

# Package ‘fabCI’

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**Title** FAB Confidence Intervals

**Version** 0.1

**Description** Frequentist assisted by Bayes (FAB) confidence interval construction. See 'Adaptive multigroup confidence intervals with constant coverage' by Yu and Hoff <<https://arxiv.org/abs/1612.08287>>.

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## R topics documented:

fabtCI . . . . .	2
fabzCI . . . . .	3
hhetmodel . . . . .	4
hhommodel . . . . .	4
multifabCI . . . . .	5
multifabCIhom . . . . .	6
radon . . . . .	7
<b>Index</b>	<b>9</b>

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fabtCI	<i>FAB t-interval</i>
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### Description

Computation of a 1-alpha FAB t-interval.

### Usage

```
fabtCI(y, psi = c(0, 100, 1, 2), alpha = 0.05)
```

### Arguments

y	a numeric vector with at least two non-missing values
psi	a length-four vector of hyperparameters for the prior
alpha	the type I error rate, so 1-alpha is the coverage rate

### Details

A FAB interval is the "frequentist" interval procedure that is Bayes optimal: It minimizes the prior expected interval width among all interval procedures with exact 1-alpha frequentist coverage. This function computes the FAB t-interval for the mean of a normal population with an unknown variance, given a user-specified prior distribution determined by psi. The prior is that the population mean and variance are independently distributed as normal and inverse-gamma random variables. Referring to the elements of psi as mu, t2, s20, nu0, the prior is determined as follows:

1. mu is the prior expectation of the mean
2. t2 is the prior variance of the mean
3. the population variance is inverse-gamma(nu0/2, nu0 s20/2)

### Author(s)

Peter Hoff

### Examples

```
y<-rnorm(10)
fabtCI(y,c(0,10,1,5))
fabtCI(y,c(0,1/10,1,5))
fabtCI(y,c(2,10,1,5))
fabtCI(y,c(0,1/10,1,5))
```

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fabzCI	<i>FAB z-interval</i>
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**Description**

Computation of a 1-alpha FAB z-interval.

**Usage**

```
fabzCI(y, mu, t2, s2, alpha = 0.05)
```

**Arguments**

y	a numeric scalar
mu	a numeric scalar
t2	a positive numeric scalar
s2	a positive numeric scalar
alpha	the type I error rate, so 1-alpha is the coverage rate

**Details**

A FAB interval is the "frequentist" interval procedure that is Bayes optimal: It minimizes the prior expected interval width among all interval procedures with exact 1-alpha frequentist coverage. This function computes the FAB z-interval for the mean of a normal population with an known variance, given a user-specified prior distribution determined by psi. The prior is that the population mean is normally distributed. Referring to the elements of psi as mu, t2, s2, the prior and population variance are determined as follows:

1. mu is the prior expectation of the mean
2. t2 is the prior variance of the mean
3. s2 is the population variance

**Author(s)**

Peter Hoff

**Examples**

```
y<-0
fabzCI(y,0,10,1)
fabzCI(y,0,1/10,1)
fabzCI(y,2,10,1)
fabzCI(y,0,1/10,1)
```

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`hhetmodel`*Hierarchical heteroscedastic model estimates*

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**Description**

Estimate across-group heterogeneity of means and variances.

**Usage**

```
hhetmodel(y, g)
```

**Arguments**

`y` a numeric vector of data  
`g` a group membership vector, of the same length as `y`

**Details**

This function estimates parameters in a hierarchical model for normally distributed groups, where the across-group model for means is normal and the across group model for variances is inverse-gamma.

**Value**

A vector  $(\mu, t^2, s^2, \nu_0)$ , where

1.  $\mu$  is the mean of the group means
2.  $t^2$  is the variance of the group means
3. the the distribution of group variances is  $\text{inverse-gamma}(\nu_0/2, \nu_0 s^2/2)$

**Author(s)**

Peter Hoff

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`hhommodel`*Hierarchical homoscedastic model estimates*

---

**Description**

Estimate across-group heterogeneity of means.

**Usage**

```
hhommodel(y, g, group, p1)
```

**Arguments**

y	a numeric vector of data
g	a group membership vector, of the same length as y
group	the index of the group
p1	number of groups used to pool sample variance

**Details**

This function estimates parameters in a hierarchical model for normally distributed groups, where the across-group model for means is normal and the variance is the same across groups.

**Value**

A vector (s2,df,muw,t2w,s2w), where

1. s2 is the pooled variance
2. df is the degree of freedom of the t-quantiles
3. muw is the estimate mean of the group means
4. t2w is the estimate variance of the group means
5. s2w is the estimate within-group variance

**Author(s)**

Chaoyu Yu

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multifabCI

*Multigroup FAB t-intervals*

---

**Description**

Computation of 1-alpha FAB t-intervals for heteroscedastic multigroup data.

**Usage**

```
multifabCI(y, g, alpha = 0.05)
```

**Arguments**

y	a numeric vector of data
g	a group membership vector, of the same length as y
alpha	the type I error rate, so 1-alpha is the coverage rate

**Details**

For each group  $j$ , this function computes an estimate of the parameters in a hierarchical model for means and variances from data other than group  $j$ , and uses this information to construct a FAB t-interval for group  $j$ . These intervals have  $1-\alpha$  frequentist coverage, assuming within-group normality.

**Author(s)**

Peter Hoff

**Examples**

```
## -- simulated data
p<-10 ; n<-10
y<-rnorm(n*p) ; g<-rep(1:p,n)

## -- more interesting data takes longer
# data(radon) ; y<-radon[,2] ; g<-radon[,1]

## -- FAB t-intervals
FCI<-multifabCI(y,g)

## -- UMAU t-intervals
ybar<-tapply(y,g,mean) ; ssd<-tapply(y,g,sd) ; n<-table(g)
qtn<-cbind( qt(.025,n-1), qt(.975,n-1) )
UCI<-sweep(sweep(qtn,1,ssd/sqrt(n),"*"),1,ybar,"+")

mean( (UCI[,2]-UCI[,1])/(FCI[,2]-FCI[,1]) , na.rm=TRUE)
```

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multifabCIhom

*Multigroup FAB t-intervals for the homoscedastic model*

---

**Description**

Computation of  $1-\alpha$  FAB t-intervals for homoscedastic multigroup data.

**Usage**

```
multifabCIhom(y, g, alpha = 0.05, prop = 0.5)
```

**Arguments**

y	a numeric vector of data
g	a group membership vector, of the same length as y
alpha	the type I error rate, so $1-\alpha$ is the coverage rate
prop	the proportion of groups to obtain the sample variance estimate

**Details**

For each group  $j$ , this function computes an estimate of the parameters in a hierarchical model for means using data from other groups, and uses this information to construct a FAB t-interval for group  $j$ . These intervals have  $1-\alpha$  frequentist coverage, assuming within-group normality and that the within group variance is the same across groups.

**Author(s)**

Chaoyu Yu

**Examples**

```
## -- simulate the data
mu = 0; sigma2 = 10; tau2 = 1; p = 100;
theta = rnorm(p,mu,sqrt(tau2))
ns = round(runif(p,2,18))
Y=c()
for(i in 1:p){
  d2 = rnorm(ns[i],theta[i],sqrt(sigma2))
  d1 = rep(i,ns[i])
  d = cbind(d1,d2)
  Y = rbind(Y,d)}
y = Y[,2]
g = Y[,1]

## -- FAB t-intervals
FCI = multifabCIhom(y,g)

## -- UMAU t-intervals
ybar<-tapply(y,g,mean) ; ssd<-tapply(y,g,sd) ; n<-table(g)
qtn<-cbind( qt(.025,n-1), qt(.975,n-1) )
UCI<-sweep(sweep(qtn,1,ssd/sqrt(n),"*"),1,ybar,"+")

mean( (UCI[,2]-UCI[,1])/(FCI[,2]-FCI[,1]) , na.rm=TRUE)
```

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radon

*Minnesota Radon Dataset*

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**Description**

Radon levels in 919 homes from 85 Minnesota counties

**Usage**

data(radon)

**Format**

A numeric matrix

**Source**

<http://www.stat.columbia.edu/~gelman/arm/software/>



# Index

\*Topic **datasets**

radon, [7](#)

\*Topic **htest**

fabtCI, [2](#)

fabzCI, [3](#)

hhetmodel, [4](#)

hhommodel, [4](#)

multifabCI, [5](#)

multifabCIhom, [6](#)

[fabtCI, 2](#)

[fabzCI, 3](#)

[hhetmodel, 4](#)

[hhommodel, 4](#)

[multifabCI, 5](#)

[multifabCIhom, 6](#)

[radon, 7](#)