

BMI-585R: Final R package Test and Usage

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Installation and Loading

```
#devtools::install_git("https://github.com/satpathysarthak/FinalPackageBMI585R.git", force = T)
library(FinalPackageBMI585R)
```

boxMuller

```
head(boxMuller(500))
```

```
## [1] -1.5164315  0.3023574 -1.2772155 -1.0212607  0.7777790  0.8058745
```

twoSidedT(t,n)

```
twoSidedT(-.785,14)
```

```
## [1] 0.4455351
```

twoSidedZ(z)

```
twoSidedZ(-.785)
```

```
## [1] 0.4324536
```

effectSize(x,g)

```
set.seed(24)
x = c(rnorm(50,mean=10,sd=2),rnorm(50,mean=3,sd=6))
g = c(rep('M',50),rep('F',50))
#g = as.factor(g)
effectSize(x,g)
```

```
## [1] 1.269001
```

welchT(x,y)

```
welchT(1:10, y = c(7:20)) # 0.000019
```

```
##    p.value estimate      dof
## 0.000019  5.435000 22.000000
welchT(1:10, y = c(7:20, 200)) # 0.124513
```

```
##    p.value estimate      dof
## 0.124513  1.633000 14.200000
```

minimumN(d)

```
minimumN(d = 1)

## [1] 16.71477
```

chiSquareCounts(tib)

```
data = readr::read_csv('https://jluasmckay.bmi.emory.edu/global/bmi585/demographics.csv')

## Rows: 436 Columns: 4
## -- Column specification -----
## Delimiter: ","
## chr (3): sex, icd, group
## dbl (1): age
##
## i Use `spec()` to retrieve the full column specification for this data.
## i Specify the column types or set `show_col_types = FALSE` to quiet this message.
data = subset(data, select = c('sex', 'group'))
chiSquareCounts(data)

##
##           Essential tremor      Holmes Parkinson's disease
## Female           64.000000      8.000000           89.000000
## Male            44.782110      1.892202          126.777523
## [1] 1.23083e-13
```

postHocPower(d,n1,n2)

```
set.seed(2021)
postHocPower(0.2,1000,1500) # 0.974

## [1] 0.974
```

bhAdjust(p)

```
pval <- c(0.0050,0.0025,0.0075,0.0100,0.0125,0.0150,0.0175,0.0200,0.0225,0.0250)
bhAdjust(pval) # TRUE TRUE FALSE FALSE FALSE FALSE FALSE FALSE FALSE
## [1] TRUE TRUE FALSE FALSE FALSE FALSE FALSE FALSE FALSE
```

fdrAdjust(p)

```
fdrAdjust(pval)
```

```
## [1] TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE
```

r2(pred,truth)

```
model = lm(Sepal.Width ~ Sepal.Length+Petal.Length, data = iris)
truth = iris$Sepal.Width
pred = model$fitted.values
r2(pred,truth)
```

```
## [1] 0.456415
```

adjR2(pred,truth)

```
adjR2(pred,truth,d = 2)
```

```
## [1] 0.4490193
```

sensitivity(pred,truth)

```
truth = c(T,T,T,T,T,F,F,F,F,F)
pred = c(T,F,T,T,F,T,T,T,F,F)
sensitivity(pred,truth)
```

```
## [1] 0.6
```

specificity(pred,truth)

```
specificity(pred,truth)
```

```
## [1] 0.4
```

accuracy(pred,truth)

```
accuracy(pred,truth)
```

```
## [1] 0.5
```

ppv(pred,truth)

```
ppv(pred,truth)
```

```
## [1] 0.5
```

f1(pred,truth)

```
f1(pred,truth)
```

```
## [1] 0.5454545
```

unscale(x)

```
set.seed(1)
x = matrix(sample(1:12), ncol= 3)
xs = scale(x, center = TRUE, scale = TRUE)
unscale(xs)
```

```
##      [,1] [,2] [,3]
## [1,]    9    2    6
## [2,]    4    5   11
## [3,]    7    3   12
## [4,]    1    8   10
```

pcApprox(x, npc)

```
data = iris[,1:4]
head(pcApprox(data,3))
```

```
##      Sepal.Length Sepal.Width Petal.Length Petal.Width
## [1,]    5.094788    3.501297    1.434079    0.1903865
## [2,]    4.877788    3.005527    1.545247    0.1590267
## [3,]    4.693881    3.201523    1.340014    0.1887124
## [4,]    4.614223    3.096461    1.406998    0.2262353
## [5,]    5.007746    3.598073    1.349346    0.2142891
## [6,]    5.398575    3.900355    1.709318    0.3973714
```

pcLollipop(x)

```
data = iris[,1:4]
pcLollipop(data)
```

