R Function Guide

Load Packages

The **NCStats** and **ggplot2** packages should ALWAYS be loaded with `library()` at the top of your new script in RStudio.

```
> library(NCStats)
> library(ggplot2)
```

Random Individuals

EXPERIMENT – Randomly order **N** individuals.

```
sample(N)
```

OBSERVATIONAL STUDY – Randomly select **n** from **N** individuals.

```
sample(N,n)
```

```
> sample(10)        # randomly order 1 to 10
[1]  6  7  9  8  1  2 10  5  3  4
> sample(10,3)      # randomly select 3 from 1 to 10
[1] 10  4  5
```

Normal Distributions

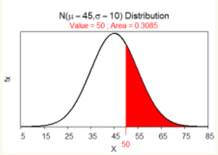
```
distrib(val,mean=mnval,sd=sdval,lower.tail=FALSE,type="q")
```

- **val** is a value of the quantitative variable (x) or an area (i.e., a percentage, but entered as a proportion)
- **mnval** is the population mean (μ)
- **sdval** is the standard deviation (σ) or error (SE)
  - For SE use (where **nval** is the sample size):

```
sd=sdval/sqrt(nval)
```

- `lower.tail=FALSE` is included for "right-of" calculations
- `type="q"` is included for reverse calculations

```
> distrib(50,mean=45,sd=10,lower.tail=FALSE)   #forward-right
```



```
> distrib(50,mean=45,sd=10)                    #forward-left
> distrib(0.05,mean=45,sd=10,type="q")         #reverse-left
> distrib(0.2,mean=45,sd=10,type="q",lower.tail=FALSE) #rev-rgt
> distrib(50,mean=45,sd=10/sqrt(30))           #using SE
> distrib(0.95,mean=45,sd=10/sqrt(30),
        type="q",lower.tail=FALSE)             #using SE

> distrib(.025,type="q")                     #Z*, not =, alpha=.05
```

Hints:

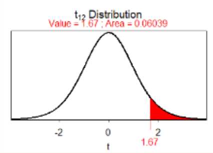
- Green code typed exactly as shown
- Red code is optional or must be replaced with context-specific name or value
- Replace **qvar** with quantitative variable name
- Replace **cvar** with categorical variable name
- Replaced **#** with numeric value

t Distributions

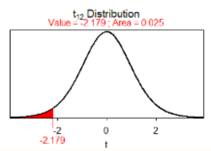
```
distrib(val,distrib="t",df=dfval,lower.tail=FALSE,type="q")
```

- **val** is a value of the t test statistic (for computing the p-value) or an area as a proportion (for computing t* for confidence region)
- **dfval** is the degrees-of-freedom (df)
- `lower.tail=FALSE` is included for "right-of" calculations
- `type="q"` is included for reverse (confidence region) calculations

```
> distrib(1.67,distrib="t",df=12,lower.tail=FALSE)  # p-value
```



```
> distrib(0.025,distrib="t",df=12,type="q")         # t-star
```

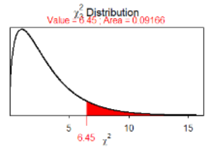


χ^2 Distributions

```
distrib(val,distrib="chisq",df=dfval,lower.tail=FALSE)
```

- **val** is a value of the χ^2 test statistic (for computing the p-value)
- **dfval** is the degrees-of-freedom (df)
- `lower.tail=FALSE` is included for ALL calculations

```
> distrib(6.45,distrib="chisq",df=3,lower.tail=FALSE)  # p-value
```



Get and Load Data

ENTER RAW DATA:

1. In Excel, enter variables in columns with variable names in the first row, each individual's data in rows below that (do not use spaces or special characters).
2. Save as "Comma Separated Values (*.CSV)" file in your local directory/folder.

DATA PROVIDED BY PROFESSOR:

1. Goto the MTH107 Resources webpage.
2. Save "data" link (right-click) to your local directory/folder.

LOAD THE EXTERNAL CSV FILE INTO R:

1. Start script and save it in the same folder with the CSV file.
2. Select *Session, Set Working Directory, To Source File …* menus
3. Copy resulting **`setwd()`** code to your script.
4. Use **`read.csv()`** to load data in *filename.csv* into **dfobj**.

```
dfobj <- read.csv("filename.csv")
```

5. Observe the structure of **dfobj**.

```
str(dfobj)
```

```
> setwd("C:/aaaWork/Web/GitHub/NCMTH107")
> dfcar <- read.csv("93cars.csv")
> str(dfcar)
'data.frame':    93 obs. of  26 variables:
  $ Type    : Factor w/ 6 levels "Compact","Large": 4 3 3 ...
  $ HMPG    : int  31 25 26 26 30 31 28 25 27 25...
  $ Manual  : Factor w/ 2 levels "No","Yes": 2 2 2 2 2 1 1 ...
  $ Weight  : int  2705 3560 3375 3405 3640 2880 3470 ...
  $ Domestic: Factor w/ 2 levels "No","Yes": 1 1 1 1 1 2 2 ...
```

Filter Individuals

Individuals may be selected from the **dfobj** data.frame and put in the **newdf** data.frame according to a **condition** with

```
newdf <- filterD(dfobj,condition)
```

where **condition** may be as follows

var == value	# equal to
var != value	# not equal to
var > value	# greater than
var >= value	# greater than or equal
var %in% c("value", "value", "value")	# in the list
cond, cond	# both conditions met

with **var** replaced by a variable name and **value** replaced by a number or category name (*if not a number then must be in quotes*).

```
> justSporty <- filterD(dfcar,Type=="Sporty")
> noDomestic <- filterD(dfcar,Domestic!="Yes")
> justHMPGgt30 <- filterD(dfcar,HMPG>30)
> Sp_or_Sm <- filterD(dfcar,Type %in% c("Sporty","Small") )
> Sprty_n_gt30 <- filterD(dfcar,Type=="Sporty",HMPG>30)
> justWTlteq3000 <- filterD(dfcar,Weight<=3000)

> justNum17 <- dfcar[17,]
> notNum17 <- dfcar[-17,]
```

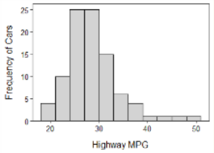
Univariate EDA - Quantitative

Summary statistics (mean, median, SD, Q1, Q3, etc.) and histogram of **qvar** quantitative variable in **dfobj** data.frame.

```
Summarize(~qvar,data=dfobj,digits=#)
ggplot(data=dfobj,mapping=aes(x=qvar)) +
  geom_histogram(binwidth=#,boundary=0,
                 color="black",fill="lightgray") +
  labs(x="better qvar label",y="Frequency of XXX") +
  scale_y_continuous(expand=expansion(mult=c(0,0.05)) +
  theme_NCStats()
```

- **#** in `digits=` is the desired number of decimal places
- **#** in `binwidth=` is the desired width of bins/bars
- **XXX** in `labs()` is a label/description of an individual

```
> Summarize(~HMPG,data=dfcar,digits=1)
      n   mean     sd    min     Q1  median     Q3    max 
   93.0   29.1    5.3   20.0   26.0   28.0   31.0   50.0 
> ggplot(data=dfcar,mapping=aes(x=HMPG)) +
    geom_histogram(binwidth=3,boundary=0,
                   color="black",fill="lightgray") +
    labs(x="Highway MPG",y="Frequency of Cars") +
    scale_y_continuous(expand=expansion(mult=c(0,0.05))) +
    theme_NCStats()
```

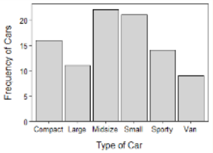


Univariate EDA - Categorical

Frequency & percentage tables, bar chart of **cvar** categorical variable.

```
( freq1 <- xtabs(~cvar,data=dfobj) )
percTable(freq1)
ggplot(data=dfobj,mapping=aes(x=cvar)) +
  geom_bar(color="black",fill="lightgray") +
  labs(x="better cvar label",y="Frequency of XXX") +
  scale_y_continuous(expand=expansion(mult=c(0,0.05)) +
  theme_NCStats()
```

```
> ( freq1 <- xtabs(~Type,data=dfcar) )
 Compact   Large Midsize   Small  Sporty     Van 
      16      11      22      21      14       9 
> percTable(freq1)
 Compact   Large Midsize   Small  Sporty     Van 
    17.2    11.8    23.7    22.6    15.1     9.7 
> ggplot(data=dfcar,mapping=aes(x=Type)) +
    geom_bar(color="black",fill="lightgray") +
    labs(x="Type of Car",y="Frequency of Cars") +
    scale_y_continuous(expand=expansion(mult=c(0,0.05))) +
    theme_NCStats()
```



Univariate EDA – Quant by Groups

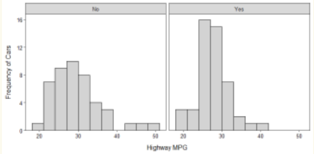
Separate summary statistics of **qvar** by groups in **cvar**.

```
Summarize(qvar~cvar,data=dfobj,digits=#)
```

Separate histograms by "adding" this to code for a single histogram.

```
facet_wrap(vars(cvar))
```

```
> Summarize(HMPG~Domestic,data=dfcar,digits=1)
  Domestic  n mean  sd min Q1 median Q3 max
1       No 45 30.1 6.2  21 25     30 33  50
2      Yes 48 28.1 4.2  20 26     28 30  41
> ggplot(data=dfcar,mapping=aes(x=HMPG)) +
    geom_histogram(binwidth=3,boundary=0,
                   color="black",fill="lightgray") +
    labs(x="Highway MPG",y="Frequency of Cars") +
    scale_y_continuous(expand=expansion(mult=c(0,0.05))) +
    theme_NCStats() +
    facet_wrap(vars(Domestic))
```



Bivariate EDA - Categorical

Frequency and percentage tables for **cvarRow** and **cvarCol** variables.

```
( freq2 <- xtabs(~cvarRow+cvarCol, data=dfobj) )
addmargins(freq2)                # append totals
percTable(freq2)                 # total/table %
percTable(freq2,margin=1)        # row %
percTable(freq2,margin=2)        # column %
```

```
> ( freq2 <- xtabs(~Domestic+Manual,data=dfcar) )
        Manual
Domestic No Yes
     No   6  39
     Yes 26  22
> addmargins(freq2)
        Manual
Domestic No Yes Sum
     No   6  39  45
     Yes 26  22  48
     Sum 32  61  93

> percTable(freq2)
        Manual
Domestic    No   Yes   Sum
     No    6.5  41.9  48.4
     Yes  28.0  23.7  51.7
     Sum  34.5  65.6 100.1
> percTable(freq2,margin=1)
        Manual
Domestic    No   Yes   Sum
     No   13.3  86.7 100.0
     Yes  54.2  45.8 100.0
> percTable(freq2,margin=2)
        Manual
Domestic    No   Yes
     No   18.8  63.9
     Yes  81.2  36.1
     Sum 100.0 100.0
```

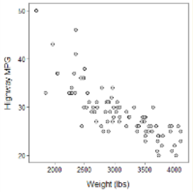
Bivariate EDA - Quantitative

Correlation coefficient (r) and scatterplot for **qvar1** and **qvar2**.

```
corr(~qvar1+qvar2,data=dfobj,digits=3)
ggplot(data=dfobj,mapping=aes(x=qvar1,y=qvar2)) +
  geom_point(pch=21,color="black",fill="lightgray") +
  labs(x="better qvar1 label",y="better qvar2 label") +
  theme_NCStats()
```

```
> corr(~HMPG+Weight,data=dfcar,digits=3)
  [1] -0.811

> ggplot(data=dfcar,mapping=aes(x=Weight,y=HMPG)) +
    geom_point(pch=21,color="black",fill="lightgray") +
    labs(x="Weight (lbs)",y="Highway MPG") +
    theme_NCStats()
```



Linear Regression

The coefficients for the best-fit line between the **qvarResp** response and **qvarExpl** explanatory variables.

```
( bfl <- lm(qvarResp~qvarExpl,data=dfobj) )
```

The coefficient of determination (r^2) value.

```
rSquared(bfl)
```

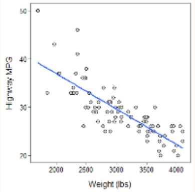
Plot best-fit line by "adding" this to code for a scatterplot.

```
geom_smooth(method="lm",se=FALSE)
```

```
> ( bfl <- lm(HMPG~Weight,data=dfcar) )
  Coefficients:
  (Intercept)       Weight  
    51.601365    -0.007327  

> rSquared(bfl)
  [1] 0.6571665

> ggplot(data=dfcar,mapping=aes(x=Weight,y=HMPG)) +
    geom_point(pch=21,color="black",fill="lightgray") +
    labs(x="Weight (lbs)",y="Highway MPG") +
    theme_NCStats() +
    geom_smooth(method="lm",se=FALSE)
```



1-Sample t-Test

```
t.test(~qvar,data=dfobj,mu=mu0,alt=HA, conf.level=cnfval)
```

- **qvar** is the quantitative response variable in **dfobj**
- **mu0** is the population mean in H_0
- **HA** is replaced with **`"two.sided"`** for not equals, **`"less"`** for less than, or **`"greater"`** for greater than alternative hypotheses (H_A)
- **cnfval** is the confidence level as a proportion (e.g., 0.95)

```
> t.test(~HMPG,data=dfcar,mu=26,alt="two.sided",
         conf.level=0.99)
   t = 5.5818, df = 92, p-value = 2.387e-07
   alternative hypothesis: true mean is not equal to 26
   99 percent confidence interval:
    27.63178 30.54026
   sample estimates:
   mean of x
    29.08602
```

NOTE: if n<40 then you may need to construct a histogram.

```
> ggplot(data=dfcar,mapping=aes(x=HMPG)) +
    geom_histogram(binwidth=3,boundary=0,
                   color="black",fill="lightgray") +
    labs(x="Highway MPG",y="Frequency of Cars") +
    scale_y_continuous(expand=expansion(mult=c(0,0.05))) +
    theme_NCStats()
```

2-Sample t-Test

```
levenesTest(qvar~cvar,data=dfobj)
t.test(qvar~cvar,data=dfobj,alt=HA,conf.level=cnfval,
          var.equal=TRUE)
```

- **qvar** is the quantitative response variable in **dfobj**
- **cvar** is the categorical variable that identifies the two groups
- **HA** is replaced with **`"two.sided"`** for not equals, **`"less"`** for less than, or **`"greater"`** for greater than alternative hypotheses (H_A)
- **cnfval** is the confidence level as a proportion (e.g., 0.95)
- **`var.equal`=TRUE** if the popn variances are thought to be equal

```
> levenesTest(HMPG~Manual,data=dfcar)
          Df F value   Pr(>F)
   group  1  7.6663 0.006818
          91

> t.test(HMPG~Manual,data=dfcar,alt="less",conf.level=0.99,
         var.equal=TRUE)
   t = -4.2183, df = 91, p-value = 2.904e-05
   alt. hypothesis: true difference in means is less than 0
   99 percent confidence interval:
         -Inf -1.980103
   sample estimates:
    mean in group No mean in group Yes
            26.12500          30.63934
```

NOTE: if $n_1+n_2<40$ then you may need to construct histograms.

```
> ggplot(data=dfcar,mapping=aes(x=HMPG)) +
    geom_histogram(binwidth=3,boundary=0,
                   color="black",fill="lightgray") +
    labs(x="Highway MPG",y="Frequency of Cars") +
    scale_y_continuous(expand=expansion(mult=c(0,0.05))) +
    theme_NCStats()+
    facet_wrap(vars(Manual))
```

Chi-square Test

Two-way frequency table with **cvarResp** categorical response variable in columns and **cvarPop** populations as rows.

```
( obstbl <- xtabs(~cvarPop+cvarResp,data=dfobj) )
```

Compute chi-square test results from **obstbl**.

```
( chi <- chisq.test(obstbl,correct=FALSE) )
```

Extract expected values.

```
chi$expected
```

Compute row percentages table (i.e., percentage of individuals in each level of the response variable for each population).

```
percTable(obstbl,margin=1)
```

```
> ( freq2 <- xtabs(~Domestic+Manual,data=dfcar) )
          Manual
  Domestic No Yes
       No   6  39
       Yes 26  22

> ( chi <- chisq.test(freq2,correct=FALSE) )
  Pearson's Chi-squared test with freq2
  X-squared = 17.1588, df = 1, p-value = 3.438e-05

> chi$expected
          Manual
  Domestic       No      Yes
       No  15.48387 29.51613
       Yes 16.51613 31.48387

> percTable(freq2,margin=1)
          Manual
  Domestic    No   Yes   Sum
       No   13.3  86.7 100.0
       Yes  54.2  45.8 100.0
```

NOTE: *If data were summarized*, then enter frequencies (reading vertically) into a vector with **`c()`** and then into a table with **`matrix()`**, making sure to identify the number of rows in **`nrow=`**.

```
obstbl <- matrix(c(#, #, #, …),nrow=#)
```

Name rows and columns with **`rownames()`** and **`colnames()`**.

```
rownames(obstbl) <- c("name","name", …)
colnames(obstbl) <- c("name","name", …)
```

Then proceed with **obstbl** as above.

```
> freq2 <- matrix(c(6,26,39,22),nrow=2)
> rownames(freq2) <- c("No","Yes")
> colnames(freq2) <- c("No","Yes")
> freq2
     No Yes
 No   6  39
 Yes 26  22
```

Goodness-of-Fit Test

One-way frequency table of **cvarResp** categorical response variable

```
( obstbl <- xtabs(~cvarResp,data=dfobj) )
```

Expected proportions (or ratios or values) in **exp.p**.

```
( exp.p <- c(lvl1=#, lvl2=#, lvl3=#,…) )
```

Compute GOF test results from **obstbl** and **exp.p**.

```
( gof <- chisq.test(obstbl,p=exp.p,rescale.p=TRUE, correct=FALSE) )
```

Extract expected values.

```
gof$expected
```

Construct table of observed proportions in each level along with confidence intervals and expected proportions.

```
gofCI(gof,digits=3)
```

```
> ( freq1 <- xtabs(~Type,data=dfcar) )
 Compact   Large Midsize   Small  Sporty     Van
      16      11      22      21      14       9

> ( exp <- c(Compact=1,Large=1,Midsize=1,
             Small=1,Sporty=1,Van=1) )
 Compact   Large Midsize   Small  Sporty     Van
       1       1       1       1       1       1

> ( gof <- chisq.test(freq1,p=exp,rescale.p=TRUE,
                      correct=FALSE) )
 Chi-squared test for given probabilities with freq1
 X-squared = 8.871, df = 5, p-value = 0.1143

> gof$expected
 Compact   Large Midsize   Small  Sporty     Van
    15.5    15.5    15.5    15.5    15.5    15.5

> gofCI(gof,digits=3)
  p.obs p.LCI p.UCI p.exp
 Compact 0.172 0.109 0.261 0.167
 Large   0.118 0.067 0.199 0.167
 Midsize 0.237 0.162 0.332 0.167
 Small   0.226 0.153 0.321 0.167
 Sporty  0.151 0.092 0.237 0.167
 Van     0.097 0.052 0.174 0.167
```

NOTE: *If data were summarized*, then enter frequencies into a named vector with **`c()`**.

```
( obstbl <- c(lvl1=#, lvl2=#, lvl3=#,…) )
```

Then proceed with **obstbl** as above.

```
> ( freq1 <- c(Compact=16,Large=11,Midsize=22,
               Small=21,Sporty=14,Van=9) )
 Compact   Large Midsize   Small  Sporty     Van
      16      11      22      21      14       9
```