

Homework 9 -

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Import Adiantum quantitative ecological data

```
adDat <- read.table("QuantitativeDataAdiantum1.csv",sep=";",header=T,stringsAsFactors = F)
head(adDat)
```

```
## SitePatch SpeciesID Elevation PercentCanopyCover MicroSlope MicroAspect
## 1 1.1 P 231.00 85.44 30 110
## 2 1.2 P 224.59 88.82 31 102
## 3 2.1 P 384.00 88.82 5 211
## 4 2.2 P 379.00 87.26 7 179
## 5 3.1 P 594.00 85.70 3 70
## 6 4.1 P 575.00 87.52 24 76
## MacroSlope MacroAspect AvgLitterDepth AvgDepth0 AvgDepthA AvgDepthB
## 1 27.0 102 4.00 3.7500 13.000 NA
## 2 29.0 108 2.00 2.7500 7.000 10.16
## 3 7.5 90 2.80 3.2500 10.000 NA
## 4 10.0 292 1.25 2.5000 5.900 4.90
## 5 15.0 94 3.50 3.0000 13.660 7.00
## 6 22.0 70 2.50 1.3125 7.875 9.30
## AvgSoilDepth pH Ompct P K Ca Mg Zn B Mn Cu Fe Al
## 1 27.0000 4.80 3.965 2.40 36 154 25 1.55 0.20 10.3 0.20 24.9 343
## 2 27.3000 4.89 6.240 2.05 60 406 74 8.20 0.25 49.8 0.20 27.6 125
## 3 5.6250 6.10 8.606 1.10 34 2010 89 3.60 0.15 30.0 0.10 2.5 25
## 4 7.2000 6.06 4.966 1.05 34 1525 67 3.00 0.20 12.4 0.15 5.2 79
## 5 10.0000 5.47 11.518 1.10 24 458 40 2.25 0.10 21.2 0.40 7.2 549
## 6 11.3125 5.82 4.966 0.90 44 989 128 2.05 0.15 12.9 0.10 9.5 60
## Na S ExchAcid ECEC CaBaseSat MgBaseSat KBaseSat Pb Ni Cd Cr
## 1 9 20 7.06 1.07 9.47 2.56 1.14 NA NA NA NA
## 2 87 17 6.39 2.80 22.09 6.71 1.67 NA NA NA NA
## 3 13 6 2.71 10.88 73.96 5.46 0.64 NA NA NA NA
## 4 9 9 2.28 8.27 72.25 5.29 0.83 NA NA NA NA
## 5 12 14 7.38 2.68 22.75 3.31 0.61 NA NA NA NA
## 6 6 4 2.96 6.12 54.44 11.74 1.24 NA NA NA NA
```

```
tail(adDat)
```

```
## SitePatch SpeciesID Elevation PercentCanopyCover MicroSlope MicroAspect
## 24 9.2 A 364.8456 58.40 42 258
## 25 9.3 V 309.9800 85.18 15 298
## 26 9.4 3x 352.1600 71.14 42 275
## 27 10.1 V 392.5824 66.20 5 0
## 28 10.2 A&V 434.6448 85.44 33 250
## 29 10.3 P 391.6680 83.62 18 273
## MacroSlope MacroAspect AvgLitterDepth AvgDepth0 AvgDepthA AvgDepthB
## 24 45 270 1.916667 1.666700 2.333333 3.000000
## 25 14 309 1.785714 3.300000 3.250000 6.666667
## 26 36 285 1.950000 1.944444 2.100000 NA
```

```
## 27      6      0      1.750000  2.375000 10.875000  5.500000
## 28     25     257      2.625000  2.812500  2.857143  1.125000
## 29     20     270      2.100000  3.800000  4.400000 11.700000
##      AvgSoilDepth  pH  Ompct      P      K      Ca      Mg      Zn      B      Mn      Cu      Fe      Al
## 24      4.50000  6.40 28.899  4.70  86  394 1501 0.75 0.35 11.2 0.05 2.5  2
## 25     11.71429  5.94 14.157  2.15  33  247 1234 1.80 0.10  8.8 0.05 2.8  7
## 26      3.30000  5.36 53.287 12.85 125  836  993 3.35 0.10 13.2 0.05 3.8  5
## 27     38.10000  7.04  7.150  1.75  52  358 1213 0.95 0.25  7.6 0.55 2.2 31
## 28      5.87500  6.63 19.799  3.40  53  661 1282 0.75 0.30  7.6 0.10 3.2  4
## 29     20.00000  6.69  8.515  3.55  61 1183  923 5.60 0.25 18.4 0.05 2.6  6
##      Na  S  ExchAcid  ECEC  CaBaseSat  MgBaseSat  KBaseSat  Pb  Ni  Cd  Cr
## 24  8 7      5.94 14.70      9.54      60.60      1.07 0.90 3.00 0.10 0.10
## 25  8 5      4.30 11.60      7.77      64.66      0.53 0.75 6.85 0.10 0.05
## 26  9 9     14.32 12.78     15.43     30.54      1.18 3.50 2.80 0.10 0.10
## 27  8 4      0.00 12.03     14.88     84.01      1.11 0.05 0.95 0.05 0.05
## 28 11 7     3.32 14.12     18.95     61.24      0.78 0.30 3.00 0.05 0.10
## 29  8 7      0.77 13.76     40.70     52.92      1.08 0.05 5.95 0.25 0.10
```

Clean up data set by changing NA values to 0 - justified for this data-set where the missing values are 0
Transform NA values to 0

```
adDat[is.na(adDat)]<- 0
head(adDat)
```

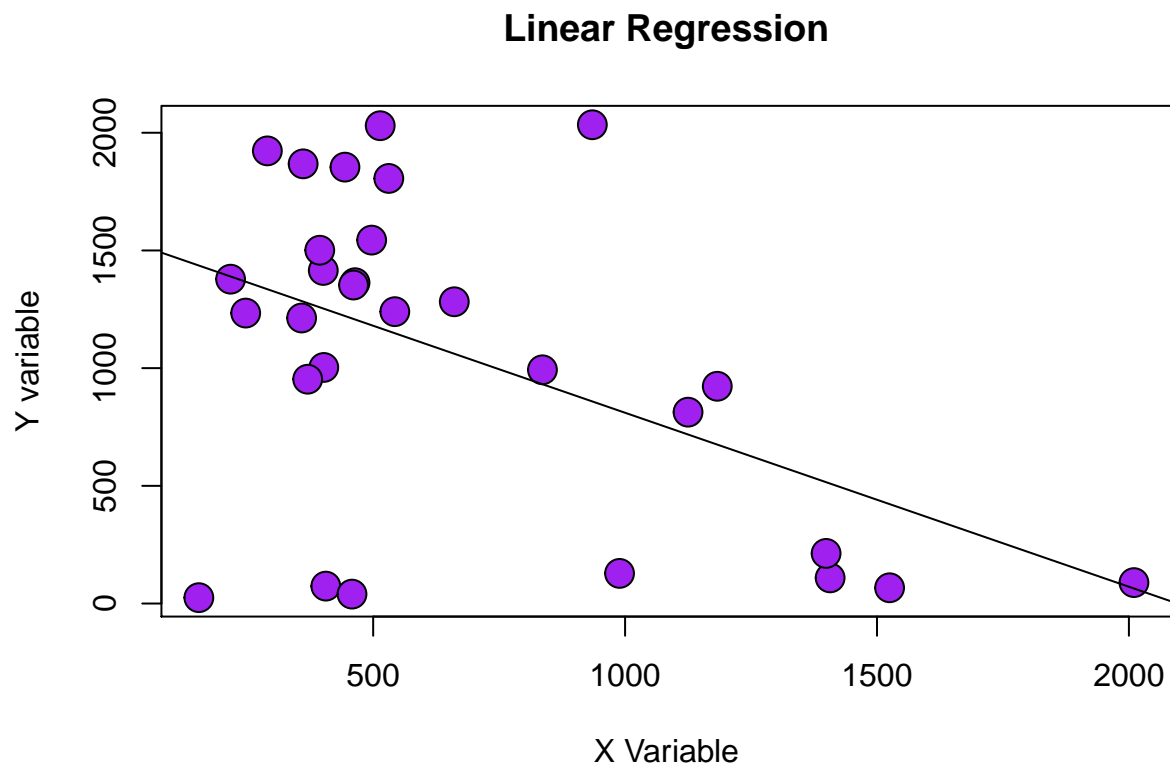
```
##      SitePatch SpeciesID Elevation PercentCanopyCover MicroSlope MicroAspect
## 1      1.1      P      231.00      85.44      30      110
## 2      1.2      P      224.59      88.82      31      102
## 3      2.1      P      384.00      88.82      5      211
## 4      2.2      P      379.00      87.26      7      179
## 5      3.1      P      594.00      85.70      3      70
## 6      4.1      P      575.00      87.52     24      76
##      MacroSlope MacroAspect AvgLitterDepth AvgDepth0 AvgDepthA AvgDepthB
## 1      27.0      102      4.00      3.7500      13.000      0.00
## 2      29.0      108      2.00      2.7500      7.000      10.16
## 3      7.5      90      2.80      3.2500     10.000      0.00
## 4     10.0     292      1.25      2.5000      5.900      4.90
## 5     15.0      94      3.50      3.0000     13.660      7.00
## 6     22.0      70      2.50      1.3125      7.875      9.30
##      AvgSoilDepth  pH  Ompct      P      K      Ca      Mg      Zn      B      Mn      Cu      Fe      Al
## 1     27.0000  4.80  3.965  2.40  36  154  25 1.55 0.20 10.3 0.20 24.9 343
## 2     27.3000  4.89  6.240  2.05  60  406  74 8.20 0.25 49.8 0.20 27.6 125
## 3      5.6250  6.10  8.606  1.10  34 2010  89 3.60 0.15 30.0 0.10  2.5  25
## 4      7.2000  6.06  4.966  1.05  34 1525  67 3.00 0.20 12.4 0.15  5.2  79
## 5     10.0000  5.47 11.518  1.10  24  458  40 2.25 0.10 21.2 0.40  7.2 549
## 6     11.3125  5.82  4.966  0.90  44  989 128 2.05 0.15 12.9 0.10  9.5  60
##      Na  S  ExchAcid  ECEC  CaBaseSat  MgBaseSat  KBaseSat  Pb  Ni  Cd  Cr
## 1  9 20      7.06  1.07      9.47      2.56      1.14  0  0  0  0
## 2  87 17      6.39  2.80     22.09      6.71      1.67  0  0  0  0
## 3 13  6      2.71 10.88     73.96      5.46      0.64  0  0  0  0
## 4  9  9      2.28  8.27     72.25      5.29      0.83  0  0  0  0
## 5 12 14      7.38  2.68     22.75      3.31      0.61  0  0  0  0
## 6  6  4      2.96  6.12     54.44     11.74      1.24  0  0  0  0
```

```
dim(adDat)
```

```
## [1] 29 36
```

Linear Regression of Ca:Mg ratio

```
# Use the linear regression function to test the relationship between soil concentrations of Ca and Mg,  
linReg(xVar=adDat$Ca,yVar=adDat$Mg)  
  
##          slope          pValue  
## -0.739283171  0.006017112  
  
# plot results using linRegPlot  
linRegPlot(xVar=adDat$Ca,yVar=adDat$Mg)
```



```
## NULL
```

Logistic Regression of Depth A Soil Layer between *A. aleuticum* & *A. viridimontanum*

```
““
```

```
# subset out just the serpentine maidenhair data from adDat  
serpDataA <- subset(adDat,SpeciesID=="A")  
serpDatV <- subset(adDat,SpeciesID=="V")  
  
# create new species id column so that to get rid of categorical letter id variable so that A. aleuticum  
dim(serpDataA)
```

```
## [1] 6 36
```

```
dim(serpDatV)
```

```
## [1] 9 36
```

```
id <- rep("0",length=6)
```

```
serpDatA <- cbind(serpDatA,id)
```

```
id <- rep("1",length=9)
```

```
serpDatV <- cbind(serpDatV,id)
```

```
# combine both subsets into a single data frame serpDat
```

```
serpDat <- rbind(serpDatA,serpDatV)
```

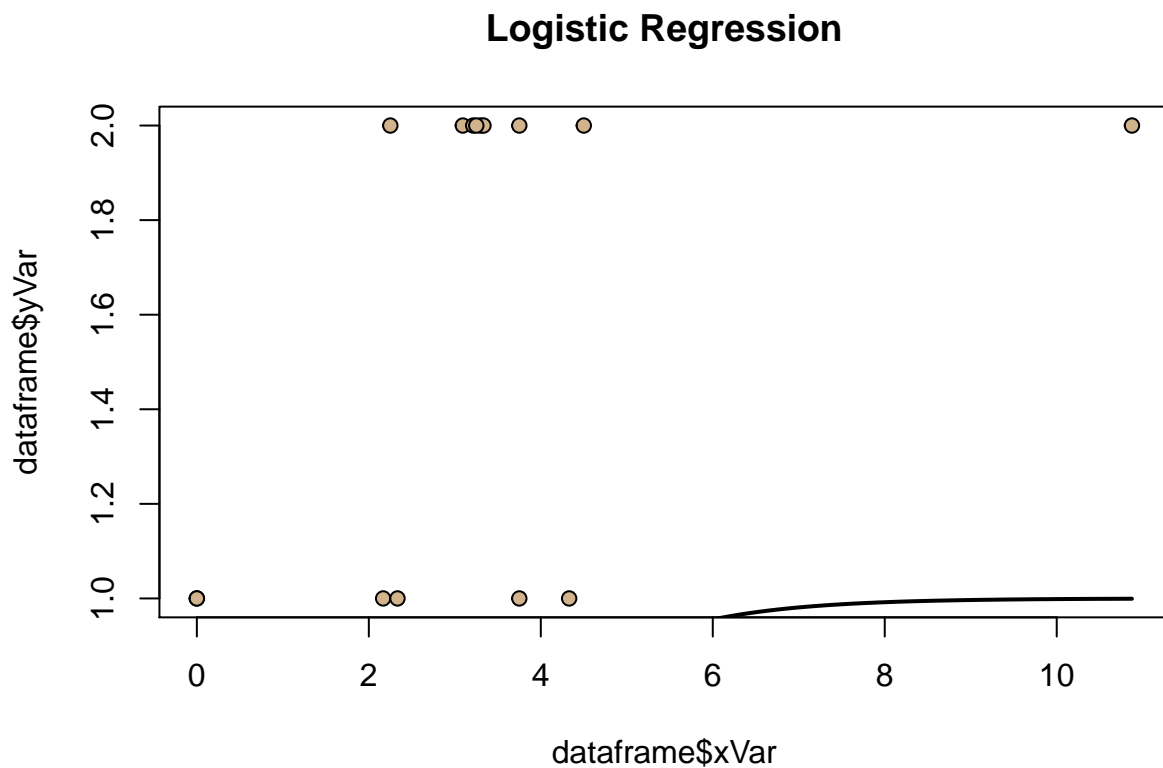
```
# Test the difference in depth of the A soil layer between the two serpentine maidenheads using logisti
```

```
logReg(xVar=serpDat$AvgDepthA,yVar=serpDat$id)
```

```
## xVarEst pValue
```

```
## 0.8765369 0.1363388
```

```
logRegPlot(xVar=serpDat$AvgDepthA,yVar=serpDat$id)
```



```
## $x
```

```
## [1] 0.00000 0.10875 0.21750 0.32625 0.43500 0.54375 0.65250
```

```
## [8] 0.76125 0.87000 0.97875 1.08750 1.19625 1.30500 1.41375
```

```
## [15] 1.52250 1.63125 1.74000 1.84875 1.95750 2.06625 2.17500
```

```
## [22] 2.28375 2.39250 2.50125 2.61000 2.71875 2.82750 2.93625
```

```
## [29] 3.04500 3.15375 3.26250 3.37125 3.48000 3.58875 3.69750
## [36] 3.80625 3.91500 4.02375 4.13250 4.24125 4.35000 4.45875
## [43] 4.56750 4.67625 4.78500 4.89375 5.00250 5.11125 5.22000
## [50] 5.32875 5.43750 5.54625 5.65500 5.76375 5.87250 5.98125
## [57] 6.09000 6.19875 6.30750 6.41625 6.52500 6.63375 6.74250
## [64] 6.85125 6.96000 7.06875 7.17750 7.28625 7.39500 7.50375
## [71] 7.61250 7.72125 7.83000 7.93875 8.04750 8.15625 8.26500
## [78] 8.37375 8.48250 8.59125 8.70000 8.80875 8.91750 9.02625
## [85] 9.13500 9.24375 9.35250 9.46125 9.57000 9.67875 9.78750
## [92] 9.89625 10.00500 10.11375 10.22250 10.33125 10.44000 10.54875
## [99] 10.65750 10.76625 10.87500
##
## $y
##      1      2      3      4      5      6      7
## 0.1004828 0.1094327 0.1190743 0.1294420 0.1405682 0.1524834 0.1652143
##      8      9     10     11     12     13     14
## 0.1787839 0.1932101 0.2085048 0.2246731 0.2417123 0.2596110 0.2783486
##     15     16     17     18     19     20     21
## 0.2978944 0.3182076 0.3392366 0.3609197 0.3831850 0.4059514 0.4291293
##     22     23     24     25     26     27     28
## 0.4526223 0.4763283 0.5001415 0.5239540 0.5476580 0.5711479 0.5943215
##     29     30     31     32     33     34     35
## 0.6170824 0.6393413 0.6610170 0.6820379 0.7023422 0.7218787 0.7406065
##     36     37     38     39     40     41     42
## 0.7584951 0.7755239 0.7916819 0.8069662 0.8213822 0.8349417 0.8476628
##     43     44     45     46     47     48     49
## 0.8595684 0.8706855 0.8810443 0.8906775 0.8996195 0.9079057 0.9155720
##     50     51     52     53     54     55     56
## 0.9226546 0.9291890 0.9352100 0.9407518 0.9458470 0.9505271 0.9548220
##     57     58     59     60     61     62     63
## 0.9587602 0.9623687 0.9656727 0.9686961 0.9714610 0.9739883 0.9762973
##     64     65     66     67     68     69     70
## 0.9784058 0.9803306 0.9820869 0.9836890 0.9851500 0.9864819 0.9876959
##     71     72     73     74     75     76     77
## 0.9888021 0.9898098 0.9907277 0.9915637 0.9923248 0.9930178 0.9936486
##     78     79     80     81     82     83     84
## 0.9942227 0.9947452 0.9952207 0.9956534 0.9960470 0.9964051 0.9967309
##     85     86     87     88     89     90     91
## 0.9970273 0.9972968 0.9975420 0.9977650 0.9979678 0.9981522 0.9983199
##     92     93     94     95     96     97     98
## 0.9984724 0.9986111 0.9987373 0.9988519 0.9989562 0.9990510 0.9991372
##     99    100    101
## 0.9992156 0.9992869 0.9993517
```

Test variation in depth of the A layer between species groups using ANOVA

Run ANOV & ANOVplot functions from HW8

```
ANOV <- function(xVar=as.factor(rep(c("A","B","C","D","E"),each=3)),
                 yVar=c(rgamma(10,shape=5,scale=5),rgamma(5,shape=5,scale=10))){
  df=data.frame(xVar,yVar)
  aovMod <- aov(yVar~xVar,data=df)
```

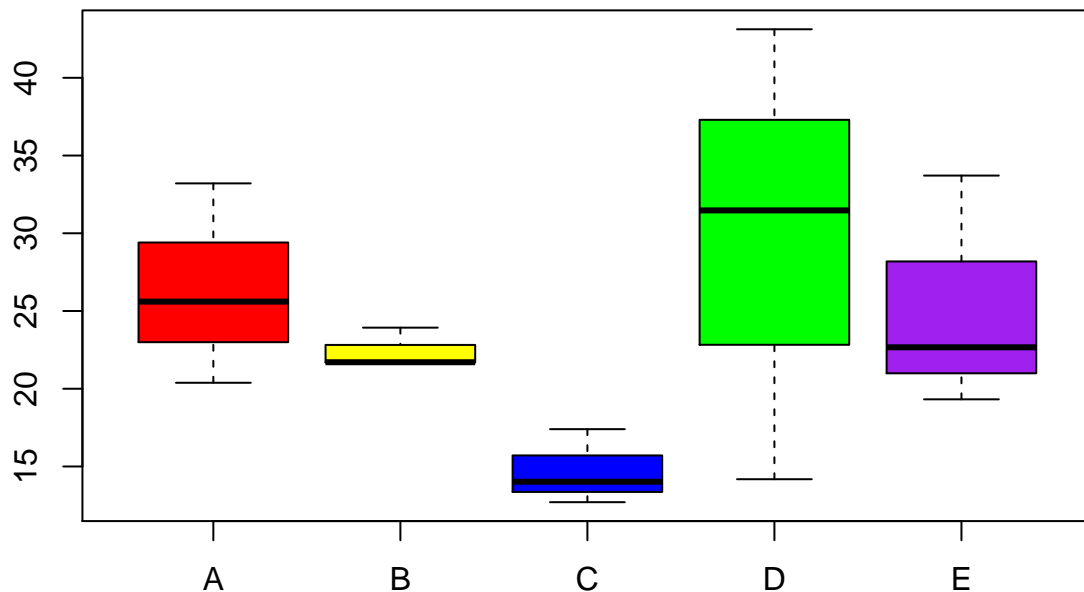
```

    aovOut <- summary(aovMod)[[1]][["Pr(>F)"]][1]
    return(aovOut)}

ANOVPLOT <- function(xVar=as.factor(rep(c("A","B","C","D","E"),each=3)),yVar=c(rgamma(15,shape=5,scale=
df <- data.frame(xVar,yVar)
aovMod <- aov(yVar~xVar,data=df)
aovPlot <- boxplot(yVar~xVar,
                    data=df,
                    col=c("red","yellow","blue","green","purple"),
                    xlab=names(xVar),ylab=names(yVar))
    return(aovPlot)}

ANOVPLOT()

```



```

## $stats
##      [,1]      [,2]      [,3]      [,4]      [,5]
## [1,] 20.38504 21.68080 12.70454 14.18129 19.31944
## [2,] 22.99550 21.69299 13.36213 22.82708 20.99314
## [3,] 25.60596 21.70519 14.01972 31.47286 22.66684
## [4,] 29.40754 22.81808 15.71014 37.29727 28.18973
## [5,] 33.20912 23.93096 17.40055 43.12167 33.71262
##
## $n
## [1] 3 3 3 3 3
##
## $conf

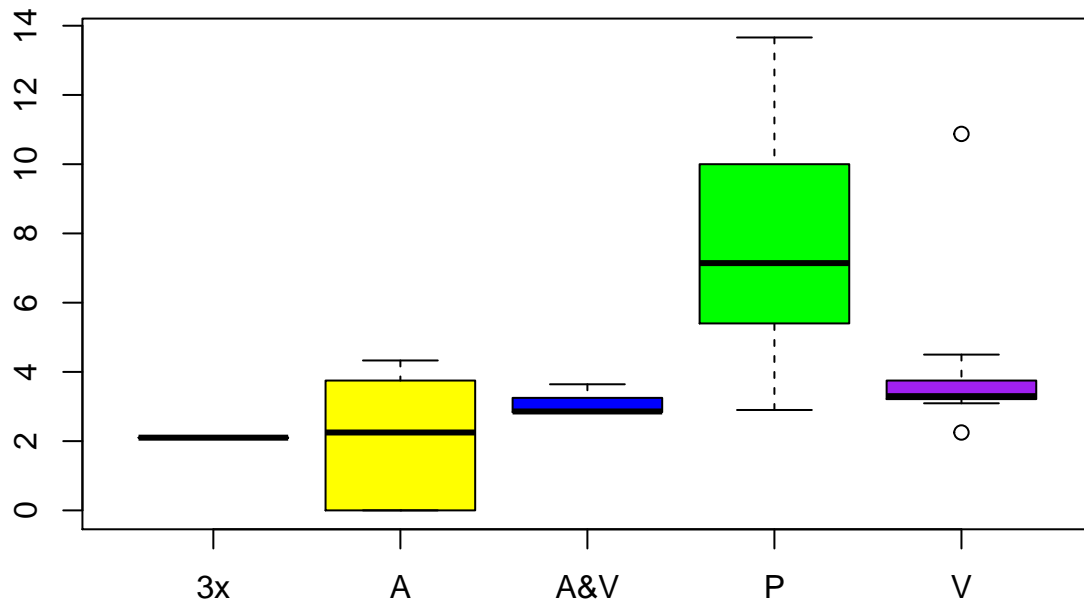
```

```
##           [,1]      [,2]      [,3]      [,4]      [,5]
## [1,] 19.75682 20.67887 11.87784 18.27296 16.10202
## [2,] 31.45511 22.73150 16.16161 44.67277 29.23167
##
## $out
## numeric(0)
##
## $group
## numeric(0)
##
## $names
## [1] "A" "B" "C" "D" "E"
```

```
ANOVA(xVar=adDat$SpeciesID,yVar=adDat$AvgDepthA)
```

```
## [1] 0.00480182
```

```
ANOVAplot(xVar=adDat$SpeciesID,yVar=adDat$AvgDepthA)
```



```
## $stats
##           [,1] [,2]      [,3]      [,4]      [,5]
## [1,]  2.1  0.00  2.818182   2.900000  3.093000
## [2,]  2.1  0.00  2.837662   5.400000  3.214286
## [3,]  2.1  2.25  2.857143   7.142857  3.300000
## [4,]  2.1  3.75  3.250000  10.000000  3.750000
## [5,]  2.1  4.33  3.642857  13.660000  4.500000
##
## $n
```

```
## [1] 1 6 3 10 9
##
## $conf
##      [,1]      [,2]      [,3]      [,4]      [,5]
## [1,] 2.1 -0.1688711 2.481003 4.844514 3.017857
## [2,] 2.1 4.6688711 3.233283 9.441201 3.582143
##
## $out
## [1] 2.250 10.875
##
## $group
## [1] 5 5
##
## $names
## [1] "3x" "A" "A&V" "P" "V"
```

Construct random data set with the same structure as original data

```
library(MASS)
fitMg <- fitdistr(adDat$Mg,"gamma")

## Warning in densfun(x, parm[1], parm[2], ...): NaNs produced
## Warning in densfun(x, parm[1], parm[2], ...): NaNs produced
## Warning in densfun(x, parm[1], parm[2], ...): NaNs produced
ranMg <- rnorm(30,mean=1050,sd=670)

fitdistr(adDat$Ca,"normal")

##      mean      sd
## 675.24138 451.42622
## ( 83.82774) ( 59.27517)
ranCa <- rnorm(30,mean=675,sd=451)

randomData <- cbind(ranCa,ranMg)
head(randomData)

##      ranCa      ranMg
## [1,] 495.7974 943.5656
## [2,] 464.0230 1841.1826
## [3,] 1260.5745 1602.3561
## [4,] 481.5407 809.7799
## [5,] 1174.9180 959.9166
## [6,] 1459.5267 1391.7099
```

Construct random data set with same structure as original data using dgamma

```
library(MASS)
# use the fitdistr function to get parameters of percent organic matter in soil using gamma distribution
fitom <- fitdistr(adDat$Ompct,"gamma")
```



```

# make a new randomly generated %OM variable using parameters from above
randOM <- rgamma(30,fitom$estimate[1],fitom$estimate[2])

# Create vector of species id's and assign to randomly generated randOM values
spID <- c("A","V")
ranSpID <- rep(spID,length=30)
ranDat <- data.frame(ranSpID,randOM)

#Run ANOVA with randomly generated values - returns non-significant result
ANOV(xVar=ranDat$ranSpID,yVar=ranDat$randOM)

## [1] 0.2364415

```