Package ‘ANOVAreplciation’

July 18, 2019

Type Package

Version 1.1.4

Title Test ANOVA Replications by Means of the Prior Predictive p-Value

Description Allows for the computation of a prior predictive p-value to test replication of relevant features of original ANOVA studies. Relevant features are captured in informative hypotheses. The package also allows for the computation of sample sizes for new studies, post-hoc power calculations, and comes with a Shiny application in which all calculations can be conducted as well. The statistical underpinnings are described in Zondervan-Zwijnenburg (2019) <doi:10.31234/osf.io/6myqh>.

License GPL (>= 3)

Depends quadprog, graphics, grDevices, shiny, stats, utils

Suggests knitr, rmarkdown, testthat

VignetteBuilder knitr

Encoding UTF-8

LazyData true

URL https://dx.doi.org/10.17605/OSF.IO/6H8X3

NeedsCompilation no

Author M.A.J. Zondervan-Zwijnenburg [aut, cre],
        Herbert Hoijtink [ths],
        Caspar J van Lissa [ctb],
        Consortium Individual Development [fnd] (NWO grant number 024.001.003)

Maintainer M.A.J. Zondervan-Zwijnenburg <m.a.j.zwijnenburg@uu.nl>

Repository CRAN

Date/Publication 2019-07-18 06:37:04 UTC

R topics documented:

Fbar.dif ................................................................. 2
Fbar.exact ............................................................. 3
Fbar.ineq ............................................................... 4
Fbar.dif

F-bar for inequality constraints with minimum differences between means

Description

The function calculates F-bar for inequality constrained hypotheses with minimum differences between means (Type B). See Silvapulle & Sen (2011) for background on the F-bar statistic. The code of Vanbrabant (2017) is the basis to this Fbar function.

Usage

Fbar.dif(data, Amat, difmin, effectsize=FALSE)

Arguments

data

A dataframe with two variables: (1) a dependent variable, and (2) a grouping variable. Groups are labeled consecutively, starting at 1.

Amat

A p by q matrix, where p is the number of means in the ANOVA model, and q is the number of constraints to be imposed on the model. Each row represents one constraint where the parameter with the lower value according to the constraint receives the value -1, and the parameter with the higher value according to the constraint receives the value 1. Other parameters within the same row obtain the value 0.

difmin

A vector of length q with the minimum difference per constraint as specified in Amat.

effectsize

Logical; If TRUE the values in difmin are interpreted as Cohen’s d.

Value

The value for the F-bar statistic

Author(s)

M. A. J. Zondervan-Zwijnenburg
Fbar.exact

References


See Also

See also runShiny, Fbar.ineq, and Fbar.exact.

Examples

data <- data.frame(y=ChickWeight$weight,g=ChickWeight$Diet)
aggregate(data$y,by=list(data$g),mean)

#create matrices HR: g4>(g1,g2,g3). g4-g1>0.8, g4-g2>0.5, g4-g3>0.2
HR <- create_matrices(varnames = c("g1","g2","g3","g4"),
  hyp = "g4-g1>0.8 & g4-g2>0.5 & g4-g3>0.2")
Fbar.dif(data,Amat=HR$Amat,difmin=HR$difmin,effectsize=TRUE)

#make Amat with constraints: 1<4,2<4,3<4 (last constraint is not true)
Amat <- (rbind(c(-1,0,0,1),c(0,-1,0,1),c(0,0,-1,1)))
#minimal differences for each constraint
difmin=c(30,15,1)
Fbar.dif(data,Amat,difmin=difmin)

Fbar.exact

F-bar for exact constraints

Description

The function calculates F-bar for hypotheses constrained with exact values (Type B). See Silvapulle & Sen (2011) for background on the F-bar statistic. The code of Vanbrabant (2017) is the basis to this Fbar function.

Usage

Fbar.exact(data,exact)

Arguments

data A dataframe with two variables: (1) a dependent variable, and (2) a grouping variable.
exact A vector of length p, where p is the number of means in the ANOVA model, with the exact values of the constrained hypothesis.
Value

The value for the F-bar statistic

Author(s)

M. A. J. Zondervan-Zwijnenburg

References


See Also

See also runShiny, Fbar.ineq and Fbar.dif.

Examples

data <- data.frame(y=ChickWeight$weight,g=ChickWeight$Diet)
aggregate(data$y,by=list(data$g),mean)

#specify exact values to be evaluated. Hi: mu1=102,mu2=123,mu3=143,mu4=135.
exact <- c(102,123,143,135)
Fbar.exact(data,exact)

Fbar.ineq

F-bar for inequality constraints

Description

The function calculates F-bar for inequality constrained hypotheses (Type B). See Silvapulle & Sen (2011) for background on the F-bar statistic. The code of Vanbrabant (2017) is the basis to this Fbar function.

Usage

Fbar.ineq(data,Amat)
generate.data

Arguments

data A dataframe with two variables: (1) a dependent variable, and (2) a grouping variable.

Amat A p by q matrix, where p is the number of means in the ANOVA model, and q is the number of constraints to be imposed on the model. Each row represents one constraint where the parameter with the lower value according to the constraint receives the value -1, and the parameter with the higher value according to the constraint receives the value 1. Other parameters within the same row obtain the value 0.

Value

The value for the F-bar statistic.

Author(s)

M. A. J. Zondervan-Zwijnenburg

References


See Also

See also runShiny, Fbar.dif, and Fbar.exact.

Examples

data <- data.frame(y=ChickWeight$weight,g=ChickWeight$Diet)
aggregate(data$y,by=list(data$g),mean)

# create matrices HR: g4>(g1,g2,g3)
HR <- create_matrices(varnames = c("g1","g2","g3","g4"),
                      hyp = "g4>(g1,g2,g3")
Fbar.ineq(data,Amat=HR$Amat)

generate.data Generate Data

Description

Generates data of sample size n with the exact specified mean and standard deviation.
Usage

generate.data(n,mean,sd)

Arguments

n integer; sample size.
mean integer; mean of the data.
sd integer; standard deviation of the data.

Examples

#simple example
data1 <- generate.data(n=10,mean=5,sd=1)

#multiple independent groups
means = c(0.36,-0.19,-0.18)
sds = c(1.08,0.53,0.81)
n = c(28,28,28) #N = 84
y <- list(NA)
for (i in 1:3){y[[i]] <- generate.data(n[i],means[i],sds[i])}
y <- unlist(y)
group <- c(rep(0,n[1]),rep(1,n[2]),rep(2,n[3]))
p <- length(unique(group))
data=data.frame(y=y,g=group)
aggregate(data$y,by=list(data$g),mean)

Gibbs.ANOVA

Gibbs sampler

Description

Samples from the posterior distribution of the data by means of a Gibbs sampler (derived from Lynch, 2007, p. 170-172).

Usage

Gibbs.ANOVA(data,it=5000,burnin=500,seed=0)

Arguments

data a data frame with a variable y and a variable g, where y is the dependent variable, and g is the grouping variable for the ANOVA. Groups are labeled consecutively, starting at 1.

it the number of (post-burnin) iterations for each of the two chains. The default uses 5.000 iterations.

burnin the number of iterations for the function to use for the burnin phase in each of the two chains. The default uses 500 burnin iterations.

seed integer; seed value. If seed==0, no seed is set.
pooled.sd

Value

output_m  a matrix with all samples from the posterior for each parameter.

Returns a matrix with the mean, median, and standard deviation (in columns) for the it samples from the conditional posterior distributions of the group means and pooled standard deviation (rows).

Produces traceplots of each parameter and the associated samples from the posterior distribution.

Author(s)

M. A. J. Zondervan-Zwijnenburg

References


Examples

data <- data.frame(y=ChickWeight$weight,g=ChickWeight$Diet)
Gibbs.ANOVA(data)

pooled.sd  

Description

Calculates the pooled standard deviation.

Usage

pooled.sd(data)

Arguments

data  A dataframe with two variables: the dependent variable in the first column, and the grouping variable in the second column.

Value

Returns the pooled standard deviation.

Author(s)

M.A.J. Zondervan-Zwijnenburg
Examples

data <- data.frame(y=ChickWeight$weight,g=ChickWeight$Diet)
pooled.sd(data)

power.calc

Description

Calculates the power for the prior predictive check

Usage

power.calc(n.r,posterior,g.m,p.sd,
    statistic,Amat=0L,exact=0L,difmin=0L,effectsize=FALSE,
    alpha=.05)

Arguments

  n.r vector with the sample size per group (i.e., n_{jr}) for new study (i.e., y_r).
  posterior matrix (e.g., the output of Gibbs.ANOVA) with samples from the posterior based
    on the original data (i.e., y_o).
  g.m vector; the population values the alternative distribution. To calculate the power
    to reject replication if the means are equal specify the grand mean of the study
    variables in the original dataset.
  p.sd integer; the population value for the pooled standard deviation in the alternative
    distribution. We advice to specify the pooled standard deviation for the study
    variables in the original dataset.
  statistic the type of hypothesis to be evaluated: "ineq" for inequality constrained means,
    "dif" for inequality constraints plus minimum differences between means, "ex-
    act" for specific values for the means.
  Amat p by q matrix, where p is the number of means in the ANOVA model, and q is
    the number of constraints to be imposed on the model. Each row represents one
    constraint where the parameter with the lower value according to the constraint
    receives the value -1, and the parameter with the higher value according to the
    constraint receives the value 1. Other parameters within the same row obtain the
    value 0. The create_matrices function can be used to obtain Amat.
  exact vector of length p, where p is the number of means in the ANOVA model, with
    the exact values of the constrained hypothesis.
  difmin vector of length q with the minimum difference per constraint as specified in
    Amat. The create_matrices function can be used to obtain difmin. Default =
    0L, indicating that only the ordering of means is evaluated.
  effectsize logical; If TRUE the values in difmin are interpreted as Cohen’s d.
  alpha integer; the level of alpha that should be taken into account while calculating the
    required sample size.
prior.predictive.check

Value

- **power**: The acquired power given the input
- **rejection.value**: The 1-alpha’th percentile of the null distribution. The proportion of H1 larger than this value constitutes power.

Author(s)
M. A. J. Zondervan-Zwijnenburg, H. Hoijtink

References

See Also
See also runShiny, Gibbs.ANOVA, Fbar.ineq, Fbar.dif, and Fbar.exact, create_matrices, prior.predictive.check, sample.size.calc.

Examples

```r
# analysis original data
data_o <- data.frame(y=ChickWeight$weight,g=ChickWeight$Diet)
g.m <- rep(mean(data_o$y),3)
# compute pooled sd
sd.g <- aggregate(data_o$y,by=list(data_o$g),sd)
[,2]
n.g <- table(data_o$g)
p.sd <- pooled.sd(data_o)

means <- aggregate(data_o$y,by=list(data_o$g),mean)
[,2]

post <- Gibbs.ANOVA(data_o)

power.calc(n.r=c(20,21,22,23),posterior=post$posterior,g.m=g.m,p.sd=p.sd,
statistic="exact",exact=means, alpha=.05)
```

---

prior.predictive.check

**Prior predictive check**

Description
Uses the prior predictive check to test replication for ANOVA models.
prior.predictive.check

Usage

prior.predictive.check(n, posterior, statistic, obs=TRUE, F_n, Amat=0L, exact=0L, difmin=0L, effectsize=FALSE, seed=0)

Arguments

n
vector with the sample size per group (i.e., n_jr) for new study (i.e., y_r).

posterior
a matrix (e.g., the output of Gibbs.ANOVA) with samples from the posterior based on the original data (i.e., y_o).

statistic
the type of hypothesis to be evaluated: "ineq" for inequality constrained means, "dif" for inequality constraints plus minimum differences between means, "exact" for specific values for the means.

obs
logic; If FALSE, the prior predictive check does not calculate a p-value, because no observed statistic is provided. Used by the sample.size.calculator function.

F_n
The Fbar value for the new data.

Amat
a p by q matrix, where p is the number of means in the ANOVA model, and q is the number of constraints to be imposed on the model. Each row represents one constraint where the parameter with the lower value according to the constraint receives the value -1, and the parameter with the higher value according to the constraint receives the value 1. Other parameters within the same row obtain the value 0.

exact
a vector of length p, where p is the number of means in the ANOVA model, with the exact values of the constrained hypothesis.

difmin
a vector of length q with the minimum difference per constraint as specified in Amat.

effectsize
logical; If TRUE the values in difmin are interpreted as Cohen’s d.

seed
integer; seed value. If seed==0, no seed is set.

Value

Generates a histogram of F_sim in which F_n is indicated with a vertical line. The proportion of F_sim at the right of this line constitutes the prior predictive p-value.

sumFdist
a summary of F_sim

ppp
the prior predictive p-value

F_sim
a vector with F-bar values for all simulated datasets

Author(s)

M. A. J. Zondervan-Zwijnenburg

References

runShiny

See Also

See also runShiny, Gibbs.ANOVA, Fbar.ineq, Fbar.dif, and Fbar.exact, sample.size.calc, power.calc.

Examples

```r
#analysis original data
data_o <- data.frame(y=ChickWeight$weight, g=ChickWeight$Diet)
post <- Gibbs.ANOVA(data_o)

#analysis new data
data_r <- data.frame(y=rnorm(660, mean(data_o$y), sd=sd(data_o$y)), g=round(runif(660,1,4)))
n.r = as.numeric(table(data_r$g))

#create matrices HR: g4>(g1,g2,g3). g4-g1>0.8, g4-g2>0.5, g4-g3>0.2
HR <- create_matrices(varnames = c("g1","g2","g3","g4"),
hyp = "g4-g1>0.8 & g4-g2>0.5 & g4-g3>0.2")
Amat <- HR$Amat
difmin <- HR$difmin
r.F.dif.efsz <- Fbar.dif(data_r, Amat, difmin, effectsize=TRUE)

#prior predictive check
result <- prior.predictive.check(n=n.r, posterior=post$posterior, F_n=r.F.dif.efsz, statistic="dif",
effectsize=TRUE, Amat=Amat, difmin=difmin, seed=1)

result$sumFdist #summary of the f(F_y_sim)
result$ppp #the prior predictive p-value
```

Description

Launches a Shiny application for the replication test.

Usage

```r
runShiny()
```

Value

In the Shiny application Gibbs.ANOVA can be ran, which prints convergence plots, samples of the posterior, and a summary table.
Subsequently, the sample size calculator can be used, which prints a matrix with two columns. The first column contains the sample size per group and the second column the associated power. Furthermore, sample.size.calc produces a histogram to illustrate power as evaluated in the last iteration. Detailed descriptions are provided in the Shiny application. Alternatively, the power for a specific combination of group sample sizes can be calculated with the power calculator (power.calc).

If information for a new study is provided, the prior predictive check can be used to compute the prior predictive p-value. The prior predictive check generates a histogram of F_sim in which F_n is indicated with a vertical line. The proportion of F_sim at the right of this line constitutes the prior predictive p-value. The user can download this histogram and sumFdist: a summary of F_sim.

See Also

See also Gibbs.ANOVA, sample.size.calc, power.calc, prior.predictive.check, Fbar.ineq, Fbar.dif, and Fbar.exact.

---

sample.size.calc  Sample size calculator for the prior.predictive.check function

Description

Calculates the required sample size for a new study to conduct the prior predictive check with sufficient statistical power.

Usage

```r
sample.size.calc(start_n, itmax=10, nmax=600, powtarget=.825, powmargin=.025, posterior, g.m, p.sd,
                 statistic, Amat=0L, exact=0L, difmin=0L, effectsize=FALSE, alpha=.05)
```

Arguments

- `start_n`  integer; the starting value for the sample size per group.
- `itmax`  integer; the maximum number of iterations for the function.
- `nmax`  integer; the maximum total sample size to evaluate.
- `powtarget`  integer; the target power for which the sample size is to be obtained.
- `powmargin`  integer; the margin around the target power for which results are to be returned.
- `posterior`  a matrix (e.g., the output of Gibbs.ANOVA) with samples from the posterior based on the original data (i.e., y_o).
- `g.m`  vector; the population values the alternative distribution. To calculate the power to reject replication if the means are equal specify the grand mean of the study variables in the original dataset.
- `p.sd`  integer; the population value for the pooled standard deviation in the alternative distribution. We advice to specify the pooled standard deviation for the study variables in the original dataset.
the type of hypothesis to be calculated: "ineq" for inequality constrained means, "dif" for inequality constraints plus minimum differences between means, "exact" for specific values for the means.

A matrix where is the number of means in the ANOVA model, and is the number of constraints to be imposed on the model. Each row represents one constraint where the parameter with the lower value according to the constraint receives the value -1, and the parameter with the higher value according to the constraint receives the value 1. Other parameters within the same row obtain the value 0.

a vector of length where is the number of means in the ANOVA model, with the exact values of the constrained hypothesis.

A vector of length with the minimum difference per constraint as specified in .

logical; If TRUE the values in are interpreted as Cohen’s d.

integer; the level of alpha that should be taken into account while calculating the required sample size.

Prints iterations while calculating. Prints a matrix with two columns. The first column contains the sample size per group and the second column the associated power. Furthermore, produces a histogram with the null (i.e., the red distribution) and alternative distribution (i.e., the blue distribution) for the last iteration afterwards. The vertical line indicates which is the 1-alpha’th percentile of the null distribution. The proportion of the alternative distribution on the right side of which constitutes the statistical power.

M.A.J. Zondervan-Zwijnenburg


See also runShiny, prior.predictive.check, power.calc, Fbar.ineq, Fbar.dif, and Fbar.exact.

#analysis original data
data_o <- data.frame(y=ChickWeight$weight,g=ChickWeight$Diet)
#compute pooled sd
sd.g <- aggregate(data_o$y,by=list(data_o$g),sd)
  n.g <- table(data_o$g)
p.sd <- pooled.sd(data_o)

Gibbs.ANOVA(data_o)
# create matrices HR: g4>(g1,g2,g3). g4-g1>0.8, g4-g2>0.5, g4-g3>0.2
HR <- create_matrices(varnames = c("g1","g2","g3","g4"),
                      hyp = "g4-g1>0.8 & g4-g2>0.5 & g4-g3>0.2")

Amat <- HR$Amat
difmin <- HR$difmin

# sample size calculator
sample.size.calc(start_n=30, powtarget=.825, powmargin=.025, posterior=output_m,
g.m=rep(mean(data_o$y),4), p.sd=p.sd,
statistic="dif", effectsize=TRUE, Amat=Amat, difmin=difmin)