sample size required to reach a decision at the corresponding standardized effec size in `nReplicate` replicated studies.

Author(s)

Sandipan Pramanik and Valen E. Johnson

References

Pramanik, S. and Johnson, V. (2022). *Efficient Alternatives for Bayesian Hypothesis Tests in Psychology. Psychological Methods. Just accepted.*

Johnson, V. and Rossell, R. (2010). *On the use of non-local prior densities in Bayesian hypothesis tests. Journal of the Royal Statistical Society: Series B, 72:143-170.* [Article]

Examples

```
out = SBFNAP_twot(n1max = 100, n2max = 100, es = c(0, 0.3), nCore = 1)
```

SBFNAP_twoz *Sequential Bayes Factor using the NAP for two-sample z-tests*

Description

In case of two independent populations $N(\mu_1, \sigma_0^2)$ and $N(\mu_2, \sigma_0^2)$ with known common variance σ_0^2, consider the two-sample z-test for testing the point null hypothesis of difference in their means $H_0 : \mu_2 - \mu_1 = 0$ against $H_1 : \mu_2 - \mu_1 \neq 0$. This function calculates the operating characteristics (OC) and average sample number (ASN) of the Sequential Bayes Factor design when a *normal moment prior* is assumed on the difference between standardized effect sizes $(\mu_2 - \mu_1)/\sigma_0$ under the alternative.

Usage

```
SBFNAP_twoz(es = c(0, 0.2, 0.3, 0.5), n1min = 1, n2min = 1,
            n1max = 5000, n2max = 5000,
            tau.NAP = 0.3/sqrt(2), sigma0 = 1,
            RejectH1.threshold = exp(-3), RejectH0.threshold = exp(3),
            batch1.size.increment, batch2.size.increment,
            nReplicate = 50000, nCore)
```

Arguments

`es` Numeric vector. Standardized effect size differences $(\mu_2 - \mu_1)/\sigma_0$ where OC and ASN are desired. **Default:** `c(0,0.2,0.3,0.5)`.

`n1min` Positive integer. Minimum sample size from Group-1 in the sequential comparison. **Default:** 1.

`n2min` Positive integer. Minimum sample size from Group-2 in the sequential comparison. **Default:** 1.

`n1max` Positive integer. Maximum sample size from Group-1 in the sequential comparison. **Default:** 1.

`n2max` Positive integer. Maximum sample size from Group-2 in the sequential comparison. **Default:** 1.

`tau.NAP` Positive numeric. Parameter in the moment prior. **Default:** $0.3/\sqrt{2}$. This places the prior modes of $(\mu_2 - \mu_1)/\sigma_0$ at 0.3 and -0.3.

`sigma0` Positive numeric. Known common standard deviation of the populations. **Default:** 1.

`RejectH1.threshold`
Positive numeric. H_0 is accepted if $BF \leq$`RejectH1.threshold`. **Default:** `exp(-3)`.

`RejectH0.threshold`
Positive numeric. H_0 is rejected if $BF \geq$`RejectH0.threshold`. **Default:** `exp(3)`.

`batch1.size.increment`
: function. Increment in sample size from Group-1 at each sequential step. **Default:** `function(narg){20}`. This means an increment of 20 samples at each step.

`batch2.size.increment`
: function. Increment in sample size from Group-2 at each sequential step. **Default:** `function(narg){20}`. This means an increment of 20 samples at each step.

`nReplicate`
: Positve integer. Number of replicated studies based on which the OC and ASN are calculated. **Default:** 50,000.

`nCore`
: Positive integer. **Default:** One less than the total number of available cores.

Value

A list with three components named `summary`, `BF`, and `N`.

`$summary` is a data frame with columns `effect.size` containing the values in `es`. At those values, `acceptH0` contains the proportion of times `H_0` is accepted, `rejectH0` contains the proportion of times `H_0` is rejected, `inconclusive` contains the proportion of times the test is inconclusive, `ASN` contains the ASN, and `avg.logBF` contains the expected weight of evidence values.

`$BF` is a matrix of dimension `length(es)` by `nReplicate`. Each row contains the Bayes factor values at the corresponding standardized effec size in `nReplicate` replicated studies.

`$N` is a matrix of the same dimension as `$BF`. Each row contains the sample size required to reach a decision at the corresponding standardized effec size in `nReplicate` replicated studies.

Author(s)

Sandipan Pramanik and Valen E. Johnson

References

Pramanik, S. and Johnson, V. (2022). *Efficient Alternatives for Bayesian Hypothesis Tests in Psychology. Psychological Methods. Just accepted.*

Johnson, V. and Rossell, R. (2010). *On the use of non-local prior densities in Bayesian hypothesis tests. Journal of the Royal Statistical Society: Series B, 72:143-170.* [Article]

Examples

```
out = SBFNAP_twoz(n1max = 100, n2max = 100, es = c(0, 0.3), nCore = 1)
```

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