R code compilation

Description

[su_spoiler title="? Collapse this information to display the page content" open="yes" style="fancy" icon="folder-2"]

This project was funded by the EU Marie Curie Initial Training Network FP7-PEOPLE-2013-ITN-604764

Image not found or type unknown https://www.cognovo.eu/people/research-fellows/christopher-germann.php

? Primary goals of research and innovation policy as defined by the European Comission: **Open Innovation, Open Science, Open to the World.**
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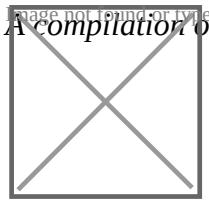
[/su_spoiler]

[su_spacer size=”20?] R-code.ml



A compilation of code snippets, scripts, packages, instructions, lectures, & more…

Keywords: [su_label]Statistical computing[/su_label][su_label]Open-source software[/su_label][su_label]Bayesian analysis[/su_label][su_label]Markov chain Monte Carlo methods[/su_label][su_label]Data visualisation[/su_label][su_label]Logical inference[/su_label][su_label]Hypothesis testing[/su_label][su_label]Deductive reasoning[/su_label][su_label]Abduction[/su_label][su_label]Credibility intervals[/su_label][su_label]Probability theory[/su_label][su_label]Decision algorithms[/su_label][su_label]New statistics[/su_label][su_label]Replication crisis[/su_label][su_label]Creative statistics[/su_label]

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S

[su_spoiler title="Add R code to this repository" style="fancy" icon="folder-1?][/su_spoiler] [su_spoiler title="Frequentist inference" open="yes" style="default" icon="plus" anchor="frequentist" class=""] [su_tabs vertical="yes"] [su_tab title="Fixed-effects ANOVA" disabled="no" anchor="" url="" target="blank" class=""]

```
data(ToothGrowth)

## Example plot from ?ToothGrowth

coplot(len ~ dose | supp, data = ToothGrowth, panel = panel.smooth,
       xlab = "ToothGrowth data: length vs dose, given type of supplement")
## Treat dose as a factor
ToothGrowth$dose = factor(ToothGrowth$dose)
levels(ToothGrowth$dose) = c("Low", "Medium", "High")

summary(aov(len ~ supp*dose, data=ToothGrowth))


#install.packages("xtable")
library(xtable)
xtable(x, caption = NULL, label = NULL, align = NULL, digits = NULL,
       display = NULL, auto = FALSE, ...)

print(xtable(d), type="html")
print(xtable(d), type="latex") # anova table to latex
#https://cran.r-project.org/web/packages/xtable/index.html
#https://rmarkdown.rstudio.com/
```

[/su_tab] [su_tab title="General linear models: mixing continuous and categorical covariates" disabled="no" anchor="" url="" target="blank" class=""]

```
data(ToothGrowth)

# model log2 of dose instead of dose directly
ToothGrowth$dose = log2(ToothGrowth$dose)

# Classical analysis for comparison
lmToothGrowth <- lm(len ~ supp + dose + supp:dose, data=ToothGrowth)
summary(lmToothGrowth)
```

[/su_tab] [su_tab title="Output plot as PDF" disabled="no" anchor="" url="" target="blank" class=""]

```
x<- (1:5)
y<- (1:111)
pdf(file=file.choose())
hist(x)
plot(x, type='o')
dev.off()
```

Notes

`file.choose()` is a very handy command which saves the work associated with defining absolute

and relative paths which can be quite cumbersome.
`list.files` for non-interactive selection.
`choose.files` for selecting multiple files interactively.
More
www.rdocumentation.org/packages/base/versions/3.5.2/topics/file.choose
[/su_tab] [su_tab title="Simple linear regression" disabled="no" anchor="" url="" target="blank" class=""]

```
# http://wiki.math.yorku.ca/index.php/VR4:_Chapter_1_summary
x <- seq( 1, 20, 0.5)   # sequence from 1 to 20 by 0.5
x                       # print it
w <- 1 + x/2            # a weight vector
y <- x + w*rnorm(x)     # generate y with standard deviations
                          #    equal to w

dum <- data.frame( x, y, w )     # make a data frame of 3 columns
dum                     # typing it's name shows the object
rm( x, y, w )           # remove the original variables


fm <- lm ( y ~ x, data = dum)   # fit a simple linear regression (between x an
summary( fm )                   # and look at the analysis



fm1 <- lm( y ~ x, data = dum, weight = 1/w^2 )  # a weighted regression
summary(fm1)

lrf <- loess( y ~ x, dum)    # a smooth regression curve using a
                               #   modern local regression function
attach( dum )                # make the columns in the data frame visible
                               #   as variables (Note: before this command, ty
                               #   y would yield errors)
plot( x, y)                  # a standard scatterplot to which we will
                               #   fit regression curves
lines( spline( x, fitted (lrf)), col = 2)  # add in the local regression using
                                             #  interpolation between calculat
                                             #  points
abline(0, 1, lty = 3, col = 3)    # add in the true regression line (lty=3: re
                                    #   col=3: read colour=green; type "?par"
abline(fm, col = 4)               # add in the unweighted regression line
abline(fm1, lty = 4, col = 5)     # add in the weighted regression line
plot( fitted(fm), resid(fm),
       xlab = "Fitted Values",
       ylab = "Residuals")          # a standard regression diagnostic plot
                                    # to check for heteroscedasticity.
                                    # The data were generated from a
                                    # heteroscedastic process. Can you see
                                    # it from this plot?
qqnorm( resid(fm) )               # Normal scores to check for skewness,
                                    #   kurtosis and outliers.  How would you
                                    #   expect heteroscedasticity to show up?
search()                          # Have a look at the search path
detach()                          # Remove the data frame from the search path
search()                          # Have another look. How did it change?
```

```
rm(fm, fm1, lrf, dum)             # Clean up (this is not that important in R
                                    #    for reasons we will understand later)



library(rgl)
rgl.open()
rgl.bg(col='white')
x <- sort(rnorm(1000))
y <- rnorm(1000)
z1 <- atan2(x,y)
z <- rnorm(1000) + atan2(x, y)
plot3d(x, y, z1, col = rainbow(1000), size = 2)
bbox3d()
```

[/su_tab] [su_tab title=”Skewness & Kurtosis” disabled=”no” anchor=”” url=”” target=”blank” class=””]

```
skew(x, na.rm = TRUE)
kurtosi(x, na.rm = TRUE)

#x A data.frame or matrix
#na.rm how to treat missing data

## The function is currently defined as
function (x, na.rm = TRUE)
{
    if (length(dim(x)) == 0) {
        if (na.rm) {
            x <- x[!is.na(x)]
           }

        mx <- mean(x)
         sdx <- sd(x,na.rm=na.rm)
        kurt <- sum((x - mx)^4)/(length(x) * sd(x)^4)  -3
        } else {

    kurt <- rep(NA,dim(x)[2])
    mx <- colMeans(x,na.rm=na.rm)
     sdx <- sd(x,na.rm=na.rm)
    for (i in 1:dim(x)[2]) {
    kurt[i] <- sum((x[,i] - mx[i])^4,  na.rm = na.rm)/((length(x[,i]) - sum(is
            }
    }
    return(kurt)
  }
```

[/su_tab] [/su_tabs] [/su_spoiler] [su_divider style=”dashed” divider_color=”#000? link_color=”#000? size=”1? margin=”0?] [su_spoiler title=”Bayes Factor analysis” open=”no” style=”default” icon=”plus” anchor=”bayesfactor” class=””] [su_tabs vertical=”yes”] [su_tab title=”ttestBF function (one sample)” disabled=”no” anchor=”” url=”” target=”blank” class=””]

```
#https://richarddmorey.github.io/BayesFactor/
bf = ttestBF(x = diffScores)
## Equivalently:
## bf = ttestBF(x = sleep$extra[1:10],y=sleep$extra[11:20], paired=TRUE)
bf
```

Comment

ttestBF function, which performs the “JZS” t test described by Rouder, Speckman, Sun, Morey, and Iverson (2009).
[/su_tab] [su_tab title=” BFmcmc function” disabled=”no” anchor=”” url=”” target=”blank” class=””]

```
#https://richarddmorey.github.io/BayesFactor/
chains2 = recompute(chains, iterations = 10000)
plot(chains2[,1:2])
```

Comment
The posterior function returns a object of type BFmcmc, which inherits the methods of the mcmc class from the coda package.
[/su_tab] [su_tab title=”ttestBF function (two sample)” disabled=”no” anchor=”” url=”” target=”blank” class=””]

```
#https://richarddmorey.github.io/BayesFactor/
## Compute Bayes factor
bf = ttestBF(formula = weight ~ feed, data = chickwts)
bf
###
chains = posterior(bf, iterations = 10000)
plot(chains[,2])
```

[/su_tab] [su_tab title=”Bayesian meta analysis” disabled=”no” anchor=”” url=”” target=”blank” class=””]

```
#https://richarddmorey.github.io/BayesFactor/
## Bem's t statistics from four selected experiments
t = c(-.15, 2.39, 2.42, 2.43)
N = c(100, 150, 97, 99)
###
## Do analysis again, without nullInterval restriction
bf = meta.ttestBF(t=t, n1=N, rscale=1)

## Obtain posterior samples
chains = posterior(bf, iterations = 10000)
plot(chains)
```

Comment
ttestBF function, which performs the “JZS” t test described by Rouder, Speckman, Sun, Morey, and Iverson (2009).
[/su_tab] [su_tab title=”Bayes factor robustness analysis, one-sided” disabled=”no” anchor=”” url=”” target=”blank” class=””]

```
## This source code is licensed under the FreeBSD license
## (c) 2013 Felix Schönbrodt
```

```
#' @title Plots a comparison of a sequence of priors for t test Bayes factors
#'
#' @details
#'
#'
#' @param ts A vector of t values
#' @param ns A vector of corresponding sample sizes
#' @param rs The sequence of rs that should be tested. r should run up to 2 (h
#' @param labels Names for the studies (displayed in the facet headings)
#' @param dots Values of r's which should be marked with a red dot
#' @param plot If TRUE, a ggplot is returned. If false, a data frame with the
#' @param sides If set to "two" (default), a two-sided Bayes factor is compute
#' @param nrow Number of rows of the faceted plot.
#' @param forH1 Defines the direction of the BF. If forH1 is TRUE, BF > 1 spea
#'
#' @references
#'
#' Rouder, J. N., Speckman, P. L., Sun, D., Morey, R. D., & Iverson, G. (2009)
#' Wagenmakers, E.-J., & Morey, R. D. (2013). Simple relation between one-side
#' Wagenmakers, E.-J., Wetzels, R., Borsboom, D., Kievit, R. & van der Maas, H

BFrobustplot <- function(
    ts, ns, rs=seq(0, 2, length.out=200), dots=1, plot=TRUE,
    labels=c(), sides="two", nrow=2, xticks=3, forH1=TRUE)
{
    library(BayesFactor)

    # compute one-sided p-values from ts and ns
    ps <- pt(ts, df=ns-1, lower.tail = FALSE)   # one-sided test

    # add the dots location to the sequences of r's
    rs <- c(rs, dots)

    res <- data.frame()
    for (r in rs) {

        # first: calculate two-sided BF
        B_e0 <- c()
        for (i in 1:length(ts))
            B_e0 <- c(B_e0, exp(ttest.tstat(t = ts[i], n1 = ns[i], rscale=r)$b

        # second: calculate one-sided BF
        B_r0 <- c() for (i in 1:length(ts)) { if (ts[i] > 0) {
                # correct direction
                B_r0 <- c(B_r0, (2 - 2*ps[i])*B_e0[i])
            } else {
                # wrong direction
                B_r0 <- c(B_r0, (1 - ps[i])*2*B_e0[i])
            }
        }

        res0 <- data.frame(t=ts, n=ns, BF_two=B_e0, BF_one=B_r0, r=r) if (leng
            res0$labels <- labels
            res0$heading <- factor(1:length(labels), labels=paste0(labels, "\n
```

```
        } else {
            res0$heading <- factor(1:length(ts), labels=paste0("t = ", ts, ",
        }
        res <- rbind(res, res0)
    }

    # define the measure to be plotted: one- or two-sided?
    res$BF <- res[, paste0("BF_", sides)]


    # Flip BF if requested
    if (forH1 == FALSE) {
        res$BF <- 1/res$BF
    }


    if (plot==TRUE) {
        library(ggplot2)
        p1 <- ggplot(res, aes(x=r, y=log(BF))) + geom_line() + facet_wrap(~hea
        p1 <- p1 + geom_hline(yintercept=c(c(-log(c(30, 10, 3)), log(c(3, 10,
        p1 <- p1 + geom_hline(yintercept=log(1), linetype="dashed", color="dar

        # add the dots
        p1 <- p1 + geom_point(data=res[res$r %in% dots,], aes(x=r, y=log(BF)),

        # add annotation
        p1 <- p1 + annotate("text", x=max(rs)*1.8, y=-2.85, label=paste0("Stro
        p1 <- p1 + annotate("text", x=max(rs)*1.8, y=-1.7 , label=paste0("Mode
        p1 <- p1 + annotate("text", x=max(rs)*1.8, y=-.55 , label=paste0("Anec
        p1 <- p1 + annotate("text", x=max(rs)*1.8, y=2.86 , label=paste0("Stro
        p1 <- p1 + annotate("text", x=max(rs)*1.8, y=1.7  , label=paste0("Mode
        p1 <- p1 + annotate("text", x=max(rs)*1.8, y=.55  , label=paste0("Anec

        # set scale ticks
        p1 <- p1 + scale_y_continuous(breaks=c(c(-log(c(30, 10, 3)), 0, log(c(
        p1 <- p1 + scale_x_continuous(breaks=seq(min(rs), max(rs), length.out=

        return(p1)
    } else {
        return(res)
    }
}
```

References

Rouder, J. N., Speckman, P. L., Sun, D., Morey, R. D., & Iverson, G. (2009). Bayesian t-tests for accepting and rejecting the null hypothesis. Psychonomic Bulletin and Review, 16, 225-237

[/su_tab] [su_tab title="Animating Robustness-Check of Bayes Factor Priors" disabled="no" anchor="" url="" target="blank" class=""]

```
#https://jimgrange.wordpress.com/2015/11/27/animating-robustness-check-of-baye
### plots of prior robustness check

# gif created from PNG plots using http://gifmaker.me/
```

```
# clear R's memory
rm(list = ls())

# load the Bayes factor package
library(BayesFactor)

# set working directory (will be used to save files here, so make sure
# this is where you want to save your plots!)
setwd <- "D:/Work//Blog_YouTube code//Blog/Prior Robust Visualisation/plots"

#------------------------------------------------------------------------
### declare some variables for the analysis

# what is the t-value for the data?
tVal <- 3.098

# how many points in the prior should be explored?
nPoints <- 1000

# what Cauchy rates should be explored?
cauchyRates <- seq(from = 0.01, to = 1.5, length.out = nPoints)

# what effect sizes should be plotted?
effSize <- seq(from = -2, to = 2, length.out = nPoints)

# get the Bayes factor for each prior value
bayesFactors <- sapply(cauchyRates, function(x)
  exp(ttest.tstat(t = tVal, n1 = 76, rscale = x)[['bf']]))
#------------------------------------------------------------------------

#------------------------------------------------------------------------
### do the plotting

# how many plots do we want to produce?
nPlots <- 50
plotWidth <- round(seq(from = 1, to = nPoints, length.out = nPlots), 0)

# loop over each plot
for(i in plotWidth){

  # set up the file
  currFile <- paste(getwd(), "/plot_", i, ".png", sep = "")

  # initiate the png file
  png(file = currFile, width = 1200, height = 1000, res = 200)

  # change the plotting window so plots appear side-by-side
  par(mfrow = c(1, 2))

  #----
  # do the prior density plot
  d <- dcauchy(effSize, scale = cauchyRates[i])
  plot(effSize, d, type = "l", ylim = c(0, 5), xlim = c(-2, 2),
       ylab = "Density", xlab = "Effect Size (d)", lwd = 2, col = "gray48",
```

```
      main = paste("Rate (r) = ", round(cauchyRates[i], 3), sep = ""))

  #-----
  # do the Bayes factor plot
  plot(cauchyRates, bayesFactors, type = "l", lwd = 2, col = "gray48",
       ylim = c(0, max(bayesFactors)), xaxt = "n",
                 xlab = "Cauchy Prior Width (r)", ylab = "Bayes Factor (10)")
  abline(h = 0, lwd = 1)
  abline(h = 6, col = "black", lty = 2, lwd = 2)
  axis(1, at = seq(0, 1.5, 0.25))

  # add the BF at the default Cauchy point
  points(0.707, 9.97, col = "black", cex = 1.5, pch = 21, bg = "red")

  # add the BF for the Cauchy prior currently being plotted
  points(cauchyRates[i], bayesFactors[i], col = "black", pch = 21, cex = 1.3,
         bg = "cyan")

  # add legend
  legend(x = 0.25, y = 3, legend = c("r = 0.707", paste("r = ",
                                                        round(cauchyRates[i], 3)
                                                              sep = "")),
         pch = c(21, 21), lty = c(NA, NA), lwd = c(NA, NA), pt.cex = c(1, 1),
         col = c("black", "black"), pt.bg = c("red", "cyan"), bty = "n")

  # save the current plot
  dev.off()

}
#-------------------------------------------------------------------------------
```

[/su_tab] [su_tab title=”Skewness & Kurtosis” disabled=”no” anchor=”” url=”” target=”blank” class=””]

```
skew(x, na.rm = TRUE)
kurtosi(x, na.rm = TRUE)

#x A data.frame or matrix
#na.rm how to treat missing data

## The function is currently defined as
function (x, na.rm = TRUE)
{
    if (length(dim(x)) == 0) {
        if (na.rm) {
            x <- x[!is.na(x)]
           }

        mx <- mean(x)
         sdx <- sd(x,na.rm=na.rm)
        kurt <- sum((x - mx)^4)/(length(x) * sd(x)^4)  -3
        } else {

    kurt <- rep(NA,dim(x)[2])
    mx <- colMeans(x,na.rm=na.rm)
     sdx <- sd(x,na.rm=na.rm)
```

```
    for (i in 1:dim(x)[2]) {
    kurt[i] <- sum((x[,i] - mx[i])^4,  na.rm = na.rm)/((length(x[,i]) - sum(is
            }
    }
    return(kurt)
  }
```

[/su_tab] [su_tab title=”anovaBF function” disabled=”no” anchor=”” url=”” target=”blank” class=””]

```
#https://richarddmorey.github.io/BayesFactor/
data(ToothGrowth)

## Example plot from ?ToothGrowth

coplot(len ~ dose | supp, data = ToothGrowth, panel = panel.smooth,
       xlab = "ToothGrowth data: length vs dose, given type of supplement")
bf = anovaBF(len ~ supp*dose, data=ToothGrowth)
bf
plot(bf[3:4] / bf[2])

#reduce number of comparisons (alpha inflation)
bf = anovaBF(len ~ supp*dose, data=ToothGrowth, whichModels="top")
bf
```

[su_tab title=”lmBF function” disabled=”no” anchor=”” url=”” target=”blank” class=””]

```
bfMainEffects = lmBF(len ~ supp + dose, data = ToothGrowth)
bfInteraction = lmBF(len ~ supp + dose + supp:dose, data = ToothGrowth)
## Compare the two models
bf = bfInteraction / bfMainEffects
bf
##
newbf = recompute(bf, iterations = 500000)
newbf

# posterior function
## Sample from the posterior of the full model
chains = posterior(bfInteraction, iterations = 10000)
## 1:13 are the only "interesting" parameters
summary(chains[,1:13])
#lot posterior of selected effects
plot(chains[,4:6])
```

Comment

Reduce number of comparisons by specifyig the xact model of interest a priori.

[/su_tab] [/su_tab] [/su_tabs] [/su_spoiler] [su_divider style=”dashed” divider_color=”#000? link_color=”#000? size=”1? margin=”0?] [su_spoiler title=”Markov chain Monte Carlo methods” open=”no” style=”default” icon=”plus” anchor=”mcmc” class=””] [su_tabs vertical=”yes”] [su_tab title=”MCMC 1G” disabled=”no” anchor=”” url=”” target=”blank” class=””]

```
# MODIFIED FROM BEST.R FOR ONE GROUP INSTEAD OF TWO.
# Version of Dec 02, 2015.
# John K. Kruschke
# johnkruschke@gmail.com
# http://www.indiana.edu/~kruschke/BEST/
```

```
#
# This program is believed to be free of errors, but it comes with no guarante
# The user bears all responsibility for interpreting the results.
# Please check the webpage above for updates or corrections.
#
### ************************************************************
### ******** SEE FILE BEST1Gexample.R FOR INSTRUCTIONS ************
### ************************************************************

source("openGraphSaveGraph.R") # graphics functions for Windows, Mac OS, Linux

BEST1Gmcmc = function( y , numSavedSteps=100000, thinSteps=1, showMCMC=FALSE)
  # This function generates an MCMC sample from the posterior distribution.
  # Description of arguments:
  # showMCMC is a flag for displaying diagnostic graphs of the chains.
  #    If F (the default), no chain graphs are displayed. If T, they are.

  require(rjags)

  #-----------------------------------------------------------------------------
  # THE MODEL.
  modelString = "
  model {
    for ( i in 1:Ntotal ) {
      y[i] ~ dt( mu , tau , nu )
    }
    mu ~ dnorm( muM , muP )
    tau <- 1/pow( sigma , 2 )
    sigma ~ dunif( sigmaLow , sigmaHigh )
    nu ~ dexp(1/30)
}
  " # close quote for modelString
  # Write out modelString to a text file
  writeLines( modelString , con="BESTmodel.txt" )

  #-----------------------------------------------------------------------------
  # THE DATA.
  # Load the data:
  Ntotal = length(y)
  # Specify the data in a list, for later shipment to JAGS:
  dataList = list(
    y = y ,
    Ntotal = Ntotal ,
    muM = mean(y) ,
    muP = 0.000001 * 1/sd(y)^2 ,
    sigmaLow = sd(y) / 1000 ,
    sigmaHigh = sd(y) * 1000
  )

  #-----------------------------------------------------------------------------
  # INTIALIZE THE CHAINS.
  # Initial values of MCMC chains based on data:
  mu = mean(y)
  sigma = sd(y)
  # Regarding initial values in next line: (1) sigma will tend to be too big i
```

```
  # the data have outliers, and (2) nu starts at 5 as a moderate value. These
  # initial values keep the burn-in period moderate.
  initsList = list( mu = mu , sigma = sigma , nu = 5 )

  #-----------------------------------------------------------------------------
  # RUN THE CHAINS

  parameters = c( "mu" , "sigma" , "nu" )     # The parameters to be monitored
  adaptSteps = 500              # Number of steps to "tune" the samplers
  burnInSteps = 1000
  nChains = 3
  nIter = ceiling( ( numSavedSteps * thinSteps ) / nChains )
  # Create, initialize, and adapt the model:
  jagsModel = jags.model( "BESTmodel.txt" , data=dataList , inits=initsList ,
                          n.chains=nChains , n.adapt=adaptSteps )
  # Burn-in:
  cat( "Burning in the MCMC chain...\n" )
  update( jagsModel , n.iter=burnInSteps )
  # The saved MCMC chain:
  cat( "Sampling final MCMC chain...\n" )
  codaSamples = coda.samples( jagsModel , variable.names=parameters ,
                              n.iter=nIter , thin=thinSteps )
  # resulting codaSamples object has these indices:
  #   codaSamples[[ chainIdx ]][ stepIdx , paramIdx ]

  #-----------------------------------------------------------------------------
  # EXAMINE THE RESULTS
  if ( showMCMC ) {
    openGraph(width=7,height=7)
    autocorr.plot( codaSamples[[1]] , ask=FALSE )
    show( gelman.diag( codaSamples ) )
    effectiveChainLength = effectiveSize( codaSamples )
    show( effectiveChainLength )
  }

  # Convert coda-object codaSamples to matrix object for easier handling.
  # But note that this concatenates the different chains into one long chain.
  # Result is mcmcChain[ stepIdx , paramIdx ]
  mcmcChain = as.matrix( codaSamples )
  return( mcmcChain )

} # end function BESTmcmc

#===============================================================================

BEST1Gplot = function( y , mcmcChain , compValm=0.0 , ROPEm=NULL ,
                       compValsd=NULL , ROPEsd=NULL ,
                       ROPEeff=NULL , showCurve=FALSE , pairsPlot=FALSE ) {
  # This function plots the posterior distribution (and data).
  # Description of arguments:
  # y is the data vector.
  # mcmcChain is a list of the type returned by function BEST1G.
  # compValm is hypothesized mean for comparing with estimated mean.
  # ROPEm is a two element vector, such as c(-1,1), specifying the limit
  #   of the ROPE on the mean.
```

```
# ROPEsd is a two element vector, such as c(14,16), specifying the limit
#   of the ROPE on the difference of standard deviations.
# ROPEeff is a two element vector, such as c(-1,1), specifying the limit
#   of the ROPE on the effect size.
# showCurve is TRUE or FALSE and indicates whether the posterior should
#   be displayed as a histogram (by default) or by an approximate curve.
# pairsPlot is TRUE or FALSE and indicates whether scatterplots of pairs
#   of parameters should be displayed.
mu = mcmcChain[,"mu"]
sigma = mcmcChain[,"sigma"]
nu = mcmcChain[,"nu"]

if ( pairsPlot ) {
  # Plot the parameters pairwise, to see correlations:
  openGraph(width=7,height=7)
  nPtToPlot = 1000
  plotIdx = floor(seq(1,length(mu),by=length(mu)/nPtToPlot))
  panel.cor = function(x, y, digits=2, prefix="", cex.cor, ...) {
    usr = par("usr"); on.exit(par(usr))
    par(usr = c(0, 1, 0, 1))
    r = (cor(x, y))
    txt = format(c(r, 0.123456789), digits=digits)[1]
    txt = paste(prefix, txt, sep="")
    if(missing(cex.cor)) cex.cor <- 0.8/strwidth(txt)
    text(0.5, 0.5, txt, cex=1.25 ) # was cex=cex.cor*r
  }
  pairs( cbind( mu , sigma , log10(nu) )[plotIdx,] ,
         labels=c( expression(mu) ,
                   expression(sigma) ,
                   expression(log10(nu)) ) ,
         lower.panel=panel.cor , col="skyblue" )
}

# Define matrix for storing summary info:
summaryInfo = NULL

source("plotPost.R")
# Set up window and layout:
openGraph(width=6.0,height=5.0)
layout( matrix( c(3,3,4,4,5,5, 1,1,1,1,2,2) , nrow=6, ncol=2 , byrow=FALSE )
par( mar=c(3.5,3.5,2.5,0.5) , mgp=c(2.25,0.7,0) )

# Select thinned steps in chain for plotting of posterior predictive curves:
chainLength = NROW( mcmcChain )
nCurvesToPlot = 30
stepIdxVec = seq( 1 , chainLength , floor(chainLength/nCurvesToPlot) )
xRange = range( y )
xLim = c( xRange[1]-0.1*(xRange[2]-xRange[1]) ,
          xRange[2]+0.1*(xRange[2]-xRange[1]) )
xVec = seq( xLim[1] , xLim[2] , length=200 )
maxY = max( dt( 0 , df=max(nu[stepIdxVec]) ) / min(sigma[stepIdxVec]) )
# Plot data y and smattering of posterior predictive curves:
stepIdx = 1
plot( xVec , dt( (xVec-mu[stepIdxVec[stepIdx]])/sigma[stepIdxVec[stepIdx]] ,
                 df=nu[stepIdxVec[stepIdx]] )/sigma[stepIdxVec[stepIdx]] ,
```

```
      ylim=c(0,maxY) , cex.lab=1.75 ,
      type="l" , col="skyblue" , lwd=1 , xlab="y" , ylab="p(y)" ,
      main="Data w. Post. Pred." )
for ( stepIdx in 2:length(stepIdxVec) ) {
  lines(xVec, dt( (xVec-mu[stepIdxVec[stepIdx]])/sigma[stepIdxVec[stepIdx]]
                  df=nu[stepIdxVec[stepIdx]] )/sigma[stepIdxVec[stepIdx]] ,
        type="l" , col="skyblue" , lwd=1 )
}
histBinWd = median(sigma)/2
histCenter = mean(mu)
histBreaks = sort( c( seq( histCenter-histBinWd/2 , min(xVec)-histBinWd/2 ,
                           -histBinWd ),
                      seq( histCenter+histBinWd/2 , max(xVec)+histBinWd/2 ,
                           histBinWd ) , xLim ) )
histInfo = hist( y , plot=FALSE , breaks=histBreaks )
yPlotVec = histInfo$density
yPlotVec[ yPlotVec==0.0 ] = NA
xPlotVec = histInfo$mids
xPlotVec[ yPlotVec==0.0 ] = NA
points( xPlotVec , yPlotVec , type="h" , lwd=3 , col="red" )
text( max(xVec) , maxY , bquote(N==.(length(y))) , adj=c(1.1,1.1) )

# Plot posterior distribution of parameter nu:
paramInfo = plotPost( log10(nu) , col="skyblue" , # breaks=30 ,
                      showCurve=showCurve ,
                      xlab=bquote("log10("*nu*")") , cex.lab = 1.75 , showMod
                      main="Normality" ) #  (<0.7 suggests kurtosis)
summaryInfo = rbind( summaryInfo , paramInfo )
rownames(summaryInfo)[NROW(summaryInfo)] = "log10(nu)"

# Plot posterior distribution of parameters mu1, mu2, and their difference:
xlim = range( c( mu , compValm ) )
paramInfo = plotPost( mu ,  xlim=xlim , cex.lab = 1.75 , ROPE=ROPEm ,
                      showCurve=showCurve , compVal = compValm ,
                      xlab=bquote(mu) , main=paste("Mean") ,
                      col="skyblue" )
summaryInfo = rbind( summaryInfo , paramInfo )
rownames(summaryInfo)[NROW(summaryInfo)] = "mu"

# Plot posterior distribution of sigma:
xlim=range( sigma )
paramInfo = plotPost( sigma ,  xlim=xlim , cex.lab = 1.75 , ROPE=ROPEsd ,
                      showCurve=showCurve , compVal=compValsd ,
                      xlab=bquote(sigma) , main=paste("Std. Dev.") ,
                      col="skyblue" , showMode=TRUE )
summaryInfo = rbind( summaryInfo , paramInfo )
rownames(summaryInfo)[NROW(summaryInfo)] = "sigma"

# Plot of estimated effect size:
effectSize = ( mu - compValm ) / sigma
paramInfo = plotPost( effectSize , compVal=0 ,  ROPE=ROPEeff ,
                      showCurve=showCurve ,
                      xlab=bquote( (mu-.(compValm)) / sigma ),
                      showMode=TRUE , cex.lab=1.75 , main="Effect Size" , col
summaryInfo = rbind( summaryInfo , paramInfo )
```

```
  rownames(summaryInfo)[NROW(summaryInfo)] = "effSz"

  return( summaryInfo )

  } # end of function BEST1Gplot

#==============================================================================
```

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```
# MODIFIED 2015 DEC 02.
# John K. Kruschke
# johnkruschke@gmail.com
# http://www.indiana.edu/~kruschke/BEST/
#
# This program is believed to be free of errors, but it comes with no guarante
# The user bears all responsibility for interpreting the results.
# Please check the webpage above for updates or corrections.
#
### ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
### ~~~~~~~~ SEE FILE BESTexample.R FOR INSTRUCTIONS ~~~~~~~~~~~~~~
### ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~

# Load various essential functions:
source("DBDA2E-utilities.R")

BESTmcmc = function( y1 , y2 ,
                     priorOnly=FALSE , showMCMC=FALSE ,
                     numSavedSteps=20000 , thinSteps=1 ,
                     mu1PriorMean = mean(c(y1,y2)) ,
                     mu1PriorSD = sd(c(y1,y2))*5 ,
                     mu2PriorMean = mean(c(y1,y2)) ,
                     mu2PriorSD = sd(c(y1,y2))*5 ,
                     sigma1PriorMode = sd(c(y1,y2)) ,
                     sigma1PriorSD = sd(c(y1,y2))*5 ,
                     sigma2PriorMode = sd(c(y1,y2)) ,
                     sigma2PriorSD = sd(c(y1,y2))*5 ,
                     nuPriorMean = 30 ,
                     nuPriorSD = 30 ,
                     runjagsMethod=runjagsMethodDefault ,
                     nChains=nChainsDefault ) {
  # This function generates an MCMC sample from the posterior distribution.
  # Description of arguments:
  # showMCMC is a flag for displaying diagnostic graphs of the chains.
  #    If F (the default), no chain graphs are displayed. If T, they are.

  #------------------------------------------------------------------------
  # THE DATA.
  # Load the data:
  y = c( y1 , y2 ) # combine data into one vector
  x = c( rep(1,length(y1)) , rep(2,length(y2)) ) # create group membership cod
  Ntotal = length(y)
  # Specify the data and prior constants in a list, for later shipment to JAGS
  if ( priorOnly ) {
```

```
  dataList = list(
    #  y = y ,
    x = x ,
    Ntotal = Ntotal ,
    mu1PriorMean = mu1PriorMean ,
    mu1PriorSD = mu1PriorSD ,
    mu2PriorMean = mu2PriorMean ,
    mu2PriorSD = mu2PriorSD ,
    Sh1 = gammaShRaFromModeSD( mode=sigma1PriorMode ,
                               sd=sigma1PriorSD )$shape ,
    Ra1 = gammaShRaFromModeSD( mode=sigma1PriorMode ,
                               sd=sigma1PriorSD )$rate ,
    Sh2 = gammaShRaFromModeSD( mode=sigma2PriorMode ,
                               sd=sigma2PriorSD )$shape ,
    Ra2 = gammaShRaFromModeSD( mode=sigma2PriorMode ,
                               sd=sigma2PriorSD )$rate ,
    ShNu = gammaShRaFromMeanSD( mean=nuPriorMean , sd=nuPriorSD )$shape ,
    RaNu = gammaShRaFromMeanSD( mean=nuPriorMean , sd=nuPriorSD )$rate
  )
} else {
  dataList = list(
    y = y ,
    x = x ,
    Ntotal = Ntotal ,
    mu1PriorMean = mu1PriorMean ,
    mu1PriorSD = mu1PriorSD ,
    mu2PriorMean = mu2PriorMean ,
    mu2PriorSD = mu2PriorSD ,
    Sh1 = gammaShRaFromModeSD( mode=sigma1PriorMode ,
                               sd=sigma1PriorSD )$shape ,
    Ra1 = gammaShRaFromModeSD( mode=sigma1PriorMode ,
                               sd=sigma1PriorSD )$rate ,
    Sh2 = gammaShRaFromModeSD( mode=sigma2PriorMode ,
                               sd=sigma2PriorSD )$shape ,
    Ra2 = gammaShRaFromModeSD( mode=sigma2PriorMode ,
                               sd=sigma2PriorSD )$rate ,
    ShNu = gammaShRaFromMeanSD( mean=nuPriorMean , sd=nuPriorSD )$shape ,
    RaNu = gammaShRaFromMeanSD( mean=nuPriorMean , sd=nuPriorSD )$rate
  )
}

#------------------------------------------------------------------------------
# THE MODEL.
modelString = "
model {
  for ( i in 1:Ntotal ) {
    y[i] ~ dt( mu[x[i]] , 1/sigma[x[i]]^2 , nu )
  }
  mu[1] ~ dnorm( mu1PriorMean , 1/mu1PriorSD^2 )  # prior for mu[1]
  sigma[1] ~ dgamma( Sh1 , Ra1 )     # prior for sigma[1]
  mu[2] ~ dnorm( mu2PriorMean , 1/mu2PriorSD^2 )  # prior for mu[2]
  sigma[2] ~ dgamma( Sh2 , Ra2 )     # prior for sigma[2]
  nu ~ dgamma( ShNu , RaNu ) # prior for nu
}
" # close quote for modelString
```

```
# Write out modelString to a text file
writeLines( modelString , con="BESTmodel.txt" )

#------------------------------------------------------------------------------
# INTIALIZE THE CHAINS.
# Initial values of MCMC chains based on data:
mu = c( mean(y1) , mean(y2) )
sigma = c( sd(y1) , sd(y2) )
# Regarding initial values in next line: (1) sigma will tend to be too big i
# the data have outliers, and (2) nu starts at 5 as a moderate value. These
# initial values keep the burn-in period moderate.
initsList = list( mu = mu , sigma = sigma , nu = 5 )

#------------------------------------------------------------------------------
# RUN THE CHAINS

parameters = c( "mu" , "sigma" , "nu" )     # The parameters to be monitored
adaptSteps = 500              # Number of steps to "tune" the samplers
burnInSteps = 1000

runJagsOut <- run.jags( method=runjagsMethod , model="BESTmodel.txt" , monit
                    / length( paramSampleVec ) )
  } else {
    pcgtCompVal=NA
  }
  return( c( meanParam , medianParam , modeParam , hdiLim , pcgtCompVal ) )
}
# Define matrix for storing summary info:
summaryInfo = matrix( 0 , nrow=9 , ncol=6 , dimnames=list(
  PARAMETER=c( "mu1" , "mu2" , "muDiff" , "sigma1" , "sigma2" , "sigmaDiff"
               "nu" , "nuLog10" , "effSz" ),
  SUMMARY.INFO=c( "mean" , "median" , "mode" , "HDIlow" , "HDIhigh" ,
                  "pcgtZero" )
) )
summaryInfo[ "mu1" , ] = mcmcSummary( mcmcChain[,"mu[1]"] )
summaryInfo[ "mu2" , ] = mcmcSummary( mcmcChain[,"mu[2]"] )
summaryInfo[ "muDiff" , ] = mcmcSummary( mcmcChain[,"mu[1]"]
                                         - mcmcChain[,"mu[2]"] ,
                                         compVal=0 )
summaryInfo[ "sigma1" , ] = mcmcSummary( mcmcChain[,"sigma[1]"] )
summaryInfo[ "sigma2" , ] = mcmcSummary( mcmcChain[,"sigma[2]"] )
summaryInfo[ "sigmaDiff" , ] = mcmcSummary( mcmcChain[,"sigma[1]"]
                                            - mcmcChain[,"sigma[2]"] ,
                                            compVal=0 )
summaryInfo[ "nu" , ] = mcmcSummary( mcmcChain[,"nu"] )
summaryInfo[ "nuLog10" , ] = mcmcSummary( log10(mcmcChain[,"nu"]) )

N1 = length(y1)
N2 = length(y2)
effSzChain = ( ( mcmcChain[,"mu[1]"] - mcmcChain[,"mu[2]"] )
               / sqrt( ( mcmcChain[,"sigma[1]"]^2
                         + mcmcChain[,"sigma[2]"]^2 ) / 2 ) )
summaryInfo[ "effSz" , ] = mcmcSummary( effSzChain , compVal=0 )
# Or, use sample-size weighted version:
# effSz = ( mu1 - mu2 ) / sqrt( ( sigma1^2 *(N1-1) + sigma2^2 *(N2-1) )
```

```
  #                                 / (N1+N2-2) )
  # Be sure also to change plot label in BESTplot function, below.
  return( summaryInfo )
}

#===============================================================================

BESTplot = function( y1 , y2 , mcmcChain , ROPEm=NULL , ROPEsd=NULL ,
                     ROPEeff=NULL , showCurve=FALSE , pairsPlot=FALSE ) {
  # This function plots the posterior distribution (and data).
  # Description of arguments:
  # y1 and y2 are the data vectors.
  # mcmcChain is a list of the type returned by function BTT.
  # ROPEm is a two element vector, such as c(-1,1), specifying the limit
  #   of the ROPE on the difference of means.
  # ROPEsd is a two element vector, such as c(-1,1), specifying the limit
  #   of the ROPE on the difference of standard deviations.
  # ROPEeff is a two element vector, such as c(-1,1), specifying the limit
  #   of the ROPE on the effect size.
  # showCurve is TRUE or FALSE and indicates whether the posterior should
  #   be displayed as a histogram (by default) or by an approximate curve.
  # pairsPlot is TRUE or FALSE and indicates whether scatterplots of pairs
  #   of parameters should be displayed.
  mu1 = mcmcChain[,"mu[1]"]
  mu2 = mcmcChain[,"mu[2]"]
  sigma1 = mcmcChain[,"sigma[1]"]
  sigma2 = mcmcChain[,"sigma[2]"]
  nu = mcmcChain[,"nu"]
  if ( pairsPlot ) {
    # Plot the parameters pairwise, to see correlations:
    openGraph(width=7,height=7)
    nPtToPlot = 1000
    plotIdx = floor(seq(1,length(mu1),by=length(mu1)/nPtToPlot))
    panel.cor = function(x, y, digits=2, prefix="", cex.cor, ...) {
      usr = par("usr"); on.exit(par(usr))
      par(usr = c(0, 1, 0, 1))
      r = (cor(x, y))
      txt = format(c(r, 0.123456789), digits=digits)[1]
      txt = paste(prefix, txt, sep="")
      if(missing(cex.cor)) cex.cor <- 0.8/strwidth(txt)
      text(0.5, 0.5, txt, cex=1.25 ) # was cex=cex.cor*r
    }
    pairs( cbind( mu1 , mu2 , sigma1 , sigma2 , log10(nu) )[plotIdx,] ,
           labels=c( expression(mu[1]) , expression(mu[2]) ,
                     expression(sigma[1]) , expression(sigma[2]) ,
                     expression(log10(nu)) ) ,
           lower.panel=panel.cor , col="skyblue" )
  }
  # source("plotPost.R") # in DBDA2E-utilities.R
  # Set up window and layout:
  openGraph(width=6.0,height=8.0)
  layout( matrix( c(4,5,7,8,3,1,2,6,9,10) , nrow=5, byrow=FALSE ) )
  par( mar=c(3.5,3.5,2.5,0.5) , mgp=c(2.25,0.7,0) )

  # Select thinned steps in chain for plotting of posterior predictive curves:
```

```
chainLength = NROW( mcmcChain )
nCurvesToPlot = 30
stepIdxVec = seq( 1 , chainLength , floor(chainLength/nCurvesToPlot) )
xRange = range( c(y1,y2) )
if ( isTRUE( all.equal( xRange[2] , xRange[1] ) ) ) {
  meanSigma = mean( c(sigma1,sigma2) )
  xRange = xRange + c( -meanSigma , meanSigma )
}
xLim = c( xRange[1]-0.1*(xRange[2]-xRange[1]) ,
          xRange[2]+0.1*(xRange[2]-xRange[1]) )
xVec = seq( xLim[1] , xLim[2] , length=200 )
maxY = max( dt( 0 , df=max(nu[stepIdxVec]) ) /
              min(c(sigma1[stepIdxVec],sigma2[stepIdxVec])) )
# Plot data y1 and smattering of posterior predictive curves:
stepIdx = 1
plot( xVec , dt( (xVec-mu1[stepIdxVec[stepIdx]])/sigma1[stepIdxVec[stepIdx]]
                 df=nu[stepIdxVec[stepIdx]] )/sigma1[stepIdxVec[stepIdx]] ,
      ylim=c(0,maxY) , cex.lab=1.75 ,
      type="l" , col="skyblue" , lwd=1 , xlab="y" , ylab="p(y)" ,
      main="Data Group 1 w. Post. Pred." )
for ( stepIdx in 2:length(stepIdxVec) ) {
  lines(xVec, dt( (xVec-mu1[stepIdxVec[stepIdx]])/sigma1[stepIdxVec[stepIdx]
                  df=nu[stepIdxVec[stepIdx]] )/sigma1[stepIdxVec[stepIdx]] ,
        type="l" , col="skyblue" , lwd=1 )
}
histBinWd = median(sigma1)/2
histCenter = mean(mu1)
histBreaks = sort( c( seq( histCenter-histBinWd/2 , min(xVec)-histBinWd/2 ,
                           -histBinWd ),
                      seq( histCenter+histBinWd/2 , max(xVec)+histBinWd/2 ,
                           histBinWd ) , xLim ) )
histInfo = hist( y1 , plot=FALSE , breaks=histBreaks )
yPlotVec = histInfo$density
yPlotVec[ yPlotVec==0.0 ] = NA
xPlotVec = histInfo$mids
xPlotVec[ yPlotVec==0.0 ] = NA
points( xPlotVec , yPlotVec , type="h" , lwd=3 , col="red" )
text( max(xVec) , maxY , bquote(N[1]==.(length(y1))) , adj=c(1.1,1.1) )
# Plot data y2 and smattering of posterior predictive curves:
stepIdx = 1
plot( xVec , dt( (xVec-mu2[stepIdxVec[stepIdx]])/sigma2[stepIdxVec[stepIdx]]
                 df=nu[stepIdxVec[stepIdx]] )/sigma2[stepIdxVec[stepIdx]] ,
      ylim=c(0,maxY) , cex.lab=1.75 ,
      type="l" , col="skyblue" , lwd=1 , xlab="y" , ylab="p(y)" ,
      main="Data Group 2 w. Post. Pred." )
for ( stepIdx in 2:length(stepIdxVec) ) {
  lines(xVec, dt( (xVec-mu2[stepIdxVec[stepIdx]])/sigma2[stepIdxVec[stepIdx]]
                  df=nu[stepIdxVec[stepIdx]] )/sigma2[stepIdxVec[stepIdx]] ,
        type="l" , col="skyblue" , lwd=1 )
}
histBinWd = median(sigma2)/2
histCenter = mean(mu2)
histBreaks = sort( c( seq( histCenter-histBinWd/2 , min(xVec)-histBinWd/2 ,
                           -histBinWd ),
                      seq( histCenter+histBinWd/2 , max(xVec)+histBinWd/2 ,
```

```
                              histBinWd ) , xLim ) )
histInfo = hist( y2 , plot=FALSE , breaks=histBreaks )
yPlotVec = histInfo$density
yPlotVec[ yPlotVec==0.0 ] = NA
xPlotVec = histInfo$mids
xPlotVec[ yPlotVec==0.0 ] = NA
points( xPlotVec , yPlotVec , type="h" , lwd=3 , col="red" )
text( max(xVec) , maxY , bquote(N[2]==.(length(y2))) , adj=c(1.1,1.1) )

# Plot posterior distribution of parameter nu:
histInfo = plotPost( log10(nu) , col="skyblue" , # breaks=30 ,
                     showCurve=showCurve ,
                     xlab=bquote("log10("*nu*")") , cex.lab = 1.75 ,
                     cenTend=c("mode","median","mean")[1] ,
                     main="Normality" ) #  (<0.7 suggests kurtosis)

# Plot posterior distribution of parameters mu1, mu2, and their difference:
xlim = range( c( mu1 , mu2 ) )
histInfo = plotPost( mu1 ,  xlim=xlim , cex.lab = 1.75 ,
                     showCurve=showCurve ,
                     xlab=bquote(mu[1]) , main=paste("Group",1,"Mean") ,
                     col="skyblue" )
histInfo = plotPost( mu2 ,  xlim=xlim , cex.lab = 1.75 ,
                     showCurve=showCurve ,
                     xlab=bquote(mu[2]) , main=paste("Group",2,"Mean") ,
                     col="skyblue" )
histInfo = plotPost( mu1-mu2 , compVal=0 ,  showCurve=showCurve ,
                     xlab=bquote(mu[1] - mu[2]) , cex.lab = 1.75 , ROPE=ROPE
                     main="Difference of Means" , col="skyblue" )

# Plot posterior distribution of param's sigma1, sigma2, and their differenc
xlim=range( c( sigma1 , sigma2 ) )
histInfo = plotPost( sigma1 ,  xlim=xlim , cex.lab = 1.75 ,
                     showCurve=showCurve ,
                     xlab=bquote(sigma[1]) , main=paste("Group",1,"Std. Dev.
                     col="skyblue" , cenTend=c("mode","median","mean")[1] )
histInfo = plotPost( sigma2 ,  xlim=xlim , cex.lab = 1.75 ,
                     showCurve=showCurve ,
                     xlab=bquote(sigma[2]) , main=paste("Group",2,"Std. Dev.
                     col="skyblue" , cenTend=c("mode","median","mean")[1] )
histInfo = plotPost( sigma1-sigma2 ,
                     compVal=0 ,  showCurve=showCurve ,
                     xlab=bquote(sigma[1] - sigma[2]) , cex.lab = 1.75 ,
                     ROPE=ROPEsd ,
                     main="Difference of Std. Dev.s" , col="skyblue" ,
                     cenTend=c("mode","median","mean")[1] )

# Plot of estimated effect size. Effect size is d-sub-a from
# Macmillan & Creelman, 1991; Simpson & Fitter, 1973; Swets, 1986a, 1986b.
effectSize = ( mu1 - mu2 ) / sqrt( ( sigma1^2 + sigma2^2 ) / 2 )
histInfo = plotPost( effectSize , compVal=0 ,  ROPE=ROPEeff ,
                     showCurve=showCurve ,
                     xlab=bquote( (mu[1]-mu[2])
                                  /sqrt((sigma[1]^2 +sigma[2]^2 )/2 ) ),
                     cenTend=c("mode","median","mean")[1] , cex.lab=1.0 , ma
```

```
                        col="skyblue" )
  # Or use sample-size weighted version:
  # Hedges 1981; Wetzels, Raaijmakers, Jakab & Wagenmakers 2009.
  # N1 = length(y1)
  # N2 = length(y2)
  # effectSize = ( mu1 - mu2 ) / sqrt( ( sigma1^2 *(N1-1) + sigma2^2 *(N2-1) )
  #                                    / (N1+N2-2) )
  # Be sure also to change BESTsummary function, above.
  # histInfo = plotPost( effectSize , compVal=0 ,  ROPE=ROPEeff ,
  #          showCurve=showCurve ,
  #          xlab=bquote( (mu[1]-mu[2])
  #          /sqrt((sigma[1]^2 *(N[1]-1)+sigma[2]^2 *(N[2]-1))/(N[1]+N[2]-2))
  #          cenTend=c("mode","median","mean")[1] , cex.lab=1.0 , main="Effect
  return( BESTsummary( y1 , y2 , mcmcChain ) )
} # end of function BESTplot

#==============================================================================

BESTpower = function( mcmcChain , N1 , N2 , ROPEm , ROPEsd , ROPEeff ,
                      maxHDIWm , maxHDIWsd , maxHDIWeff , nRep=200 ,
                      mcmcLength=10000 , saveName="BESTpower.Rdata" ,
                      showFirstNrep=0 ) {
  # This function estimates power.
  # Description of arguments:
  # mcmcChain is a matrix of the type returned by function BESTmcmc.
  # N1 and N2 are sample sizes for the two groups.
  # ROPEm is a two element vector, such as c(-1,1), specifying the limit
  #   of the ROPE on the difference of means.
  # ROPEsd is a two element vector, such as c(-1,1), specifying the limit
  #   of the ROPE on the difference of standard deviations.
  # ROPEeff is a two element vector, such as c(-1,1), specifying the limit
  #   of the ROPE on the effect size.
  # maxHDIWm is the maximum desired width of the 95% HDI on the difference
  #   of means.
  # maxHDIWsd is the maximum desired width of the 95% HDI on the difference
  #   of standard deviations.
  # maxHDIWeff is the maximum desired width of the 95% HDI on the effect size.
  # nRep is the number of simulated experiments used to estimate the power.
  #source("HDIofMCMC.R") # in DBDA2E-utilities.R
  #source("HDIofICDF.R") # in DBDA2E-utilities.R
  chainLength = NROW( mcmcChain )
  # Select thinned steps in chain for posterior predictions:
  stepIdxVec = seq( 1 , chainLength , floor(chainLength/nRep) )
  goalTally = list( HDIm.gt.ROPE = c(0) ,
                    HDIm.lt.ROPE = c(0) ,
                    HDIm.in.ROPE = c(0) ,
                    HDIm.wd.max = c(0) ,
                    HDIsd.gt.ROPE = c(0) ,
                    HDIsd.lt.ROPE = c(0) ,
                    HDIsd.in.ROPE = c(0) ,
                    HDIsd.wd.max = c(0) ,
                    HDIeff.gt.ROPE = c(0) ,
                    HDIeff.lt.ROPE = c(0) ,
                    HDIeff.in.ROPE = c(0) ,
                    HDIeff.wd.max = c(0) )
```

```
power     = list( HDIm.gt.ROPE = c(0,0,0) ,
                  HDIm.lt.ROPE = c(0,0,0) ,
                  HDIm.in.ROPE = c(0,0,0) ,
                  HDIm.wd.max = c(0,0,0) ,
                  HDIsd.gt.ROPE = c(0,0,0) ,
                  HDIsd.lt.ROPE = c(0,0,0) ,
                  HDIsd.in.ROPE = c(0,0,0) ,
                  HDIsd.wd.max = c(0,0,0) ,
                  HDIeff.gt.ROPE = c(0,0,0) ,
                  HDIeff.lt.ROPE = c(0,0,0) ,
                  HDIeff.in.ROPE = c(0,0,0) ,
                  HDIeff.wd.max = c(0,0,0) )
nSim = 0
for ( stepIdx in stepIdxVec ) {
  nSim = nSim + 1
  cat( "\n:::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::\n"
  cat( paste( "Power computation: Simulated Experiment" , nSim , "of" ,
              length(stepIdxVec) , ":\n\n" ) )
  # Get parameter values for this simulation:
  mu1Val = mcmcChain[stepIdx,"mu[1]"]
  mu2Val = mcmcChain[stepIdx,"mu[2]"]
  sigma1Val = mcmcChain[stepIdx,"sigma[1]"]
  sigma2Val = mcmcChain[stepIdx,"sigma[2]"]
  nuVal = mcmcChain[stepIdx,"nu"]
  # Generate simulated data:
  y1 = rt( N1 , df=nuVal ) * sigma1Val + mu1Val
  y2 = rt( N2 , df=nuVal ) * sigma2Val + mu2Val
  # Get posterior for simulated data:
  simChain = BESTmcmc( y1, y2, numSavedSteps=mcmcLength, thinSteps=1,
                       showMCMC=FALSE )
  if (nSim <= showFirstNrep ) { BESTplot( y1, y2, simChain, ROPEm=ROPEm, ROP
    goalTally$HDIm.gt.ROPE = goalTally$HDIm.gt.ROPE + 1 }
  if ( HDIm[2] < ROPEm[1] ) { goalTally$HDIm.lt.ROPE = goalTally$HDIm.lt.ROP
    goalTally$HDIm.in.ROPE = goalTally$HDIm.in.ROPE + 1 }
  if ( HDIm[2] - HDIm[1] < maxHDIWm ) { goalTally$HDIm.wd.max = goalTally$HD
    goalTally$HDIsd.gt.ROPE = goalTally$HDIsd.gt.ROPE + 1 }
  if ( HDIsd[2] < ROPEsd[1] ) { goalTally$HDIsd.lt.ROPE = goalTally$HDIsd.lt
    goalTally$HDIsd.in.ROPE = goalTally$HDIsd.in.ROPE + 1 }
  if ( HDIsd[2] - HDIsd[1] < maxHDIWsd ) { goalTally$HDIsd.wd.max = goalTall
    goalTally$HDIeff.gt.ROPE = goalTally$HDIeff.gt.ROPE + 1 }
  if ( HDIeff[2] < ROPEeff[1] ) { goalTally$HDIeff.lt.ROPE = goalTally$HDIef
    goalTally$HDIeff.in.ROPE = goalTally$HDIeff.in.ROPE + 1 }
  if ( HDIeff[2] - HDIeff[1] < maxHDIWeff ) { goalTally$HDIeff.wd.max = goal
  warning("pcntOut indicates more than 50% outliers; did you intend this?")
}
if ( nOut < 2 & pcntOut > 0 ) {
  stop("Combination of nPerGrp and pcntOut yields too few outliers.")
}
if ( nIn < 2 ) { stop("Too few non-outliers.") } sdN = function( x ) { sqrt(
    yOut = rnorm(n=Nout)                  # Random values for outliers
    yOut=((yOut-mean(yOut))/sdN(yOut))*(sigma*sdOutMult)+mu # Realize exactl
  }
  y = c(y,yOut)                       # Concatenate main with outliers.
  return(y)
}
```

```
  y1 = genDat( mu=mu1 , sigma=sd1 , Nin=nIn , Nout=nOut )
  y2 = genDat( mu=mu2 , sigma=sd2 , Nin=nIn , Nout=nOut )
  #
  # Set up window and layout:
  openGraph(width=7,height=7) # Plot the data.
  layout(matrix(1:2,nrow=2))
  histInfo = hist( y1 , main="Simulated Data" , col="pink2" , border="white" ,
                   xlim=range(c(y1,y2)) , breaks=30 , prob=TRUE )
  text( max(c(y1,y2)) , max(histInfo$density) ,
        bquote(N==.(nPerGrp)) , adj=c(1,1) )
  xlow=min(histInfo$breaks)
  xhi=max(histInfo$breaks)
  xcomb=seq(xlow,xhi,length=1001)
  lines( xcomb , dnorm(xcomb,mean=mu1,sd=sd1)*nIn/(nIn+nOut) +
           dnorm(xcomb,mean=mu1,sd=sd1*sdOutMult)*nOut/(nIn+nOut) , lwd=3 )
  lines( xcomb , dnorm(xcomb,mean=mu1,sd=sd1)*nIn/(nIn+nOut) ,
         lty="dashed" , col="green", lwd=3)
  lines( xcomb , dnorm(xcomb,mean=mu1,sd=sd1*sdOutMult)*nOut/(nIn+nOut) ,
         lty="dashed" , col="red", lwd=3)
  histInfo = hist( y2 , main="" , col="pink2" , border="white" ,
                   xlim=range(c(y1,y2)) , breaks=30 , prob=TRUE )
  text( max(c(y1,y2)) , max(histInfo$density) ,
        bquote(N==.(nPerGrp)) , adj=c(1,1) )
  xlow=min(histInfo$breaks)
  xhi=max(histInfo$breaks)
  xcomb=seq(xlow,xhi,length=1001)
  lines( xcomb , dnorm(xcomb,mean=mu2,sd=sd2)*nIn/(nIn+nOut) +
           dnorm(xcomb,mean=mu2,sd=sd2*sdOutMult)*nOut/(nIn+nOut) , lwd=3)
  lines( xcomb , dnorm(xcomb,mean=mu2,sd=sd2)*nIn/(nIn+nOut) ,
         lty="dashed" , col="green", lwd=3)
  lines( xcomb , dnorm(xcomb,mean=mu2,sd=sd2*sdOutMult)*nOut/(nIn+nOut) ,
         lty="dashed" , col="red", lwd=3)
  #
  return( list( y1=y1 , y2=y2 ) )
}

#==============================================================================
```

[/su_tab] [su_tab title=”BEST – Bayesian MCMC power analysis” disabled=”no” anchor=”” url=”” target=”blank” class=””]

```
# Version of May 26, 2012. Re-checked on 2015 May 08.
# John K. Kruschke
# johnkruschke@gmail.com
# http://www.indiana.edu/~kruschke/BEST/
#
# This program is believed to be free of errors, but it comes with no guarante
# The user bears all responsibility for interpreting the results.
# Please check the webpage above for updates or corrections.
#
### ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
### ~~~~~~~~ SEE FILE BESTexample.R FOR INSTRUCTIONS ~~~~~~~~~~~~~~
### ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
```

```
# OPTIONAL: Clear R's memory and graphics:
rm(list=ls())  # Careful! This clears all of R's memory!
graphics.off() # This closes all of R's graphics windows.

# Get the functions loaded into R's working memory:
source("BEST.R")

#------------------------------------------------------------------------------
# RETROSPECTIVE POWER ANALYSIS.
# !! This section assumes you have already run BESTexample.R !!
# Re-load the saved data and MCMC chain from the previously conducted
# Bayesian analysis. This re-loads the variables y1, y2, mcmcChain, etc.
load( "BESTexampleMCMC.Rdata" )
power = BESTpower( mcmcChain , N1=length(y1) , N2=length(y2) ,
                   ROPEm=c(-0.1,0.1) , ROPEsd=c(-0.1,0.1) , ROPEeff=c(-0.1,0.1)
                   maxHDIWm=2.0 , maxHDIWsd=2.0 , maxHDIWeff=0.2 , nRep=1000 ,
                   mcmcLength=10000 , saveName = "BESTexampleRetroPower.Rdata"

#------------------------------------------------------------------------------
# PROSPECTIVE POWER ANALYSIS, using fictitious strong data.
# Generate large fictitious data set that expresses hypothesis:
prospectData = makeData( mu1=108, sd1=17, mu2=100, sd2=15, nPerGrp=1000,
                         pcntOut=10, sdOutMult=2.0, rnd.seed=NULL )
y1pro = prospectData$y1 # Merely renames simulated data for convenience below.
y2pro = prospectData$y2 # Merely renames simulated data for convenience below.
# Generate Bayesian posterior distribution from fictitious data:
# (uses fewer than usual MCMC steps because it only needs nRep credible
# parameter combinations, not a high-resolution representation)
mcmcChainPro = BESTmcmc( y1pro , y2pro , numSavedSteps=2000 )
postInfoPro = BESTplot( y1pro , y2pro , mcmcChainPro , pairsPlot=TRUE )
save( y1pro, y2pro, mcmcChainPro, postInfoPro,
      file="BESTexampleProPowerMCMC.Rdata" )
# Now compute the prospective power for planned sample sizes:
N1plan = N2plan = 50 # specify planned sample size
powerPro = BESTpower( mcmcChainPro , N1=N1plan , N2=N2plan , showFirstNrep=5 ,
                    ROPEm=c(-1.5,1.5) , ROPEsd=c(-0.0,0.0) , ROPEeff=c(-0.0,0.0
                    maxHDIWm=15.0 , maxHDIWsd=10.0 , maxHDIWeff=1.0 , nRep=1000
                    mcmcLength=10000 , saveName = "BESTexampleProPower.Rdata" )

#------------------------------------------------------------------------------
```

[/su_tab] [/su_tabs] [/su_spoiler] [su_divider style=”dashed” divider_color=”#000? link_color=”#000? size=”1? margin=”0?] [su_spoiler title=”Various plots” open=”no” style=”default” icon=”plus” anchor=”plots” class=””] [su_tabs vertical=”yes”] [su_tab title=”Beanplots” disabled=”no” anchor=”” url=”” target=”blank” class=””]

```
#https://cran.r-project.org/web/packages/beanplot/beanplot.pdf
par( mfrow = c( 1, 4 ) )
with(dataexp2, beanplot(v00, ylim = c(0,10), col="lightgray", main = "v00", ke
with(dataexp2, beanplot(v01, ylim = c(0,10), col="lightgray", main = "v01", ke
with(dataexp2, beanplot(v10, ylim = c(0,10), col="darkgray", main = "v10", ker
with(dataexp2, beanplot(v11, ylim = c(0,10), col="darkgray", main = "v11", ker
```

```
#with ylim and titles
with(dataexp2, beanplot(v00, ylab = "VAS Brightness rating", xlab = "beanplot
ylim = c(0,10), col="darkgray", main = "v00", kernel = "gaussian", cut = 3, cu
overallline = "mean", horizontal = FALSE, side = "no", jitter = NULL, beanline



install.packages ("beanplot")
library("beanplot")
par( mfrow = c( 1, 2 ) )
with(dataexp2, beanplot(v00, col="darkgray", main = "v00", kernel = "gaussian"
with(dataexp2, beanplot(v01, col="darkgray", main = "v01", kernel = "gaussian"
par( mfrow = c( 1, 2 ) )
with(dataexp2, beanplot(v10, col="darkgray", main = "v10", kernel = "gaussian"
with(dataexp2, beanplot(v11, col="darkgray", main = "v11", kernel = "gaussian"

stripchart(variable ~ factor, vertical=TRUE, method="stack",
  ylab="variable", data=StackedData)

#two sided
with(dataexp1, beanplot(v00, v10, col="darkgray", main = "v00 vs. v10", kernel

#verticalpar( mfrow = c( 2, 1 ) )
install.packages ("beanplot")
library("beanplot")
par( mfrow = c( 2, 1 ) ) # layout matrix

with(dataexp1, beanplot(v00, v10, main = "v00 vs. v10", kernel = "gaussian", c
cutmin = -Inf, cutmax = Inf, overallline = "mean", horizontal = T, side = "bot

with(dataexp1, beanplot(v01, v11, main = "v01 vs. v11", kernel = "gaussian", c
cutmin = -Inf, cutmax = Inf, overallline = "mean", horizontal = T, side = "bot


#exp1
dataexp1 <-
  read.table("http://www.irrational-decisions.com/phd-thesis/dataexp1.csv",
   header=TRUE, sep=",", na.strings="NA", dec=".", strip.white=TRUE)

par( mfrow = c( 1, 2) )
with(dataexp1, beanplot(v00, ylim = c(0,7), col="lightgray", main = "v00", ker
with(dataexp1, beanplot(v10, ylim = c(0,7), col="lightgray", main = "v01", ker

par( mfrow = c( 1, 2) )
with(dataexp1, beanplot(v01, ylim = c(3,10), col="darkgray", main = "v10", ker
with(dataexp1, beanplot(v11, ylim = c(3,10), col="darkgray", main = "v11", ker
```

[/su_tab] [su_tab title=”Density and Rug plot” disabled=”no” anchor=”” url=”” target=”blank” class=””]

```
#histogram and rug plot

plot(density(dataexp2$v00))
```

```
rug(dataexp2$v00, col=2, lwd=3.5)

##############

library(MASS)
plot(density(dataexp2$v00, bw=5))
rug(dataexp2$v00+ rnorm(length(dataexp2$v00), sd=5), col=2, lwd=3.5)
```

[/su_tab] [su_tab title="Dirac function – Interdisciplinarity versus Overspecialisation" disabled="no" anchor="" url="" target="blank" class=""]

```
x = c(5)
y   = c(9)
plot(x,y,type="h",xlim=c(0,10),ylim=c(0,10),lwd=2,col="blue",ylab="knowledge",
```

[/su_tab] [su_tab title="Google Trends" disabled="no" anchor="" url="" target="blank" class=""]

```
install.packages("gtrendsR")
library(gtrendsR)
gtrends(c("bayesian inference", "p-value"), time = "all") # since 2004

res <- gtrends(c("Bayesian inference", "Markov Chain Monte Carlo", "ANOVA"), g

res <- gtrends("Markov Chain Monte Carlo", geo = c("US", "GB", "DE"))

plot(res)

#get vars

length(res)
str(res)
res$interest_over_time
ff<-res$interest_over_time

scatterplot(ff$hits~ff$date| geo, reg.line=FALSE, smooth=FALSE, spread=FALSE,

res2 <- gtrends(c("p-value", "bayes factor"))
```

[/su_tab] [su_tab title="JASP prior & posterior plot" disabled="no" anchor="" url="" target="blank" class=""]

```
library(plotrix)

.likelihoodShiftedT <- function(par, data) {

    -sum(log(dt((data - par[1])/par[2], par[3])/par[2]))

}

.dposteriorShiftedT <- function(x, parameters, oneSided) { # function that ret
            parameters[1])/parameters[2], parameters[3], lower.tail = FALSE),
            0)

    } else if (oneSided == "left") {
```

```
        ifelse(x <= 0, (dt((x - parameters[1])/parameters[2], parameters[3])/p
            parameters[1])/parameters[2], parameters[3], lower.tail = TRUE),
            0)

    }

}

.dprior <- function(x, r, oneSided = oneSided) {

    # function that returns the prior density

    if (oneSided == "right") {

        y <- ifelse(x < 0, 0, 2/(pi * r * (1 + (x/r)^2)))
        return(y)
    }

    if (oneSided == "left") {

        y <- ifelse(x > 0, 0, 2/(pi * r * (1 + (x/r)^2)))
        return(y)
    } else {

        return(1/(pi * r * (1 + (x/r)^2)))
    }
}

.plotPosterior.ttest <- function(x = NULL, y = NULL, paired = FALSE, oneSided
    BF, BFH1H0 = TRUE, iterations = 10000, rscale = "medium", lwd = 2,
    cexPoints = 1.5, cexAxis = 1.2, cexYlab = 1.5, cexXlab = 1.5, cexTextBF =
    cexCI = 1.1, cexLegend = 1.2, lwdAxis = 1.2, addInformation = TRUE,
    dontPlotData = FALSE) {

    if (addInformation) {

        par(mar = c(5.6, 5, 7, 4) + 0.1, las = 1)

    } else {

        par(mar = c(5.6, 5, 4, 4) + 0.1, las = 1)
    }

    if (dontPlotData) {

        plot(1, type = "n", xlim = 0:1, ylim = 0:1, bty = "n", axes = FALSE,
            xlab = "", ylab = "")

        axis(1, at = 0:1, labels = FALSE, cex.axis = cexAxis, lwd = lwdAxis,
            xlab = "")
        axis(2, at = 0:1, labels = FALSE, cex.axis = cexAxis, lwd = lwdAxis,
            ylab = "")

        mtext(text = "Density", side = 2, las = 0, cex = cexYlab, line = 3.25)
```

```
        mtext(expression(paste("Effect size", ~delta)), side = 1, cex = cexXla
            line = 2.5)

        return()
    }

    if (rscale == "medium") {
        r <- sqrt(2)/2
    }
    if (rscale == "wide") {
        r <- 1
    }
    if (rscale == "ultrawide") {
        r <- sqrt(2)
    }
    if (mode(rscale) == "numeric") {
        r <- rscale
    }

    if (oneSided == FALSE) {
        nullInterval <- NULL
    }
    if (oneSided == "right") {
        nullInterval <- c(0, Inf)
    }
    if (oneSided == "left") {
        nullInterval <- c(-Inf, 0)
    }

    # sample from delta posterior
    samples <- BayesFactor::ttestBF(x = x, y = y, paired = paired, posterior =
        iterations = iterations, rscale = r)

    delta <- samples[, "delta"]

    # fit shifted t distribution
    if (is.null(y)) {

        deltaHat <- mean(x)/sd(x)
        N <- length(x)
        df <- N - 1
        sigmaStart <- 1/N

    } else if (paired) {

        deltaHat <- mean(x - y)/sd(x - y)
        N <- length(x)
        df <- N - 1
        sigmaStart <- 1/N

    } else if (!is.null(y) && !paired) {

        N1 <- length(x)
        N2 <- length(y)
        sdPooled <- sqrt(((N1 - 1) * var(x) + (N2 - 1) * var(y))/(N1 +
```

```
        N2))
    deltaHat <- (mean(x) - mean(y))/sdPooled
    df <- N1 + N2 - 2
    sigmaStart <- sqrt(N1 * N2/(N1 + N2))
}

if (sigmaStart < 0.01)
    sigmaStart <- 0.01

parameters <- try(silent = TRUE, expr = optim(par = c(deltaHat, sigmaStart
    df), fn = .likelihoodShiftedT, data = delta, method = "BFGS")$par)

if (class(parameters) == "try-error") {

    parameters <- try(silent = TRUE, expr = optim(par = c(deltaHat,
        sigmaStart, df), fn = .likelihoodShiftedT, data = delta, method =
}

if (BFH1H0) {

    BF10 <- BF
    BF01 <- 1/BF10

} else {

    BF01 <- BF
    BF10 <- 1/BF01
}


# set limits plot
xlim <- vector("numeric", 2)

if (oneSided == FALSE) {

    xlim[1] <- min(-2, quantile(delta, probs = 0.01)[[1]])
    xlim[2] <- max(2, quantile(delta, probs = 0.99)[[1]])

    if (length(x) < 10) {

        if (addInformation) {

            stretch <- 1.52
        } else {

            stretch <- 1.4
        }

    } else {

        stretch <- 1.2 } } if (oneSided == "right") { # if (length(delta[d
    # possible: To few posterior samples in tested interval')

    xlim[1] <- min(-2, quantile(delta[delta >= 0], probs = 0.01)[[1]])
    xlim[2] <- max(2, quantile(delta[delta >= 0], probs = 0.99)[[1]])
```

```
    if (any(is.na(xlim))) {

        xlim[1] <- min(-2, .qShiftedT(0.01, parameters, oneSided = "right"
        xlim[2] <- max(2, .qShiftedT(0.99, parameters, oneSided = "right")

    }

    stretch <- 1.32
}

if (oneSided == "left") {

    # if (length(delta[delta <= 0]) < 10) return('Plotting is not
    # possible: To few posterior samples in tested interval')

    xlim[1] <- min(-2, quantile(delta[delta <= 0], probs = 0.01)[[1]])
    xlim[2] <- max(2, quantile(delta[delta <= 0], probs = 0.99)[[1]])

    if (any(is.na(xlim))) {

        xlim[1] <- min(-2, .qShiftedT(0.01, parameters, oneSided = "left")
        xlim[2] <- max(2, .qShiftedT(0.99, parameters, oneSided = "left"))

    }

    stretch <- 1.32
}

xticks <- pretty(xlim)

ylim <- vector("numeric", 2)

ylim[1] <- 0
dmax <- optimize(function(x) .dposteriorShiftedT(x, parameters = parameter
    oneSided = oneSided), interval = range(xticks), maximum = TRUE)$object
ylim[2] <- max(stretch * .dprior(0, r, oneSided = oneSided), stretch *
    dmax)  # get maximum density

# calculate position of 'nice' tick marks and create labels
yticks <- pretty(ylim)
xlabels <- formatC(xticks, 1, format = "f")
ylabels <- formatC(yticks, 1, format = "f")

# compute 95% credible interval & median:
if (oneSided == FALSE) {

    CIlow <- quantile(delta, probs = 0.025)[[1]]
    CIhigh <- quantile(delta, probs = 0.975)[[1]]
    medianPosterior <- median(delta)

    if (any(is.na(c(CIlow, CIhigh, medianPosterior)))) {

        CIlow <- .qShiftedT(0.025, parameters, oneSided = FALSE)
        CIhigh <- .qShiftedT(0.975, parameters, oneSided = FALSE)
```

```
        medianPosterior <- .qShiftedT(0.5, parameters, oneSided = FALSE)
    }
}

if (oneSided == "right") {

    CIlow <- quantile(delta[delta >= 0], probs = 0.025)[[1]]
    CIhigh <- quantile(delta[delta >= 0], probs = 0.975)[[1]]
    medianPosterior <- median(delta[delta >= 0])

    if (any(is.na(c(CIlow, CIhigh, medianPosterior)))) {

        CIlow <- .qShiftedT(0.025, parameters, oneSided = "right")
        CIhigh <- .qShiftedT(0.975, parameters, oneSided = "right")
        medianPosterior <- .qShiftedT(0.5, parameters, oneSided = "right")
    }
}

if (oneSided == "left") {

    CIlow <- quantile(delta[delta <= 0], probs = 0.025)[[1]]
    CIhigh <- quantile(delta[delta <= 0], probs = 0.975)[[1]]
    medianPosterior <- median(delta[delta <= 0])

    if (any(is.na(c(CIlow, CIhigh, medianPosterior)))) {

        CIlow <- .qShiftedT(0.025, parameters, oneSided = "left")
        CIhigh <- .qShiftedT(0.975, parameters, oneSided = "left")
        medianPosterior <- .qShiftedT(0.5, parameters, oneSided = "left")
    }

}

posteriorLine <- .dposteriorShiftedT(x = seq(min(xticks), max(xticks),
    length.out = 1000), parameters = parameters, oneSided = oneSided)

xlim <- c(min(CIlow, range(xticks)[1]), max(range(xticks)[2], CIhigh)) plo

    mtext(text = "Density", side = 2, las = 0, cex = cexYlab, line = 4)

} else if (nchar(ylabels[length(ylabels)]) == 4) {

    mtext(text = "Density", side = 2, las = 0, cex = cexYlab, line = 3.25)

} else if (nchar(ylabels[length(ylabels)]) < 4) {

    mtext(text = "Density", side = 2, las = 0, cex = cexYlab, line = 2.85)

}

mtext(expression(paste("Effect size", ~delta)), side = 1, cex = cexXlab,
    line = 2.5)

points(0, .dprior(0, r, oneSided = oneSided), col = "black", pch = 21,
    bg = "grey", cex = cexPoints)
```

```
    if (oneSided == FALSE) {

        heightPosteriorAtZero <- .dposteriorShiftedT(0, parameters = parameter
            oneSided = oneSided)

    } else if (oneSided == "right") {

        posteriorLineLargerZero <- posteriorLine[posteriorLine > 0]
        heightPosteriorAtZero <- posteriorLineLargerZero[1]

    } else if (oneSided == "left") {

        posteriorLineLargerZero <- posteriorLine[posteriorLine > 0]
        heightPosteriorAtZero <- posteriorLineLargerZero[length(posteriorLineL
    }

    points(0, heightPosteriorAtZero, col = "black", pch = 21, bg = "grey",
        cex = cexPoints)

    ### 95% credible interval

    # enable plotting in margin
    par(xpd = TRUE)

    yCI <- grconvertY(dmax, "user", "ndc") + 0.04
    yCI <- grconvertY(yCI, "ndc", "user")

    arrows(CIlow, yCI, CIhigh, yCI, angle = 90, code = 3, length = 0.1,
        lwd = lwd)

    medianText <- formatC(medianPosterior, digits = 3, format = "f")

    if (addInformation) {

        # display BF10 value
        offsetTopPart <- 0.06

        yy <- grconvertY(0.75 + offsetTopPart, "ndc", "user")
        yy2 <- grconvertY(0.806 + offsetTopPart, "ndc", "user")

        xx <- min(xticks) if (BF10 >= 1000000 | BF01 >= 1000000) {

            BF10t <- formatC(BF10, 3, format = "e")
            BF01t <- formatC(BF01, 3, format = "e")
        }

        if (BF10 < 1000000 & BF01 < 1000000) {

            BF10t <- formatC(BF10, 3, format = "f")
            BF01t <- formatC(BF01, 3, format = "f")
        }

        if (oneSided == FALSE) {
```

```
    text(xx, yy2, bquote(BF[10] == .(BF10t)), cex = cexTextBF,
        pos = 4)
    text(xx, yy, bquote(BF[0][1] == .(BF01t)), cex = cexTextBF,
        pos = 4)
}

if (oneSided == "right") {

    text(xx, yy2, bquote(BF["+"][0] == .(BF10t)), cex = cexTextBF,
        pos = 4)
    text(xx, yy, bquote(BF[0]["+"] == .(BF01t)), cex = cexTextBF,
        pos = 4)
}

if (oneSided == "left") {

    text(xx, yy2, bquote(BF["-"][0] == .(BF10t)), cex = cexTextBF,
        pos = 4)
    text(xx, yy, bquote(BF[0]["-"] == .(BF01t)), cex = cexTextBF,
        pos = 4)
}

yy <- grconvertY(0.756 + offsetTopPart, "ndc", "user")
yy2 <- grconvertY(0.812 + offsetTopPart, "ndc", "user")

CIText <- paste("95% CI: [", bquote(.(formatC(CIlow, 3, format = "f"))
    ", ", bquote(.(formatC(CIhigh, 3, format = "f"))), "]", sep = "")
medianLegendText <- paste("median =", medianText)

text(max(xticks), yy2, medianLegendText, cex = 1.1, pos = 2)
text(max(xticks), yy, CIText, cex = 1.1, pos = 2)

# probability wheel
if (max(nchar(BF10t), nchar(BF01t)) <= 4) {
    xx <- grconvertX(0.44, "ndc", "user")
}

if (max(nchar(BF10t), nchar(BF01t)) == 5) {
    xx <- grconvertX(0.44 + 0.001 * 5, "ndc", "user")
}

if (max(nchar(BF10t), nchar(BF01t)) == 6) {
    xx <- grconvertX(0.44 + 0.001 * 6, "ndc", "user")
}

if (max(nchar(BF10t), nchar(BF01t)) == 7) {
    xx <- grconvertX(0.44 + 0.002 * max(nchar(BF10t), nchar(BF01t)),
        "ndc", "user")
}

if (max(nchar(BF10t), nchar(BF01t)) == 8) {
    xx <- grconvertX(0.44 + 0.003 * max(nchar(BF10t), nchar(BF01t)), "
    xx <- grconvertX(0.44 + 0.005 * max(nchar(BF10t), nchar(BF01t)),
        "ndc", "user")
}
```

```
    yy <- grconvertY(0.788 + offsetTopPart, "ndc", "user")

    # make sure that colored area is centered
    radius <- 0.06 * diff(range(xticks))
    A <- radius^2 * pi
    alpha <- 2/(BF01 + 1) * A/radius^2
    startpos <- pi/2 - alpha/2

    # draw probability wheel
    plotrix::floating.pie(xx, yy, c(BF10, 1), radius = radius, col = c("da
        "white"), lwd = 2, startpos = startpos)

    yy <- grconvertY(0.865 + offsetTopPart, "ndc", "user")
    yy2 <- grconvertY(0.708 + offsetTopPart, "ndc", "user")

    if (oneSided == FALSE) {

        text(xx, yy, "data|H1", cex = cexCI)
        text(xx, yy2, "data|H0", cex = cexCI)
    }

    if (oneSided == "right") {

        text(xx, yy, "data|H+", cex = cexCI)
        text(xx, yy2, "data|H0", cex = cexCI)
    }

    if (oneSided == "left") {

        text(xx, yy, "data|H-", cex = cexCI)
        text(xx, yy2, "data|H0", cex = cexCI)
    }

    # add legend
    CIText <- paste("95% CI: [", bquote(.(formatC(CIlow, 3, format = "f"))
        " ; ", bquote(.(formatC(CIhigh, 3, format = "f"))), "]", sep = "")

    medianLegendText <- paste("median =", medianText)
}

mostPosterior <- mean(delta > mean(range(xticks)))

if (mostPosterior >= 0.5) {

    legendPosition <- min(xticks)
    legend(legendPosition, max(yticks), legend = c("Posterior", "Prior"),
        lty = c(1, 3), bty = "n", lwd = c(lwd, lwd), cex = cexLegend,
        xjust = 0, yjust = 1, x.intersp = 0.6, seg.len = 1.2)
} else {

    legendPosition <- max(xticks)
    legend(legendPosition, max(yticks), legend = c("Posterior", "Prior"),
        lty = c(1, 3), bty = "n", lwd = c(lwd, lwd), cex = cexLegend,
        xjust = 1, yjust = 1, x.intersp = 0.6, seg.len = 1.2)
```

```
    }
}

### generate data ###

set.seed(1)
x <- rnorm(30, 0.15)

### calculate Bayes factor ###

library(BayesFactor)
BF <- extractBF(ttestBF(x, rscale = "medium"), onlybf = TRUE)

### plot ###

.plotPosterior.ttest(x = x, rscale = "medium", BF = BF)
```

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```
#monte carlo t test simulation


#install.packages("MonteCarlo")
library(MonteCarlo)



# Define function that generates data and applies the method of interest

ttest<-function(n,loc,scale){

  # generate sample:
    sample<-rnorm(n, loc, scale)

  # calculate test statistic:
    stat<-sqrt(n)*mean(sample)/sd(sample)

  # get test decision:
    decision<-abs(stat)>1.96

  # return result:
    return(list("decision"=decision))
}

# define parameter grid:

  n_grid<-c(50,100,250,500)
  loc_grid<-seq(0,1,0.2)
  scale_grid<-c(1,2)

# collect parameter grids in list:
  param_list=list("n"=n_grid, "loc"=loc_grid, "scale"=scale_grid)
```

```
# run simulation:

  MC_result<-MonteCarlo(func=ttest, nrep=1000, param_list=param_list)

  summary(MC_result)
```

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```
#install.packages("RWordPress", repos="http://www.omegahat.org/R", build=TRUE)
library(RWordPress)
options(WordPressLogin=c(user="password"),
        WordPressURL="http://your_wp_installation.org/xmlrpc.php")
#[code lang='r']
#...
#[/code]
knit_hooks$set(output=function(x, options) paste("\\[code\\]\n", x, "\\[/code\
knit_hooks$set(source=function(x, options) paste("\\[code lang='r'\\]\n", x, "

knit2wp <- function(file) {
    require(XML)
    content <- readLines(file)
    content <- htmlTreeParse(content, trim=FALSE)

    ## WP will add the h1 header later based on the title, so delete here
    content$children$html$children$body$children$h1 <- NULL
    content <- paste(capture.output(print(content$children$html$children$body,
                                          indent=FALSE, tagSeparator="")),
                     collapse="\n")
    content <- gsub("<?.body>", "", content)         # remove body tag

    ## enclose code snippets in SyntaxHighlighter format
    content <- gsub("<?pre><code class=\"r\">", "\\[code lang='r'\\]\\\n",
                    content)
    content <- gsub("<?pre><code class=\"no-highlight\">", "\\[code\\]\\\n",
                    content)
    content <- gsub("<?pre><code>", "\\[code\\]\\\n", content)
    content <- gsub("<?/code></pre>", "\\[/code\\]\\\n", content)
    return(content)
}

newPost(content=list(description=knit2wp('rerWorkflow.html'),
                     title='Workflow: Post R markdown to WordPress',
                     categories=c('R')),
        publish=FALSE)

postID <- 99                    # post id returned by newPost()
editPost(postID,
         content=list(description=knit2wp('rerWorkflow.html'),
                      title='Workflow: Post R markdown to WordPress',
                      categories=c('R')),
         publish=FALSE)
```

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