

# Package ‘NAP’

November 1, 2021

**Type** Package

**Title** Non-local Alternative Priors in Psychology

**Version** 1.0

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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. 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

## R topics documented:

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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. 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: 1.0  
 Date: 2021-10-30  
 License: GPL ( $\geq 2$ )

**Author(s)**

Sandipan Pramanik [aut, cre], Valen E. Johnson [aut]  
 Maintainer: Sandipan Pramanik <sandy@stat.tamu.edu>

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|                     |   |
|---------------------|---|
| fixedHajnal.oneT_es | <i>Fixed-design one-sample t-tests using Hajnal's ratio for varied sample sizes</i> |
|---------------------|---|

---

**Description**

In two-sided fixed design one-sample  $t$ -tests with *composite alternative prior* assumed on the standardized effect size  $\mu/\sigma$  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.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. <b>Default:</b> 0.   |
| es1                  | Positive numeric. <b>Default:</b> 0.3. For this, the composite alternative prior on the standardized effect size $\mu/\sigma$ takes values 0.3 and $-0.3$ each with equal probability 1/2.  |
| nmin                 | Positive integer. Minimum sample size to be considered. <b>Default:</b> 20.   |
| nmax                 | Positive integer. Maximum sample size to be considered. <b>Default:</b> 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. <b>Default:</b> function(narg){20}. This means an increment of 20 samples at each step. |
| nReplicate           | Positive integer. Number of replicated studies based on which the expected weights of evidence is calculated. <b>Default:</b> 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 | <i>Fixed-design one-sample t-tests using Hajnal's ratio and a pre-fixed sample size</i> |
|--------------------|---|

---

**Description**

In two-sided fixed design one-sample *t*-tests with *composite alternative prior* assumed on the standardized effect size  $\mu/\sigma$  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**

|                         |  |
|-------------------------|--|
| <code>es1</code>        | Positive numeric. <b>Default:</b> 0.3. For this, the composite alternative prior on the standardized effect size $\mu/\sigma$ takes values 0.3 and $-0.3$ each with equal probability 1/2. |
| <code>es</code>         | Numeric vector. Standardized effect sizes $\mu/\sigma$ where the expected weights of evidence is desired. <b>Default:</b> <code>c(0, 0.2, 0.3, 0.5)</code> .                               |
| <code>n.fixed</code>    | Positive integer. Prefixed sample size. <b>Default:</b> 20.  |
| <code>nReplicate</code> | Positive integer. Number of replicated studies based on which the expected weights of evidence is calculated. <b>Default:</b> 50,000.  |
| <code>nCore</code>      | Positive integer. <b>Default:</b> 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 effect 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**

```
## Not run:
out = fixedHajnal.oneT_n(n.fixed = 20, es = c(0, 0.3), nCore = 1)

## End(Not run)
```

---

|                     |   |
|---------------------|---|
| fixedHajnal.oneZ_es | <i>Fixed-design one-sample z-tests using Hajnal's ratio for varied sample sizes</i> |
|---------------------|---|

---

**Description**

In two-sided fixed design one-sample  $z$ -tests with *composite alternative prior* assumed on the standardized effect size  $\mu/\sigma_0$  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.oneZ_es(es = 0, es1 = 0.3, nmin = 20, nmax = 5000,
  sigma0 = 1, batch.size.increment, nReplicate = 50000)
```

**Arguments**

|                     |  |
|---------------------|--|
| <code>es</code>     | Numeric. Standardized effect size where the expected weights of evidence is desired. <b>Default:</b> 0.  |
| <code>es1</code>    | Positive numeric. <b>Default:</b> 0.3. For this, the composite alternative prior on the standardized effect size $\mu/\sigma_0$ takes values 0.3 and $-0.3$ each with equal probability 1/2. |
| <code>nmin</code>   | Positive integer. Minimum sample size to be considered. <b>Default:</b> 20.  |
| <code>nmax</code>   | Positive integer. Maximum sample size to be considered. <b>Default:</b> 5000.  |
| <code>sigma0</code> | Positive numeric. Known standard deviation in the population. <b>Default:</b> 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` Positive 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)
```

---

|                                 |   |
|---------------------------------|---|
| <code>fixedHajnal.oneZ_n</code> | <i>Fixed-design one-sample z-tests using Hajnal's ratio and a pre-fixed sample size</i> |
|---------------------------------|---|

---

### Description

In two-sided fixed design one-sample  $z$ -tests with *composite alternative prior* assumed on the standardized effect size  $\mu/\sigma_0$  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. <b>Default:</b> 0.3. For this, the composite alternative prior on the standardized effect size $\mu/\sigma_0$ takes values 0.3 and $-0.3$ each with equal probability 1/2. |
| es         | Numeric vector. Standardized effect sizes $\mu/\sigma_0$ where the expected weights of evidence is desired. <b>Default:</b> <code>c(0, 0.2, 0.3, 0.5)</code> .                               |
| n.fixed    | Positive integer. Prefixed sample size. <b>Default:</b> 20.  |
| sigma0     | Positive numeric. Known standard deviation in the population. <b>Default:</b> 1.   |
| nReplicate | Positive integer. Number of replicated studies based on which the expected weights of evidence is calculated. <b>Default:</b> 50,000.  |
| nCore      | Positive integer. <b>Default:</b> 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 effect 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

```
## Not run:
out = fixedHajnal.oneZ_n(n.fixed = 20, es = c(0, 0.3), nCore = 1)

## End(Not run)
```

---

|                     |   |
|---------------------|---|
| fixedHajnal.twoT_es | <i>Fixed-design two-sample t-tests with NAP for varied sample sizes</i> |
|---------------------|---|

---

## 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. <b>Default:</b> 0.   |
| es1                   | Positive numeric. $\delta$ as above. <b>Default:</b> 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 Grup-1 to be considered. <b>Default:</b> 20.   |
| n2min                 | Positive integer. Minimum sample size from Grup-2 to be considered. <b>Default:</b> 20.   |
| n1max                 | Positive integer. Maximum sample size from Grup-1 to be considered. <b>Default:</b> 5000.   |
| n2max                 | Positive integer. Maximum sample size from Grup-2 to be considered. <b>Default:</b> 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. <b>Default:</b> 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. <b>Default:</b> function(narg){20}. This means an increment of 20 samples from Group-2 at each step. |
| nReplicate            | Positive integer. Number of replicated studies based on which the expected weights of evidence is calculated. <b>Default:</b> 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 | <i>Fixed-design two-sample t-tests using Hajnal's ratio and a pre-fixed sample size</i> |
|--------------------|---|

---

## 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. $\delta$ as above. <b>Default:</b> 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. <b>Default:</b> $c(0, 0.2, 0.3, 0.5)$ . |
| n1.fixed   | Positive integer. Prefixed sample size from Group-1. <b>Default:</b> 20.   |
| n2.fixed   | Positive integer. Prefixed sample size from Group-2. <b>Default:</b> 20.   |
| nReplicate | Positive integer. Number of replicated studies based on which the expected weights of evidence is calculated. <b>Default:</b> 50,000.                                    |
| nCore      | Positive integer. <b>Default:</b> 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 effect 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

```
## Not run:
out = fixedHajnal.twoT_n(n1.fixed = 20, n2.fixed = 20, es = c(0, 0.3), nCore = 1)

## End(Not run)
```

---

|                     |   |
|---------------------|---|
| fixedHajnal.twoZ_es | <i>Fixed-design two-sample z-tests with NAP for varied sample sizes</i> |
|---------------------|---|

---

## 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. <b>Default:</b> 0.   |
| es1                   | Positive numeric. $\delta$ as above. <b>Default:</b> 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. <b>Default:</b> 20.  |
| n2min                 | Positive integer. Minimum sample size from Grpup-2 to be considered. <b>Default:</b> 20.  |
| n1max                 | Positive integer. Maximum sample size from Grpup-1 to be considered. <b>Default:</b> 5000.  |
| n2max                 | Positive integer. Maximum sample size from Grpup-2 to be considered. <b>Default:</b> 5000.  |
| sigma0                | Positive numeric. Known common standard deviation of the populations. <b>Default:</b> 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. <b>Default:</b> 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. <b>Default:</b> function(narg){20}. This means an increment of 20 samples from Group-2 at each step. |
| nReplicate            | Positive integer. Number of replicated studies based on which the expected weights of evidence is calculated. <b>Default:</b> 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)
```

---

|                                 |   |
|---------------------------------|---|
| <code>fixedHajnal.twoZ_n</code> | <i>Fixed-design two-sample z-tests using Hajnal's ratio and a pre-fixed sample size</i> |
|---------------------------------|---|

---

**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**

|                         |   |
|-------------------------|---|
| <code>es1</code>        | Positive numeric. <b>Default:</b> 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.                                 |
| <code>es</code>         | Numeric vector. Standardized effect size differences $(\mu_2 - \mu_1)/\sigma_0$ where the expected weights of evidence is desired. <b>Default:</b> <code>c(0, 0.2, 0.3, 0.5)</code> . |
| <code>n1.fixed</code>   | Positive integer. Prefixed sample size from Group-1. <b>Default:</b> 20.  |
| <code>n2.fixed</code>   | Positive integer. Prefixed sample size from Group-2. <b>Default:</b> 20.  |
| <code>sigma0</code>     | Positive numeric. Known common standard deviation of the populations. <b>Default:</b> 1.  |
| <code>nReplicate</code> | Positive integer. Number of replicated studies based on which the expected weights of evidence is calculated. <b>Default:</b> 50,000.   |
| <code>nCore</code>      | Positive integer. <b>Default:</b> 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 effect 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**

```
## Not run:
out = fixedHajnal.twoZ_n(n1.fixed = 20, n2.fixed = 20, es = c(0, 0.3), nCore = 1)

## End(Not run)
```

---

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  $\mu/\sigma$  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**

|                      |  |
|----------------------|--|
| <code>es</code>      | Numeric. Standardized effect size where the expected weights of evidence is desired. <b>Default:</b> 0.  |
| <code>nmin</code>    | Positive integer. Minimum sample size to be considered. <b>Default:</b> 20.  |
| <code>nmax</code>    | Positive integer. Maximum sample size to be considered. <b>Default:</b> 5000.  |
| <code>tau.NAP</code> | Positive numeric. Parameter in the moment prior. <b>Default:</b> $0.3/\sqrt{2}$ . This places the prior modes of the standardized effect size $\mu/\sigma$ 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

Positive 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

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  $\mu/\sigma$  under the alternative and a prefixed sample size, this function calculates the expected weights of evidence (that is, expected  $\log(\text{Bayes Factor})$ ) 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 $\mu/\sigma$ where the expected weights of evidence is desired. <b>Default:</b> <code>c(0, 0.2, 0.3, 0.5)</code> .                   |
| n.fixed    | Positive integer. Prefixed sample size. <b>Default:</b> 20.  |
| tau.NAP    | Positive numeric. Parameter in the moment prior. <b>Default:</b> $0.3/\sqrt{2}$ . This places the prior modes of the standardized effect size $\mu/\sigma$ at 0.3 and $-0.3$ . |
| nReplicate | Positive integer. Number of replicated studies based on which the expected weights of evidence is calculated. <b>Default:</b> 50,000.  |
| nCore      | Positive integer. <b>Default:</b> 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 effect size in `nReplicate` replicated studies.

**Author(s)**

Sandipan Pramanik and Valen E. Johnson

**References**

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**

```
## Not run:
out = fixedNAP.oneT_n(n.fixed = 20, es = c(0, 0.3), nCore = 1)

## End(Not run)
```

---

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  $\mu/\sigma_0$  under the alternative, this function calculates the expected weights of evidence (that is, expected  $\log(\text{Bayes Factor})$ ) 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. <b>Default:</b> 0.   |
| nmin                 | Positive integer. Minimum sample size to be considered. <b>Default:</b> 20.   |
| nmax                 | Positive integer. Maximum sample size to be considered. <b>Default:</b> 5000.   |
| tau.NAP              | Positive numeric. Parameter in the moment prior. <b>Default:</b> $0.3/\sqrt{2}$ . This places the prior modes of the standardized effect size $\mu/\sigma_0$ at 0.3 and $-0.3$ .  |
| sigma0               | Positive numeric. Known standard deviation in the population. <b>Default:</b> 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. <b>Default:</b> function(narg){20}. This means an increment of 20 samples at each step. |
| nReplicate           | Positive integer. Number of replicated studies based on which the expected weights of evidence is calculated. <b>Default:</b> 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**

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  $\mu/\sigma_0$  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 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 $\mu/\sigma_0$ where the expected weights of evidence is desired. <b>Default:</b> <code>c(0, 0.2, 0.3, 0.5)</code> .                   |
| n.fixed    | Positive integer. Prefixed sample size. <b>Default:</b> 20.  |
| tau.NAP    | Positive numeric. Parameter in the moment prior. <b>Default:</b> $0.3/\sqrt{2}$ . This places the prior modes of the standardized effect size $\mu/\sigma_0$ at 0.3 and $-0.3$ . |
| sigma0     | Positive numeric. Known standard deviation in the population. <b>Default:</b> 1.   |
| nReplicate | Positive integer. Number of replicated studies based on which the expected weights of evidence is calculated. <b>Default:</b> 50,000.  |
| nCore      | Positive integer. <b>Default:</b> 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 effect size in `nReplicate` replicated studies.

## Author(s)

Sandipan Pramanik and Valen E. Johnson

## References

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

```
## Not run:
out = fixedNAP.oneZ_n(n.fixed = 20, es = c(0, 0.3), nCore = 1)

## End(Not run)
```



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  $\log(\text{Bayes Factor})$ ) 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. <b>Default:</b> 0.   |
| n1min                 | Positive integer. Minimum sample size from Grup-1 to be considered. <b>Default:</b> 20.   |
| n2min                 | Positive integer. Minimum sample size from Grup-2 to be considered. <b>Default:</b> 20.   |
| n1max                 | Positive integer. Maximum sample size from Grup-1 to be considered. <b>Default:</b> 5000.   |
| n2max                 | Positive integer. Maximum sample size from Grup-2 to be considered. <b>Default:</b> 5000.   |
| tau.NAP               | Positive numeric. Parameter in the moment prior. <b>Default:</b> $0.3/\sqrt{2}$ . 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. <b>Default:</b> <code>function(narg){20}</code> . 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. <b>Default:</b> <code>function(narg){20}</code> . This means an increment of 20 samples from Group-2 at each step. |
| nReplicate            | Positive integer. Number of replicated studies based on which the expected weights of evidence is calculated. <b>Default:</b> 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**

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 | <i>Fixed-design two-sample t-tests with NAP and a pre-fixed sample size</i> |
|-----------------|---|

---

**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  $\log(\text{Bayes Factor})$ ) 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**

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

**Author(s)**

Sandipan Pramanik and Valen E. Johnson

**References**

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**

```
## Not run:
out = fixedNAP.twoT_n(n1.fixed = 20, n2.fixed = 20, es = c(0, 0.3), nCore = 1)

## End(Not run)
```

---

|                  |   |
|------------------|---|
| fixedNAP.twoZ_es | <i>Fixed-design two-sample z-tests with NAP for varied sample sizes</i> |
|------------------|---|

---

**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  $\log(\text{Bayes Factor})$ ) 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**

|                    |   |
|--------------------|---|
| <code>es</code>    | Numeric. Difference between standardized effect sizes where the expected weights of evidence is desired. <b>Default:</b> 0. |
| <code>n1min</code> | Positive integer. Minimum sample size from Grup-1 to be considered. <b>Default:</b> 20.                                     |
| <code>n2min</code> | Positive integer. Minimum sample size from Grup-2 to be considered. <b>Default:</b> 20.                                     |

|                       |   |
|-----------------------|---|
| n1max                 | Positive integer. Maximum sample size from Grup-1 to be considered. <b>Default:</b> 5000.   |
| n2max                 | Positive integer. Maximum sample size from Grup-2 to be considered. <b>Default:</b> 5000.   |
| tau.NAP               | Positive numeric. Parameter in the moment prior. <b>Default:</b> $0.3/\sqrt{2}$ . 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. <b>Default:</b> 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. <b>Default:</b> 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. <b>Default:</b> function(narg){20}. This means an increment of 20 samples from Group-2 at each step. |
| nReplicate            | Positive integer. Number of replicated studies based on which the expected weights of evidence is calculated. <b>Default:</b> 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

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  $\log(\text{Bayes Factor})$ ) 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. <b>Default:</b> <code>c(0, 0.2, 0.3, 0.5)</code> . |
| n1.fixed   | Positive integer. Prefixed sample size from Group-1. <b>Default:</b> 20.  |
| n2.fixed   | Positive integer. Prefixed sample size from Group-2. <b>Default:</b> 20.  |
| tau.NAP    | Positive numeric. Parameter in the moment prior. <b>Default:</b> $0.3/\sqrt{2}$ . 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. <b>Default:</b> 1.  |
| nReplicate | Positive integer. Number of replicated studies based on which the expected weights of evidence is calculated. <b>Default:</b> 50,000.   |
| nCore      | Positive integer. <b>Default:</b> 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 effect size differences in `nReplicate` replicated studies.

**Author(s)**

Sandipan Pramanik and Valen E. Johnson

**References**

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

```
## Not run:
out = fixedNAP.twoZ_n(n1.fixed = 20, n2.fixed = 20, es = c(0, 0.3), nCore = 1)

## End(Not run)
```

---

HajnalBF\_oneT

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


---

## Description

In a  $N(\mu, \sigma^2)$  population with unknown variance  $\sigma^2$ , 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  $\mu/\sigma$  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 <code>length(obs)</code> when numeric.   |
| mean.obs       | Numeric or numeric vector. Sample mean(s). Same as <code>mean(obs)</code> when numeric.   |
| sd.obs         | Positive numeric or numeric vector. Sample standard deviation(s). Same as <code>sd(obs)</code> when numeric.  |
| test.statistic | Numeric or numeric vector. Test-statistic value(s).   |
| es1            | Positive numeric. $\delta$ as above. <b>Default:</b> 0.3. For this, the prior on the standardized effect size $\mu/\sigma$ 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 | <i>Hajnal's ratio in one-sample z tests</i> |
|---------------|---|

---

## Description

In a  $N(\mu, \sigma_0^2)$  population with known variance  $\sigma_0^2$ , 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  $\mu/\sigma_0$  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. $\delta$ as above. <b>Default:</b> 0.3. For this, the prior on the standardized effect size $\mu/\sigma_0$ takes values 0.3 and $-0.3$ each with equal probability 1/2. |
| sigma0         | Positive numeric. Known standard deviation in the population. <b>Default:</b> 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  $\sigma^2$ , 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. $\delta$ as above. <b>Default:</b> 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 n10bs, n20bs, mean.obs1, mean.obs2, sd.obs1 and sd.obs2, or n10bs, n20bs, and test.statistic.
- If obs1 and obs2 are provided, it returns the corresponding Bayes factor value.
- If n10bs, n20bs, 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 n10bs, n20bs, 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  $\sigma_0^2$ , 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, n10bs, n20bs, 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. $\delta$ as above. <b>Default:</b> 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. <b>Default:</b> 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  $\sigma^2$ , 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  $\mu/\sigma$  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 = T, until.decision.reached = T)
```

## Arguments

|                        |  |
|------------------------|--|
| obs                    | Numeric vector. The vector of sequentially observed data.  |
| es1                    | Positive numeric. $\delta$ as above. <b>Default:</b> 0.3. For this, the prior on the standardized effect size $\mu/\sigma$ takes values 0.3 and $-0.3$ each with equal probability 1/2.                      |
| RejectH1.threshold     | Positive numeric. $H_0$ is accepted if $BF \leq \text{RejectH1.threshold}$ . <b>Default:</b> $\exp(-3)$ .  |
| RejectH0.threshold     | Positive numeric. $H_0$ is rejected if $BF \geq \text{RejectH0.threshold}$ . <b>Default:</b> $\exp(3)$ .   |
| batch.size             | Integer vector. The vector of batch sizes at each sequential comparison. <b>Default:</b> $\text{c}(2, \text{rep}(1, \text{length}(\text{obs})-2))$ .   |
| return.plot            | Logical. Whether a sequential comparison plot to be returned. <b>Default:</b> TRUE.  |
| until.decision.reached | Logical. Whether the sequential comparison is performed until a decision is reached or until the data is observed. <b>Default:</b> 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  $\sigma_0^2$ , 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  $\mu/\sigma_0$  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 = T, until.decision.reached = T)
```

## Arguments

- |                        |  |
|------------------------|--|
| obs                    | Numeric vector. The vector of sequentially observed data.  |
| es1                    | Positive numeric. $\delta$ as above. <b>Default:</b> 0.3. For this, the prior on the standardized effect size $\mu/\sigma_0$ takes values 0.3 and $-0.3$ each with equal probability 1/2.                    |
| sigma0                 | Positive numeric. Known standard deviation in the population. <b>Default:</b> 1.   |
| RejectH1.threshold     | Positive numeric. $H_0$ is accepted if $BF \leq \text{RejectH1.threshold}$ . <b>Default:</b> $\exp(-3)$ .  |
| RejectH0.threshold     | Positive numeric. $H_0$ is rejected if $BF \geq \text{RejectH0.threshold}$ . <b>Default:</b> $\exp(3)$ .   |
| batch.size             | Integer vector. The vector of batch sizes at each sequential comparison. <b>Default:</b> $\text{rep}(1, \text{length}(\text{obs}))$ .  |
| return.plot            | Logical. Whether a sequential comparison plot to be returned. <b>Default:</b> TRUE.  |
| until.decision.reached | Logical. Whether the sequential comparison is performed until a decision is reached or until the data is observed. <b>Default:</b> 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  $\sigma^2$ , 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 = T,
  until.decision.reached = T)
```

**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. $\delta$ as above. <b>Default:</b> 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 $BF \leq \text{RejectH1.threshold}$ . <b>Default:</b> $\exp(-3)$ .  |

RejectH0.threshold

Positive numeric.  $H_0$  is rejected if  $BF \geq \text{RejectH0.threshold}$ . **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:**  $c(2, \text{rep}(1, \text{length}(\text{obs1})-2))$

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:**  $c(2, \text{rep}(1, \text{length}(\text{obs2})-2))$

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  $\sigma_0^2$ , 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 = T,
  until.decision.reached = T)
```

**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.  $\delta$  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  $BF \leq \text{RejectH1.threshold}$ . **Default:**  $\exp(-3)$ .

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

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

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

**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  $\sigma^2$ , 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  $\mu/\sigma$  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 = T, until.decision.reached = T)
```

### 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  $\mu/\sigma$  at 0.3 and  $-0.3$ .

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

**RejectH0.threshold** Positive numeric.  $H_0$  is rejected if  $BF \geq \text{RejectH0.threshold}$ . **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:**  $\text{c}(2, \text{rep}(1, \text{length}(\text{obs})-2))$ .

**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

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  $\sigma_0^2$ , 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  $\mu/\sigma_0$  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 = T, until.decision.reached = T)
```

## Arguments

|                        |  |
|------------------------|--|
| obs                    | Numeric vector. The vector of sequentially observed data.  |
| tau.NAP                | Positive numeric. Parameter in the moment prior. <b>Default:</b> $0.3/\sqrt{2}$ . This places the prior modes of the standardized effect size $\mu/\sigma_0$ at 0.3 and $-0.3$ .                             |
| sigma0                 | Positive numeric. Known standard deviation in the population. <b>Default:</b> 1.   |
| RejectH1.threshold     | Positive numeric. $H_0$ is accepted if $BF \leq \text{RejectH1.threshold}$ . <b>Default:</b> $\exp(-3)$ .  |
| RejectH0.threshold     | Positive numeric. $H_0$ is rejected if $BF \geq \text{RejectH0.threshold}$ . <b>Default:</b> $\exp(3)$ .   |
| batch.size             | Integer vector. The vector of batch sizes at each sequential comparison. <b>Default:</b> $\text{rep}(1, \text{length}(\text{obs}))$ .  |
| return.plot            | Logical. Whether a sequential comparison plot to be returned. <b>Default:</b> TRUE.  |
| until.decision.reached | Logical. Whether the sequential comparison is performed until a decision is reached or until the data is observed. <b>Default:</b> 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**

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  $\sigma^2$ , 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 = T,  

  until.decision.reached = T)
```

**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. <b>Default:</b> $0.3/\sqrt{2}$ . 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 $BF \leq \text{RejectH1.threshold}$ . <b>Default:</b> $\exp(-3)$ .  |

RejectH0.threshold

Positive numeric.  $H_0$  is rejected if  $BF \geq \text{RejectH0.threshold}$ . **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:**  $c(2, \text{rep}(1, \text{length}(\text{obs1})-2))$

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:**  $c(2, \text{rep}(1, \text{length}(\text{obs2})-2))$

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

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  $\sigma_0^2$ , 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 = T,
  until.decision.reached = T)
```

**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. <b>Default:</b> $0.3/\sqrt{2}$ . 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. <b>Default:</b> 1.   |
| RejectH1.threshold     | Positive numeric. $H_0$ is accepted if $BF \leq \text{RejectH1.threshold}$ . <b>Default:</b> $\exp(-3)$ .  |
| RejectH0.threshold     | Positive numeric. $H_0$ is rejected if $BF \geq \text{RejectH0.threshold}$ . <b>Default:</b> $\exp(3)$ .   |
| batch1.size            | Integer vector. The vector of batch sizes from Group-1 at each sequential comparison. <b>Default:</b> <code>rep(1, length(obs1))</code> .  |
| batch2.size            | Integer vector. The vector of batch sizes from Group-2 at each sequential comparison. <b>Default:</b> <code>rep(1, length(obs2))</code> .  |
| return.plot            | Logical. Whether a sequential comparison plot to be returned. <b>Default:</b> TRUE.  |
| until.decision.reached | Logical. Whether the sequential comparison is performed until a decision is reached or until the data is observed. <b>Default:</b> 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**

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 results in fixed design tests.

---

```
mycombine.seq.onesample
```

*Helper function*

---

### Description

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

---

```
mycombine.seq.twosample
```

*Helper function*

---

### Description

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

---

```
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  $\sigma^2$ , 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  $\mu/\sigma$  under the alternative. Under both hypotheses, the Jeffrey's prior  $\pi(\sigma^2) \propto 1/\sigma^2$  is assumed on  $\sigma^2$ .

### Usage

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

### Arguments

|                             |  |
|-----------------------------|--|
| <code>obs</code>            | Numeric vector. Observed vector of data.   |
| <code>nObs</code>           | Numeric or numeric vector. Sample size(s). Same as <code>length(obs)</code> when numeric.  |
| <code>mean.obs</code>       | Numeric or numeric vector. Sample mean(s). Same as <code>mean(obs)</code> when numeric.  |
| <code>sd.obs</code>         | Positive numeric or numeric vector. Sample standard deviation(s). Same as <code>sd(obs)</code> when numeric.   |
| <code>test.statistic</code> | Numeric or numeric vector. Test-statistic value(s).  |
| <code>tau.NAP</code>        | Positive numeric. Parameter in the moment prior. <b>Default:</b> $0.3/\sqrt{2}$ . This places the prior modes of the standardized effect size $\mu/\sigma$ 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

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  $\sigma_0^2$ , 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  $\mu/\sigma_0$  under the alternative.

## Usage

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

## Arguments

|                             |  |
|-----------------------------|--|
| <code>obs</code>            | Numeric vector. Observed vector of data.   |
| <code>nObs</code>           | Numeric or numeric vector. Sample size(s). Same as <code>length(obs)</code> when numeric.  |
| <code>mean.obs</code>       | Numeric or numeric vector. Sample mean(s). Same as <code>mean(obs)</code> when numeric.  |
| <code>test.statistic</code> | Numeric or numeric vector. Test-statistic value(s).  |
| <code>tau.NAP</code>        | Positive numeric. Parameter in the moment prior. <b>Default:</b> $0.3/\sqrt{2}$ . This places the prior modes of the standardized effect size $\mu/\sigma_0$ at 0.3 and $-0.3$ . |
| <code>sigma0</code>         | Positive numeric. Known standard deviation in the population. <b>Default:</b> 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

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 | <i>Bayes factor in favor of the NAP in two-sample t tests</i> |
|------------|---|

---

## Description

In case of two independent populations  $N(\mu_1, \sigma^2)$  and  $N(\mu_2, \sigma^2)$  with unknown common variance  $\sigma^2$ , 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  $\sigma^2$ .

## Usage

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

## Arguments

|                    |   |
|--------------------|---|
| <code>obs1</code>  | Numeric vector. Observed vector of data from Group-1.   |
| <code>obs2</code>  | Numeric vector. Observed vector of data from Group-2.   |
| <code>n1Obs</code> | Numeric or numeric vector. Sample size(s) from Group-1. Same as <code>length(obs1)</code> 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. <b>Default:</b> $0.3/\sqrt{2}$ . 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

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  $\sigma_0^2$ , 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. <b>Default:</b> $0.3/\sqrt{2}$ . 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. <b>Default:</b> 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**

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 | <i>Sequential Bayes Factor using the Hajnal's ratio for one-sample t-tests</i> |
|----------------|--|

---

**Description**

In a  $N(\mu, \sigma^2)$  population with unknown variance  $\sigma^2$ , 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  $\mu/\sigma$  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 $\mu/\sigma$ where OC and ASN are desired. <b>Default:</b> <code>c(0, 0.2, 0.3, 0.5)</code> .   |
| es1                  | Positive numeric. $\delta$ as above. <b>Default:</b> 0.3. For this, the prior on the standardized effect size $\mu/\sigma$ 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. <b>Default:</b> 1.  |
| nmax                 | Positive integer. Maximum sample size in the sequential comparison. <b>Default:</b> 1.  |
| RejectH1.threshold   | Positive numeric. $H_0$ is accepted if $BF \leq \text{RejectH1.threshold}$ . <b>Default:</b> <code>exp(-3)</code> .   |
| RejectH0.threshold   | Positive numeric. $H_0$ is rejected if $BF \geq \text{RejectH0.threshold}$ . <b>Default:</b> <code>exp(3)</code> .  |
| batch.size.increment | function. Increment in sample size at each sequential step. <b>Default:</b> <code>function(narg){20}</code> . This means an increment of 20 samples at each step.                       |

|            |  |
|------------|--|
| nReplicate | Positive integer. Number of replicated studies based on which the OC and ASN are calculated. <b>Default:</b> 50,000. |
| nCore      | Positive integer. <b>Default:</b> 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

```
## Not run:
out = SBFHajnal_oneT(nmax = 50, es = c(0, 0.3), nCore = 1)

## End(Not run)
```

---

|                |  |
|----------------|--|
| SBFHajnal_oneZ | <i>Sequential Bayes Factor using the Hajnal's ratio for one-sample z-tests</i> |
|----------------|--|

---

### Description

In a  $N(\mu, \sigma_0^2)$  population with known variance  $\sigma_0^2$ , 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  $\mu/\sigma_0$  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 $\mu/\sigma_0$ where OC and ASN are desired. <b>Default:</b> <code>c(0, 0.2, 0.3, 0.5)</code> .   |
| es1                  | Positive numeric. $\delta$ as above. <b>Default:</b> 0.3. For this, the prior on the standardized effect size $\mu/\sigma_0$ takes values 0.3 and $-0.3$ each with equal probability 1/2. |
| nmin                 | Positive integer. Minimum sample size in the sequential comparison. <b>Default:</b> 1.  |
| nmax                 | Positive integer. Maximum sample size in the sequential comparison. <b>Default:</b> 1.  |
| sigma0               | Positive numeric. Known standard deviation in the population. <b>Default:</b> 1.  |
| RejectH1.threshold   | Positive numeric. $H_0$ is accepted if $BF \leq \text{RejectH1.threshold}$ . <b>Default:</b> <code>exp(-3)</code> .   |
| RejectH0.threshold   | Positive numeric. $H_0$ is rejected if $BF \geq \text{RejectH0.threshold}$ . <b>Default:</b> <code>exp(3)</code> .  |
| batch.size.increment | function. Increment in sample size at each sequential step. <b>Default:</b> <code>function(narg){20}</code> . This means an increment of 20 samples at each step.                         |
| nReplicate           | Positive integer. Number of replicated studies based on which the OC and ASN are calculated. <b>Default:</b> 50,000.  |
| nCore                | Positive integer. <b>Default:</b> 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 effect 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 effect 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**

```
## Not run:
out = SBFHajnal_oneZ(nmax = 100, es = c(0, 0.3), nCore = 1)

## End(Not run)
```

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  $\sigma^2$ , 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. <b>Default:</b> <code>c(0, 0.2, 0.3, 0.5)</code> .                 |
| es1                   | Positive numeric. $\delta$ as above. <b>Default:</b> 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. <b>Default:</b> 1.  |
| n2min                 | Positive integer. Minimum sample size from Group-2 in the sequential comparison. Should be at least 2. <b>Default:</b> 1.  |
| n1max                 | Positive integer. Maximum sample size from Group-1 in the sequential comparison. <b>Default:</b> 1.  |
| n2max                 | Positive integer. Maximum sample size from Group-2 in the sequential comparison. <b>Default:</b> 1.  |
| RejectH1.threshold    | Positive numeric. $H_0$ is accepted if $BF \leq \text{RejectH1.threshold}$ . <b>Default:</b> <code>exp(-3)</code> .  |
| RejectH0.threshold    | Positive numeric. $H_0$ is rejected if $BF \geq \text{RejectH0.threshold}$ . <b>Default:</b> <code>exp(3)</code> .   |
| batch1.size.increment | function. Increment in sample size from Group-1 at each sequential step. <b>Default:</b> <code>function(narg){20}</code> . 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. <b>Default:</b> <code>function(narg){20}</code> . This means an increment of 20 samples at each step. |
| nReplicate            | Positive integer. Number of replicated studies based on which the OC and ASN are calculated. <b>Default:</b> 50,000.   |
| nCore                 | Positive integer. <b>Default:</b> 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<sub>0</sub> is accepted, rejectH0 contains the proportion of times H<sub>0</sub> 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 effect 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 effect 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**

```
## Not run:
out = SBFHajnal_twoT(n1max = 100, n2max = 100, es = c(0, 0.3), nCore = 1)

## End(Not run)
```

---

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  $\sigma_0^2$ , 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. <b>Default:</b> $c(0, 0.2, 0.3, 0.5)$ .                          |
| es1                   | Positive numeric. $\delta$ as above. <b>Default:</b> 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. <b>Default:</b> 1.  |
| n2min                 | Positive integer. Minimum sample size from Group-2 in the sequential comparison. <b>Default:</b> 1.  |
| n1max                 | Positive integer. Maximum sample size from Group-1 in the sequential comparison. <b>Default:</b> 1.  |
| n2max                 | Positive integer. Maximum sample size from Group-2 in the sequential comparison. <b>Default:</b> 1.  |
| sigma0                | Positive numeric. Known common standard deviation of the populations. <b>Default:</b> 1.   |
| RejectH1.threshold    | Positive numeric. $H_0$ is accepted if $BF \leq \text{RejectH1.threshold}$ . <b>Default:</b> $\exp(-3)$ .  |
| RejectH0.threshold    | Positive numeric. $H_0$ is rejected if $BF \geq \text{RejectH0.threshold}$ . <b>Default:</b> $\exp(3)$ .   |
| batch1.size.increment | function. Increment in sample size from Group-1 at each sequential step. <b>Default:</b> <code>function(narg){20}</code> . 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. <b>Default:</b> <code>function(narg){20}</code> . This means an increment of 20 samples at each step. |
| nReplicate            | Positive integer. Number of replicated studies based on which the OC and ASN are calculated. <b>Default:</b> 50,000.   |
| nCore                 | Positive integer. <b>Default:</b> 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 effect 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 effect 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

```
## Not run:
out = SBFHajnal_twoZ(n1max = 100, n2max = 100, es = c(0, 0.3), nCore = 1)

## End(Not run)
```

---

SBFNAP\_oneT

---

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


---

## Description

In a  $N(\mu, \sigma^2)$  population with unknown variance  $\sigma^2$ , 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  $\mu/\sigma$  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 $\mu/\sigma$ where OC and ASN are desired.<br><b>Default:</b> <code>c(0, 0.2, 0.3, 0.5)</code> .                                     |
| nmin                 | Positive integer. Minimum sample size in the sequential comparison. Should be at least 2. <b>Default:</b> 1.   |
| nmax                 | Positive integer. Maximum sample size in the sequential comparison. <b>Default:</b> 1.   |
| tau.NAP              | Positive numeric. Parameter in the moment prior. <b>Default:</b> $0.3/\sqrt{2}$ . This places the prior modes of the standardized effect size $\mu/\sigma$ at 0.3 and $-0.3$ . |
| RejectH1.threshold   | Positive numeric. $H_0$ is accepted if $BF \leq \text{RejectH1.threshold}$ . <b>Default:</b> <code>exp(-3)</code> .  |
| RejectH0.threshold   | Positive numeric. $H_0$ is rejected if $BF \geq \text{RejectH0.threshold}$ . <b>Default:</b> <code>exp(3)</code> .   |
| batch.size.increment | function. Increment in sample size at each sequential step. <b>Default:</b> <code>function(narg){20}</code> . This means an increment of 20 samples at each step.              |



|            |  |
|------------|--|
| nReplicate | Positive integer. Number of replicated studies based on which the OC and ASN are calculated. <b>Default:</b> 50,000. |
| nCore      | Positive integer. <b>Default:</b> 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 effect 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 effect size in `nReplicate` replicated studies.

### Author(s)

Sandipan Pramanik and Valen E. Johnson

### References

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

```
## Not run:
out = SBFNAP_oneT(nmax = 100, es = c(0, 0.3), nCore = 1)

## End(Not run)
```

---

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  $\sigma_0^2$ , 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  $\mu/\sigma_0$  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 $\mu/\sigma_0$ where OC and ASN are desired. <b>Default:</b> <code>c(0, 0.2, 0.3, 0.5)</code> .  |
| nmin                 | Positive integer. Minimum sample size in the sequential comparison. <b>Default:</b> 1.   |
| nmax                 | Positive integer. Maximum sample size in the sequential comparison. <b>Default:</b> 1.   |
| tau.NAP              | Positive numeric. Parameter in the moment prior. <b>Default:</b> $0.3/\sqrt{2}$ . This places the prior modes of the standardized effect size $\mu/\sigma_0$ at 0.3 and $-0.3$ . |
| sigma0               | Positive numeric. Known standard deviation in the population. <b>Default:</b> 1.   |
| RejectH1.threshold   | Positive numeric. $H_0$ is accepted if $BF \leq \text{RejectH1.threshold}$ . <b>Default:</b> <code>exp(-3)</code> .  |
| RejectH0.threshold   | Positive numeric. $H_0$ is rejected if $BF \geq \text{RejectH0.threshold}$ . <b>Default:</b> <code>exp(3)</code> .   |
| batch.size.increment | function. Increment in sample size at each sequential step. <b>Default:</b> <code>function(narg){20}</code> . This means an increment of 20 samples at each step.                |
| nReplicate           | Positive integer. Number of replicated studies based on which the OC and ASN are calculated. <b>Default:</b> 50,000.   |
| nCore                | Positive integer. <b>Default:</b> 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 effect 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 effect size in `nReplicate` replicated studies.

## Author(s)

Sandipan Pramanik and Valen E. Johnson

## References

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

```
## Not run:
out = SBFNAP_oneZ(nmax = 100, es = c(0, 0.3), nCore = 1)

## End(Not run)
```

## Description

In case of two independent populations  $N(\mu_1, \sigma^2)$  and  $N(\mu_2, \sigma^2)$  with unknown common variance  $\sigma^2$ , 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. <b>Default:</b> <code>c(0, 0.2, 0.3, 0.5)</code> .                 |
| n1min                 | Positive integer. Minimum sample size from Group-1 in the sequential comparison. Should be at least 2. <b>Default:</b> 1.  |
| n2min                 | Positive integer. Minimum sample size from Group-2 in the sequential comparison. Should be at least 2. <b>Default:</b> 1.  |
| n1max                 | Positive integer. Maximum sample size from Group-1 in the sequential comparison. <b>Default:</b> 1.  |
| n2max                 | Positive integer. Maximum sample size from Group-2 in the sequential comparison. <b>Default:</b> 1.  |
| tau.NAP               | Positive numeric. Parameter in the moment prior. <b>Default:</b> $0.3/\sqrt{2}$ . 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 $BF \leq \text{RejectH1.threshold}$ . <b>Default:</b> <code>exp(-3)</code> .  |
| RejectH0.threshold    | Positive numeric. $H_0$ is rejected if $BF \geq \text{RejectH0.threshold}$ . <b>Default:</b> <code>exp(3)</code> .   |
| batch1.size.increment | function. Increment in sample size from Group-1 at each sequential step. <b>Default:</b> <code>function(narg){20}</code> . 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. <b>Default:</b> <code>function(narg){20}</code> . This means an increment of 20 samples at each step. |
| nReplicate            | Positive integer. Number of replicated studies based on which the OC and ASN are calculated. <b>Default:</b> 50,000.   |
| nCore                 | Positive integer. <b>Default:</b> 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<sub>0</sub> is accepted, rejectH0 contains the proportion of times H<sub>0</sub> 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 effect 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 effect size in nReplicate replicated studies.

## Author(s)

Sandipan Pramanik and Valen E. Johnson

## References

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

```
## Not run:
out = SBFNAP_twoT(n1max = 100, n2max = 100, es = c(0, 0.3), nCore = 1)

## End(Not run)
```

---

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  $\sigma_0^2$ , 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. <b>Default:</b> $c(0, 0.2, 0.3, 0.5)$ .                          |
| n1min                 | Positive integer. Minimum sample size from Group-1 in the sequential comparison. <b>Default:</b> 1.  |
| n2min                 | Positive integer. Minimum sample size from Group-2 in the sequential comparison. <b>Default:</b> 1.  |
| n1max                 | Positive integer. Maximum sample size from Group-1 in the sequential comparison. <b>Default:</b> 1.  |
| n2max                 | Positive integer. Maximum sample size from Group-2 in the sequential comparison. <b>Default:</b> 1.  |
| tau.NAP               | Positive numeric. Parameter in the moment prior. <b>Default:</b> $0.3/\sqrt{2}$ . 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. <b>Default:</b> 1.   |
| RejectH1.threshold    | Positive numeric. $H_0$ is accepted if $BF \leq \text{RejectH1.threshold}$ . <b>Default:</b> $\exp(-3)$ .  |
| RejectH0.threshold    | Positive numeric. $H_0$ is rejected if $BF \geq \text{RejectH0.threshold}$ . <b>Default:</b> $\exp(3)$ .   |
| batch1.size.increment | function. Increment in sample size from Group-1 at each sequential step. <b>Default:</b> <code>function(narg){20}</code> . 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. <b>Default:</b> <code>function(narg){20}</code> . This means an increment of 20 samples at each step. |
| nReplicate            | Positive integer. Number of replicated studies based on which the OC and ASN are calculated. <b>Default:</b> 50,000.   |
| nCore                 | Positive integer. <b>Default:</b> 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 effect 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 effect size in `nReplicate` replicated studies.

**Author(s)**

Sandipan Pramanik and Valen E. Johnson

**References**

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**

```
## Not run:  
out = SBFNAP_twoZ(n1max = 100, n2max = 100, es = c(0, 0.3), nCore = 1)  
  
## End(Not run)
```