R_activity_assignment_10

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```
install.packages("xfun", repos = "https://cran.rstudio.com/")
```

```
## Installing package into 'C:/Users/chemk/AppData/Local/R/win-library/4.4'
## (as 'lib' is unspecified)
```

```
## package 'xfun' successfully unpacked and MD5 sums checked
```

```
## Warning: cannot remove prior installation of package 'xfun'
```

```
## Warning in file.copy(savedcopy, lib, recursive = TRUE): problem copying
## C:\Users\chemk\AppData\Local\R\win-library\4.4\00LOCK\xfun\libs\x64\xfun.dll to
## C:\Users\chemk\AppData\Local\R\win-library\4.4\xfun\libs\x64\xfun.dll:
## Permission denied
```

```
## Warning: restored 'xfun'
```

```
##
## The downloaded binary packages are in
##  C:\Users\chemk\AppData\Local\Temp\RtmpuKm9Ht\downloaded_packages
```

```
options(repos = c(CRAN = "https://cran.rstudio.com/"))
R.home(component = "home")
```

```
## [1] "C:/PROGRA~1/R/R-44~1.2"
```

1. We will use another open source data set from the NSF Harvard Forest Long-term Ecological Research (LTER) site. These data are spiders collected in the Hemlock Removal Experiment. Remember, this experiment includes four treatments (Hemlock girdled, Hemlock logged, Hemlock control, and Hardwood control) each replicated across two (n = 2)

90 x 90 m plots. Load the data into R. We will characterize spider communities among these four treatments and between sampling methods.

```
spiders <- read.csv(file="C:/Users/chemk/Desktop/Classes/ENT6707_DataAnalysis/week12/HarvardForest_spiders.csv", header=T, na.strings=c("", ".", "NA"))
```

```
head(spiders)
```

```
##   start.date  end.date  block treatment plot replicate sampling.method
## 1  7/18/2008 7/28/2008 Valley   Girdled    1         5  Litter_sifting
## 2  5/19/2008 5/29/2008 Valley   Girdled    1         3  Litter_sifting
## 3  9/22/2008 10/2/2008 Valley   Girdled    1         1  Litter_sifting
## 4  7/18/2008 7/28/2008 Valley   Girdled    1         5  Litter_sifting
## 5  7/18/2008 7/28/2008 Valley   Girdled    1         5  Litter_sifting
## 6  7/18/2008 7/28/2008 Valley   Girdled    1         5  Litter_sifting
##         family       genus    species males females immature
## 1  LINYPHIIDAE Ceraticelus laetabilis     0       2        0
## 2   SALTICIDAE     immSalt        sp.     0       0        2
## 3  LINYPHIIDAE     immLiny        sp.     0       0       16
## 4 AMAUROBIIDAE     immAmau        sp.     0       0        4
## 5   THOMISIDAE     immThom        sp.     0       0        1
## 6    HAHNIIDAE Neoantistea      magna     1       0        0
```

```
tail(spiders)
```

```
##      start.date  end.date  block treatment plot replicate sampling.method
## 1847  7/18/2008 7/28/2008 Valley  Hardwood    8         3  Litter_sifting
## 1848  7/18/2008 7/28/2008 Valley  Hardwood    8         3  Litter_sifting
## 1849  7/18/2008 7/28/2008 Valley  Hardwood    8         3  Litter_sifting
## 1850  7/18/2008 7/28/2008 Valley  Hardwood    8         3  Litter_sifting
## 1851  7/18/2008 7/28/2008 Valley  Hardwood    8         2  Litter_sifting
## 1852  7/18/2008 7/28/2008 Valley  Hardwood    8         4  Litter_sifting
##            family     genus         species males females immature
## 1847  LINYPHIIDAE   immLiny             sp.     0       0       20
## 1848   AGELENIDAE   immAgel             sp.     0       0        2
## 1849   CORINNIDAE   immCori             sp.     0       0       11
## 1850 AMAUROBIIDAE   immAmau             sp.     0       0        2
## 1851  LINYPHIIDAE Collinsia oxypaederotipus     0       2        0
## 1852   AGELENIDAE   immAgel             sp.     0       0        1
```

```
summary(spiders)
```

```
##   start.date          end.date            block            treatment
##  Length:1852        Length:1852        Length:1852        Length:1852
##  Class :character   Class :character   Class :character   Class :character
##  Mode  :character   Mode  :character   Mode  :character   Mode  :character
##
##
##
##       plot         replicate     sampling.method       family
##  Min.   :1.000   Min.   :1.000   Length:1852        Length:1852
##  1st Qu.:3.000   1st Qu.:2.000   Class :character   Class :character
##  Median :5.000   Median :3.000   Mode  :character   Mode  :character
##  Mean   :4.917   Mean   :3.017
##  3rd Qu.:7.000   3rd Qu.:4.000
##  Max.   :8.000   Max.   :5.000
##     genus              species              males            females
##  Length:1852        Length:1852        Min.   : 0.0000   Min.   : 0.0000
##  Class :character   Class :character   1st Qu.: 0.0000   1st Qu.: 0.0000
##  Mode  :character   Mode  :character   Median : 0.0000   Median : 0.0000
##                                        Mean   : 0.6517   Mean   : 0.6463
##                                        3rd Qu.: 1.0000   3rd Qu.: 1.0000
##                                        Max.   :28.0000   Max.   :12.0000
##     immature
##  Min.   : 0.000
##  1st Qu.: 0.000
##  Median : 0.000
##  Mean   : 2.233
##  3rd Qu.: 2.000
##  Max.   :55.000
```

```
View(spiders)
str(spiders)
```

```
## 'data.frame':    1852 obs. of  13 variables:
##  $ start.date     : chr  "7/18/2008" "5/19/2008" "9/22/2008" "7/18/2008" ...
##  $ end.date       : chr  "7/28/2008" "5/29/2008" "10/2/2008" "7/28/2008" ...
##  $ block          : chr  "Valley" "Valley" "Valley" "Valley" ...
##  $ treatment      : chr  "Girdled" "Girdled" "Girdled" "Girdled" ...
##  $ plot           : int  1 1 1 1 1 1 1 1 1 1 ...
##  $ replicate      : int  5 3 1 5 5 5 1 5 1 5 ...
##  $ sampling.method: chr  "Litter_sifting" "Litter_sifting" "Litter_sifting" "Litter_sifting"
...
##  $ family         : chr  "LINYPHIIDAE" "SALTICIDAE" "LINYPHIIDAE" "AMAUROBIIDAE" ...
##  $ genus          : chr  "Ceraticelus" "immSalt" "immLiny" "immAmau" ...
##  $ species        : chr  "laetabilis" "sp." "sp." "sp." ...
##  $ males          : int  0 0 0 0 0 1 0 1 0 0 ...
##  $ females        : int  2 0 0 0 0 0 0 1 0 2 ...
##  $ immature       : int  0 2 16 4 1 0 2 0 1 0 ...
```

2. Before calculating the diversity metrics, you will have to do some data wrangling. First, create a new variable abundance by summing the counts of adult male and female spiders.

```
spiders$abundance <- spiders$males + spiders$females
```

Next, change the data set from long format to wide format using spider genus as the taxonomic resolution (i.e., each column should be a spider genus).

```
library(reshape2)
spider.matrix <- dcast(spiders, start.date + end.date + block + treatment + plot + replicate + s
ampling.method ~ genus, sum, value.var = "abundance", na.rm =TRUE)
```

Be sure that the new data frame includes the predictor and nuisance variables.

```
View(spider.matrix)
```

Then, remove any columns that do not have count data (some genera are indicated as immatures with imm), as well as three columns with unidentified spiders (LinytoID, LinyToID, and unk_toID).

```
spider_cleaned <- spider.matrix[, !grepl("imm", colnames(spider.matrix))]  # remove rows includi
ng "imm"
spider_cleaned_1 <- spider_cleaned[, !(colnames(spider_cleaned) %in% c("LinytoID", "LinyToID",
"unk_toID"))]
```

Lastly, change the variables block, plot, treatment, and sampling method to factors. Provide a summary of the data set.

```
spider_cleaned_1$block <- as.factor(spider_cleaned_1$block)
spider_cleaned_1$treatment <- as.factor(spider_cleaned_1$treatment)
spider_cleaned_1$plot <- as.factor(spider_cleaned_1$plot)
spider_cleaned_1$sampling.method <- as.factor(spider_cleaned_1$sampling.method)

levels(spider_cleaned_1$treatment)
```

```
## [1] "Girdled"  "Hardwood" "Hemlock"  "Logged"
```

How many spider genera were collected? 51

```
summary(spider_cleaned_1)
```

```
##   start.date          end.date            block        treatment       plot
##  Length:231         Length:231         Ridge :115   Girdled :58   3      :30
##  Class :character   Class :character   Valley:116   Hardwood:56   5      :30
##  Mode  :character   Mode  :character                Hemlock :59   2      :29
##                                                    Logged  :58   4      :29
##                                                                  6      :29
##                                                                  8      :29
##                                                                  (Other):55
##    replicate           sampling.method  Agelenopsis          Agroeca
##  Min.   :1.000   Litter_sifting:120    Min.   :0.000000   Min.   :0.0000
##  1st Qu.:2.000   Pitfall       :111    1st Qu.:0.000000   1st Qu.:0.0000
##  Median :3.000                         Median :0.000000   Median :0.0000
##  Mean   :2.978                         Mean   :0.008658   Mean   :0.2597
##  3rd Qu.:4.000                         3rd Qu.:0.000000   3rd Qu.:0.0000
##  Max.   :5.000                         Max.   :1.000000   Max.   :4.0000
##
##    Amaurobius       Araniella          Callobius        Castianeira
##  Min.   : 0.000   Min.   :0.000000   Min.   :0.00000   Min.   :0.00000
##  1st Qu.: 0.000   1st Qu.:0.000000   1st Qu.:0.00000   1st Qu.:0.00000
##  Median : 0.000   Median :0.000000   Median :0.00000   Median :0.00000
##  Mean   : 1.294   Mean   :0.004329   Mean   :0.06061   Mean   :0.02597
##  3rd Qu.: 2.000   3rd Qu.:0.000000   3rd Qu.:0.00000   3rd Qu.:0.00000
##  Max.   :10.000   Max.   :1.000000   Max.   :2.00000   Max.   :2.00000
##
##   Centromerus      Ceraticelus       Ceratinella       Ceratinops
##  Min.   :0.0000   Min.   : 0.0000   Min.   : 0.000   Min.   :0.00000
##  1st Qu.:0.0000   1st Qu.: 0.0000   1st Qu.: 0.000   1st Qu.:0.00000
##  Median :0.0000   Median : 0.0000   Median : 0.000   Median :0.00000
##  Mean   :0.1775   Mean   : 0.9957   Mean   : 1.126   Mean   :0.03896
##  3rd Qu.:0.0000   3rd Qu.: 1.0000   3rd Qu.: 1.000   3rd Qu.:0.00000
##  Max.   :7.0000   Max.   :11.0000   Max.   :22.000   Max.   :2.00000
##
##  Ceratinopsidis      Ceratinopsis         Cicurina         Clubiona
##  Min.   :0.000000   Min.   :0.000000   Min.   :0.0000   Min.   :0.000000
##  1st Qu.:0.000000   1st Qu.:0.000000   1st Qu.:0.0000   1st Qu.:0.000000
##  Median :0.000000   Median :0.000000   Median :0.0000   Median :0.000000
##  Mean   :0.004329   Mean   :0.004329   Mean   :0.1515   Mean   :0.004329
##  3rd Qu.:0.000000   3rd Qu.:0.000000   3rd Qu.:0.0000   3rd Qu.:0.000000
##  Max.   :1.000000   Max.   :1.000000   Max.   :7.0000   Max.   :1.000000
##
##    Collinsia          Coras            Cryphoeca         Dictyna
##  Min.   : 0.000   Min.   :0.000000   Min.   :0.0000   Min.   :0.000000
##  1st Qu.: 0.000   1st Qu.:0.000000   1st Qu.:0.0000   1st Qu.:0.000000
##  Median : 0.000   Median :0.000000   Median :0.0000   Median :0.000000
##  Mean   : 1.065   Mean   :0.004329   Mean   :0.0303   Mean   :0.004329
##  3rd Qu.: 0.500   3rd Qu.:0.000000   3rd Qu.:0.0000   3rd Qu.:0.000000
##  Max.   :30.000   Max.   :1.000000   Max.   :2.0000   Max.   :1.000000
##
##     Emblyna          Eperigone           Eris           Habronattus
##  Min.   :0.00000   Min.   :0.0000   Min.   :0.000000   Min.   :0.00000
##  1st Qu.:0.00000   1st Qu.:0.0000   1st Qu.:0.000000   1st Qu.:0.00000
##  Median :0.00000   Median :0.0000   Median :0.000000   Median :0.00000
```

```
##  Mean   :0.01299   Mean   :0.2424   Mean   :0.008658   Mean   :0.01732
##  3rd Qu.:0.00000   3rd Qu.:0.0000   3rd Qu.:0.000000   3rd Qu.:0.00000
##  Max.   :1.00000   Max.   :4.0000   Max.   :2.000000   Max.   :2.00000
##
##      Hahnia          Helophora           Hogna              Lathys
##  Min.   :0.00000   Min.   :0.00000   Min.   :0.000000   Min.   :0.00000
##  1st Qu.:0.00000   1st Qu.:0.00000   1st Qu.:0.000000   1st Qu.:0.00000
##  Median :0.00000   Median :0.00000   Median :0.000000   Median :0.00000
##  Mean   :0.02597   Mean   :0.02165   Mean   :0.008658   Mean   :0.01299
##  3rd Qu.:0.00000   3rd Qu.:0.00000   3rd Qu.:0.000000   3rd Qu.:0.00000
##  Max.   :1.00000   Max.   :2.00000   Max.   :1.000000   Max.   :1.00000
##
##    Macrargus          Meioneta        Microneta          Naphrys
##  Min.   :0.00000   Min.   :0.0000   Min.   :0.00000   Min.   :0.000000
##  1st Qu.:0.00000   1st Qu.:0.0000   1st Qu.:0.00000   1st Qu.:0.000000
##  Median :0.00000   Median :0.0000   Median :0.00000   Median :0.000000
##  Mean   :0.03463   Mean   :0.1429   Mean   :0.09524   Mean   :0.004329
##  3rd Qu.:0.00000   3rd Qu.:0.0000   3rd Qu.:0.00000   3rd Qu.:0.000000
##  Max.   :2.00000   Max.   :5.0000   Max.   :2.00000   Max.   :1.000000
##
##   Neoantistea          Neon           Ozyptila          Pardosa
##  Min.   :0.0000   Min.   :0.0000   Min.   :0.00000   Min.   : 0.0000
##  1st Qu.:0.0000   1st Qu.:0.0000   1st Qu.:0.00000   1st Qu.: 0.0000
##  Median :0.0000   Median :0.0000   Median :0.00000   Median : 0.0000
##  Mean   :0.5887   Mean   :0.1255   Mean   :0.03896   Mean   : 0.4805
##  3rd Qu.:1.0000   3rd Qu.:0.0000   3rd Qu.:0.00000   3rd Qu.: 0.0000
##  Max.   :5.0000   Max.   :3.0000   Max.   :3.00000   Max.   :19.0000
##
##    Pelegrina          Phidippus          Pholcomma       Phrurotimpus
##  Min.   :0.000000   Min.   :0.000000   Min.   :0.0000   Min.   :0.0000
##  1st Qu.:0.000000   1st Qu.:0.000000   1st Qu.:0.0000   1st Qu.:0.0000
##  Median :0.000000   Median :0.000000   Median :0.0000   Median :0.0000
##  Mean   :0.004329   Mean   :0.004329   Mean   :0.1385   Mean   :0.3939
##  3rd Qu.:0.000000   3rd Qu.:0.000000   3rd Qu.:0.0000   3rd Qu.:0.0000
##  Max.   :1.000000   Max.   :1.000000   Max.   :7.0000   Max.   :7.0000
##
##      Pirata         Pocadicnemis        Robertus        Scylaceus
##  Min.   : 0.0000   Min.   :0.00000   Min.   :0.0000   Min.   :0.00000
##  1st Qu.: 0.0000   1st Qu.:0.00000   1st Qu.:0.0000   1st Qu.:0.00000
##  Median : 0.0000   Median :0.00000   Median :0.0000   Median :0.00000
##  Mean   : 0.7835   Mean   :0.01732   Mean   :0.1991   Mean   :0.09091
##  3rd Qu.: 0.0000   3rd Qu.:0.00000   3rd Qu.:0.0000   3rd Qu.:0.00000
##  Max.   :30.0000   Max.   :2.00000   Max.   :5.0000   Max.   :7.00000
##
##    Sisicottus          Sisicus          Tapinocyba       Tenuiphantes
##  Min.   :0.000000   Min.   :0.00000   Min.   : 0.0000   Min.   :0.0000
##  1st Qu.:0.000000   1st Qu.:0.00000   1st Qu.: 0.0000   1st Qu.:0.0000
##  Median :0.000000   Median :0.00000   Median : 0.0000   Median :0.0000
##  Mean   :0.004329   Mean   :0.03896   Mean   : 0.6277   Mean   :0.3766
##  3rd Qu.:0.000000   3rd Qu.:0.00000   3rd Qu.: 0.0000   3rd Qu.:0.0000
##  Max.   :1.000000   Max.   :2.00000   Max.   :10.0000   Max.   :9.0000
##
```

```
##     Trochosa         Wadotes        Walckenaeria       Xysticus
##  Min.   :0.0000   Min.   :0.0000   Min.   :0.0000   Min.   :0.000000
##  1st Qu.:0.0000   1st Qu.:0.0000   1st Qu.:0.0000   1st Qu.:0.000000
##  Median :0.0000   Median :0.0000   Median :0.0000   Median :0.000000
##  Mean   :0.0303   Mean   :0.1905   Mean   :0.2251   Mean   :0.008658
##  3rd Qu.:0.0000   3rd Qu.:0.0000   3rd Qu.:0.0000   3rd Qu.:0.000000
##  Max.   :2.0000   Max.   :3.0000   Max.   :5.0000   Max.   :1.000000
##
##     Zelotes
##  Min.   :0.00000
##  1st Qu.:0.00000
##  Median :0.00000
##  Mean   :0.08658
##  3rd Qu.:0.00000
##  Max.   :3.00000
##
```

```
View(spider_cleaned_1)
```

3. What are the three most abundant spider genera?

Answer: Amaurobius, Ceratinella, Collinsia

```
spider_numeric <- spider_cleaned_1[sapply(spider_cleaned_1, is.numeric)]
spider_new <- spider_cleaned_1[, colSums(spider_numeric != 0) > 0]
str(spider_new)
```

```
## 'data.frame':    231 obs. of  58 variables:
##  $ start.date     : chr  "5/19/2008" "5/19/2008" "5/19/2008" "5/19/2008" ...
##  $ end.date       : chr  "5/29/2008" "5/29/2008" "5/29/2008" "5/29/2008" ...
##  $ block          : Factor w/ 2 levels "Ridge","Valley": 1 1 1 1 1 1 1 1 1 1 ...
##  $ treatment      : Factor w/ 4 levels "Girdled","Hardwood",..: 1 1 1 1 1 1 1 1 1 1 ...
##  $ plot           : Factor w/ 8 levels "1","2","3","4",..: 5 5 5 5 5 5 5 5 5 5 ...
##  $ replicate      : int  1 1 2 2 3 3 4 4 5 5 ...
##  $ sampling.method: Factor w/ 2 levels "Litter_sifting",..: 1 2 1 2 1 2 1 2 1 2 ...
##  $ Agelenopsis    : int  0 0 0 0 0 0 0 0 0 0 ...
##  $ Agroeca        : int  0 2 0 1 0 3 0 3 0 0 ...
##  $ Amaurobius     : int  3 10 1 6 0 5 1 7 1 3 ...
##  $ Araniella      : int  0 0 0 0 1 0 0 0 0 0 ...
##  $ Callobius      : int  0 0 0 0 0 0 0 0 0 0 ...
##  $ Castianeira    : int  0 0 0 0 0 0 0 0 0 0 ...
##  $ Centromerus    : int  0 0 0 0 0 0 0 0 0 0 ...
##  $ Ceraticelus    : int  5 0 1 0 3 0 2 0 0 0 ...
##  $ Ceratinella    : int  4 0 0 1 5 0 2 0 3 1 ...
##  $ Ceratinops     : int  0 0 0 0 0 0 0 0 0 0 ...
##  $ Ceratinopsidis : int  0 0 0 0 0 0 0 0 0 0 ...
##  $ Ceratinopsis   : int  0 0 0 0 0 0 0 0 0 0 ...
##  $ Cicurina       : int  0 0 0 1 0 0 0 1 0 0 ...
##  $ Clubiona       : int  0 0 0 0 0 0 0 0 0 0 ...
##  $ Collinsia      : int  4 0 0 0 6 0 30 0 10 0 ...
##  $ Coras          : int  0 0 0 0 0 0 0 0 0 0 ...
##  $ Cryphoeca      : int  0 0 0 0 0 0 0 0 0 0 ...
##  $ Dictyna        : int  0 0 0 0 0 0 0 0 0 0 ...
##  $ Emblyna        : int  0 0 0 0 0 0 0 0 0 0 ...
##  $ Eperigone      : int  0 0 0 0 1 0 0 0 0 0 ...
##  $ Eris           : int  0 0 0 0 0 0 0 0 0 0 ...
##  $ Habronattus    : int  0 0 0 0 0 0 0 0 0 0 ...
##  $ Hahnia         : int  0 0 0 0 0 0 0 0 0 0 ...
##  $ Helophora      : int  0 0 0 0 0 0 0 0 0 0 ...
##  $ Hogna          : int  0 0 0 0 0 0 0 0 0 0 ...
##  $ Lathys         : int  0 0 0 0 0 0 0 0 0 0 ...
##  $ Macrargus      : int  0 0 0 0 0 0 0 0 1 0 ...
##  $ Meioneta       : int  0 0 0 4 1 0 0 0 0 0 ...
##  $ Microneta      : int  0 0 1 0 1 0 1 0 0 0 ...
##  $ Naphrys        : int  0 0 0 0 0 0 0 0 0 0 ...
##  $ Neoantistea    : int  0 0 0 0 0 0 0 0 0 0 ...
##  $ Neon           : int  1 0 0 0 1 0 0 0 0 0 ...
##  $ Ozyptila       : int  1 0 0 0 0 0 0 0 0 0 ...
##  $ Pardosa        : int  0 0 0 2 0 1 0 1 0 1 ...
##  $ Pelegrina      : int  0 0 0 0 0 0 0 0 0 0 ...
##  $ Phidippus      : int  0 0 0 0 0 0 0 0 0 0 ...
##  $ Pholcomma      : int  0 0 0 0 0 0 0 0 0 0 ...
##  $ Phrurotimpus   : int  4 0 0 0 0 0 3 0 0 0 ...
##  $ Pirata         : int  1 3 0 0 0 2 0 6 1 1 ...
##  $ Pocadicnemis   : int  0 0 0 0 0 0 0 0 0 0 ...
##  $ Robertus       : int  0 0 0 0 0 0 0 0 0 0 ...
##  $ Scylaceus      : int  0 0 0 0 0 0 0 0 0 0 ...
##  $ Sisicottus     : int  0 0 0 0 0 0 0 0 0 0 ...
##  $ Sisicus        : int  0 0 0 0 0 0 0 0 0 0 ...
```

```
##  $ Tapinocyba     : int  0 0 1 0 7 0 4 0 3 0 ...
##  $ Tenuiphantes   : int  2 0 1 1 1 0 0 0 2 1 ...
##  $ Trochosa       : int  0 0 0 0 0 0 0 0 0 0 ...
##  $ Wadotes        : int  0 0 0 0 0 0 0 0 0 0 ...
##  $ Walckenaeria   : int  0 0 1 0 0 0 0 0 0 0 ...
##  $ Xysticus       : int  0 0 0 0 0 0 0 0 0 0 ...
##  $ Zelotes        : int  0 0 0 0 0 0 0 0 0 0 ...
```

```
spider_new[8:58] <- sapply(spider_new[8:58], as.numeric)
spider_new$totabund <- rowSums(spider_new[8:58], na.rm = TRUE)
colnames(spider_new)[8:58]
```

```
##  [1] "Agelenopsis"    "Agroeca"        "Amaurobius"     "Araniella"
##  [5] "Callobius"      "Castianeira"    "Centromerus"    "Ceraticelus"
##  [9] "Ceratinella"    "Ceratinops"     "Ceratinopsidis" "Ceratinopsis"
## [13] "Cicurina"       "Clubiona"       "Collinsia"      "Coras"
## [17] "Cryphoeca"      "Dictyna"        "Emblyna"        "Eperigone"
## [21] "Eris"           "Habronattus"    "Hahnia"         "Helophora"
## [25] "Hogna"          "Lathys"         "Macrargus"      "Meioneta"
## [29] "Microneta"      "Naphrys"        "Neoantistea"    "Neon"
## [33] "Ozyptila"       "Pardosa"        "Pelegrina"      "Phidippus"
## [37] "Pholcomma"      "Phrurotimpus"   "Pirata"         "Pocadicnemis"
## [41] "Robertus"       "Scylaceus"      "Sisicottus"     "Sisicus"
## [45] "Tapinocyba"     "Tenuiphantes"   "Trochosa"       "Wadotes"
## [49] "Walckenaeria"   "Xysticus"       "Zelotes"
```

```
colSums(spider_new[8:58])
```

```
##    Agelenopsis        Agroeca     Amaurobius      Araniella      Callobius
##              2             60            299              1             14
##    Castianeira    Centromerus    Ceraticelus    Ceratinella     Ceratinops
##              6             41            230            260              9
## Ceratinopsidis   Ceratinopsis       Cicurina       Clubiona      Collinsia
##              1              1             35              1            246
##          Coras      Cryphoeca        Dictyna        Emblyna      Eperigone
##              1              7              1              3             56
##           Eris    Habronattus         Hahnia      Helophora          Hogna
##              2              4              6              5              2
##         Lathys      Macrargus       Meioneta      Microneta        Naphrys
##              3              8             33             22              1
##    Neoantistea           Neon       Ozyptila        Pardosa      Pelegrina
##            136             29              9            111              1
##      Phidippus      Pholcomma   Phrurotimpus         Pirata   Pocadicnemis
##              1             32             91            181              4
##       Robertus      Scylaceus     Sisicottus        Sisicus     Tapinocyba
##             46             21              1              9            145
##   Tenuiphantes       Trochosa        Wadotes   Walckenaeria       Xysticus
##             87              7             44             52              2
##        Zelotes
##             20
```

```
spider_dom <- colSums(spider_new[,8:58])
spider_dom <- as.data.frame(spider_dom)
names(spider_dom)[1] <- "count"
spider_dom$genus <- rownames(spider_dom)
str(spider_dom)
```

```
## 'data.frame':    51 obs. of  2 variables:
##  $ count: num  2 60 299 1 14 6 41 230 260 9 ...
##  $ genus: chr  "Agelenopsis" "Agroeca" "Amaurobius" "Araniella" ...
```

```
spider_dom$genus <- as.factor(spider_dom$genus)
```

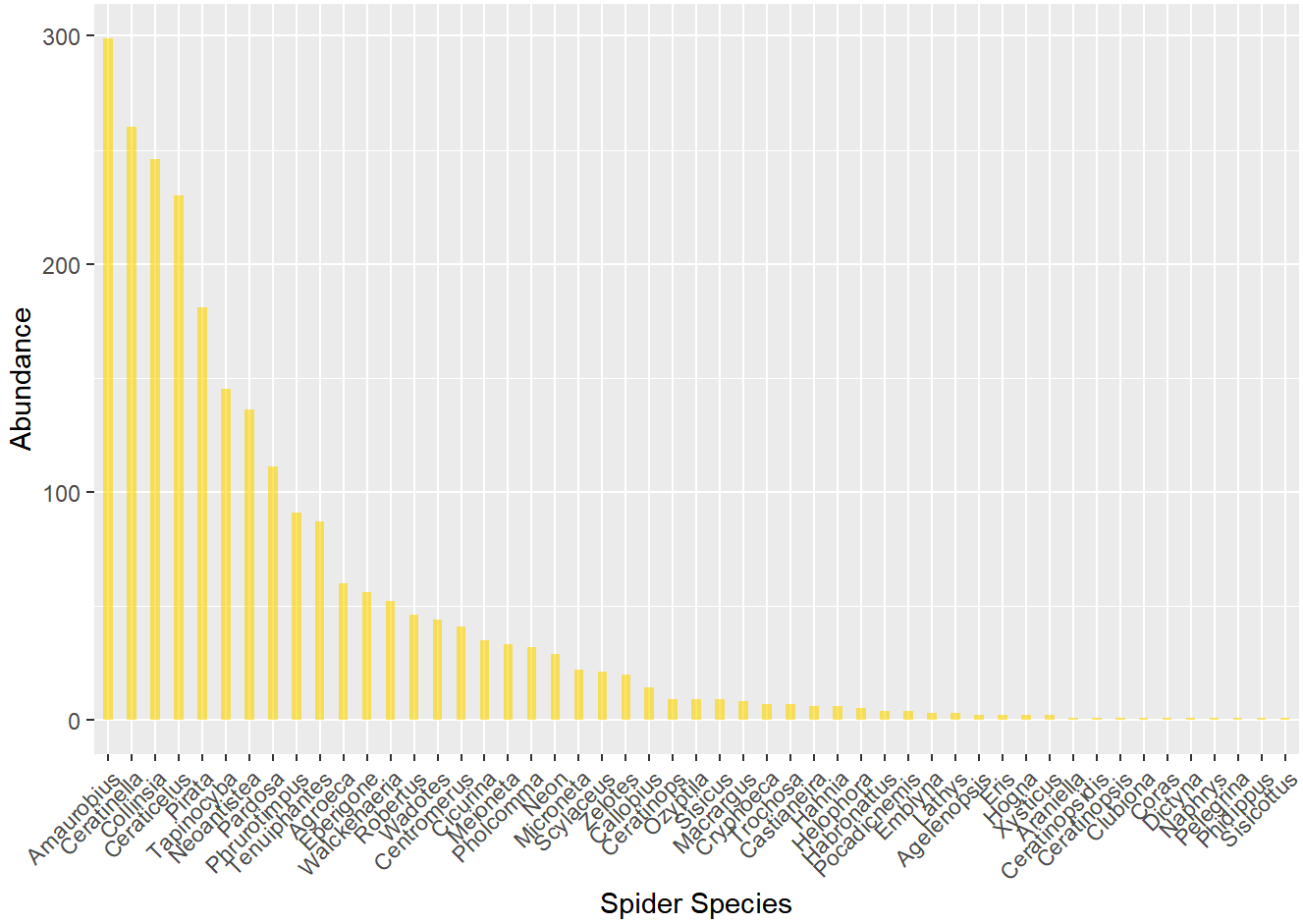
```
library(ggplot2)
library(dplyr)
```

```
##
## Attaching package: 'dplyr'
```

```
## The following objects are masked from 'package:stats':
##
##     filter, lag
```

```
## The following objects are masked from 'package:base':
##
##     intersect, setdiff, setequal, union
```

```
library(forcats)
spider_dom %>% mutate(genus =fct_reorder(genus, desc(count))) %>% ggplot(aes(x=genus, y=count))+
  geom_bar(stat="identity", fill="gold", alpha=.6, width=.4)+
  theme(axis.text.x = element_text(angle=45, vjust=1, hjust=1))+
  xlab("Spider Species")+
  ylab("Abundance")
```



4. Calculate spider genera richness for each sample, add this new variable to the data set, and create a boxplot that shows spider genera richness as a function of treatment.

```
install.packages("vegan", repos = "http://cran.us.r-project.org")
```

```
## Installing package into 'C:/Users/chemk/AppData/Local/R/win-library/4.4'
## (as 'lib' is unspecified)
```

```
## package 'vegan' successfully unpacked and MD5 sums checked
##
## The downloaded binary packages are in
##  C:\Users\chemk\AppData\Local\Temp\RtmpuKm9Ht\downloaded_packages
```

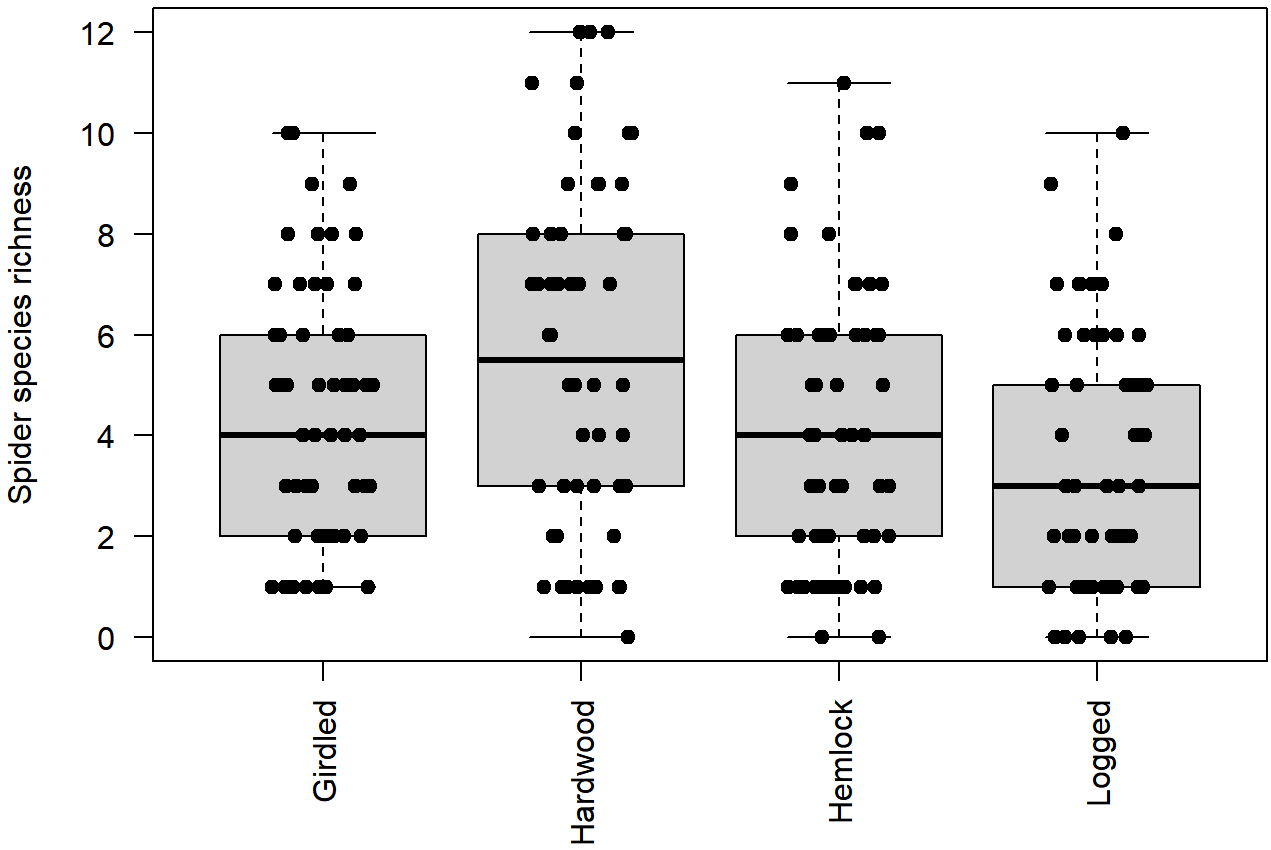
```
library(vegan)
```

```
## Loading required package: permute
```

```
## Loading required package: lattice
```

```
## This is vegan 2.6-8
```

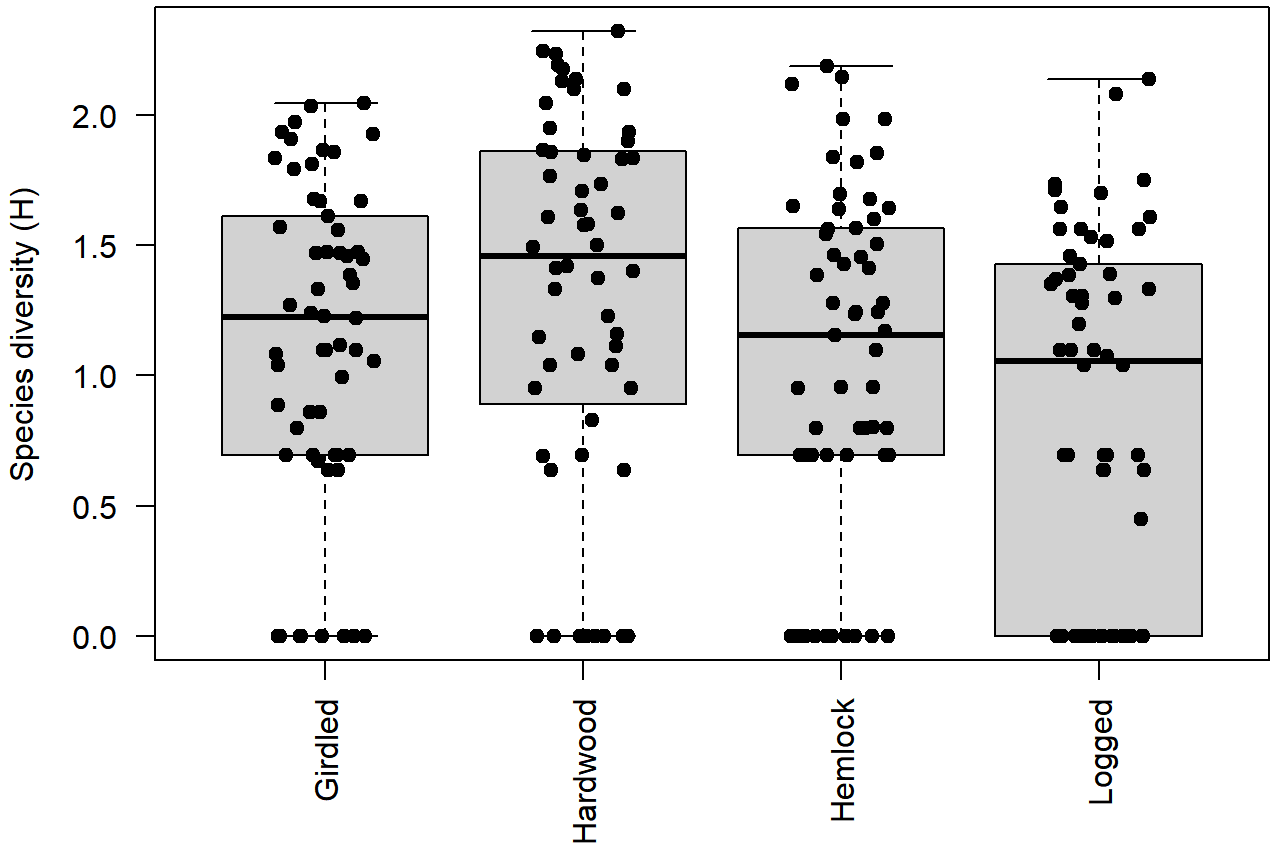
```
spider_new$sp.rich <- specnumber(spider_new[,8:58])
par(mar=c(6,4,2,2))
boxplot(sp.rich ~ treatment, data = spider_new, xlab = "", ylab = "Spider species richness", ce
x.axis = 1, las = 2)
stripchart(sp.rich ~ treatment, data = spider_new, pch = 19, add = TRUE, vertical = TRUE, method
= "jitter", jitter = 0.2)
```



5. Calculate another diversity metric of your choice and create a boxplot that shows spider genera diversity as a function of treatment.

```
library(hillR)
library(vegan)
```

```
spider_new$sh.div <- diversity(spider_new[,8:58], index = "shannon")
par(mar=c(6,4,2,2))
boxplot(sh.div ~ treatment, data = spider_new, xlab = "", ylab = "Species diversity (H)", cex.ax
is = 1, las = 2)
stripchart(sh.div ~ treatment, data = spider_new, pch = 19, add = TRUE, vertical = TRUE, method
= "jitter", jitter = 0.2)
```



6. Create a boxplot that shows spider genera diversity as a function of sampling method.

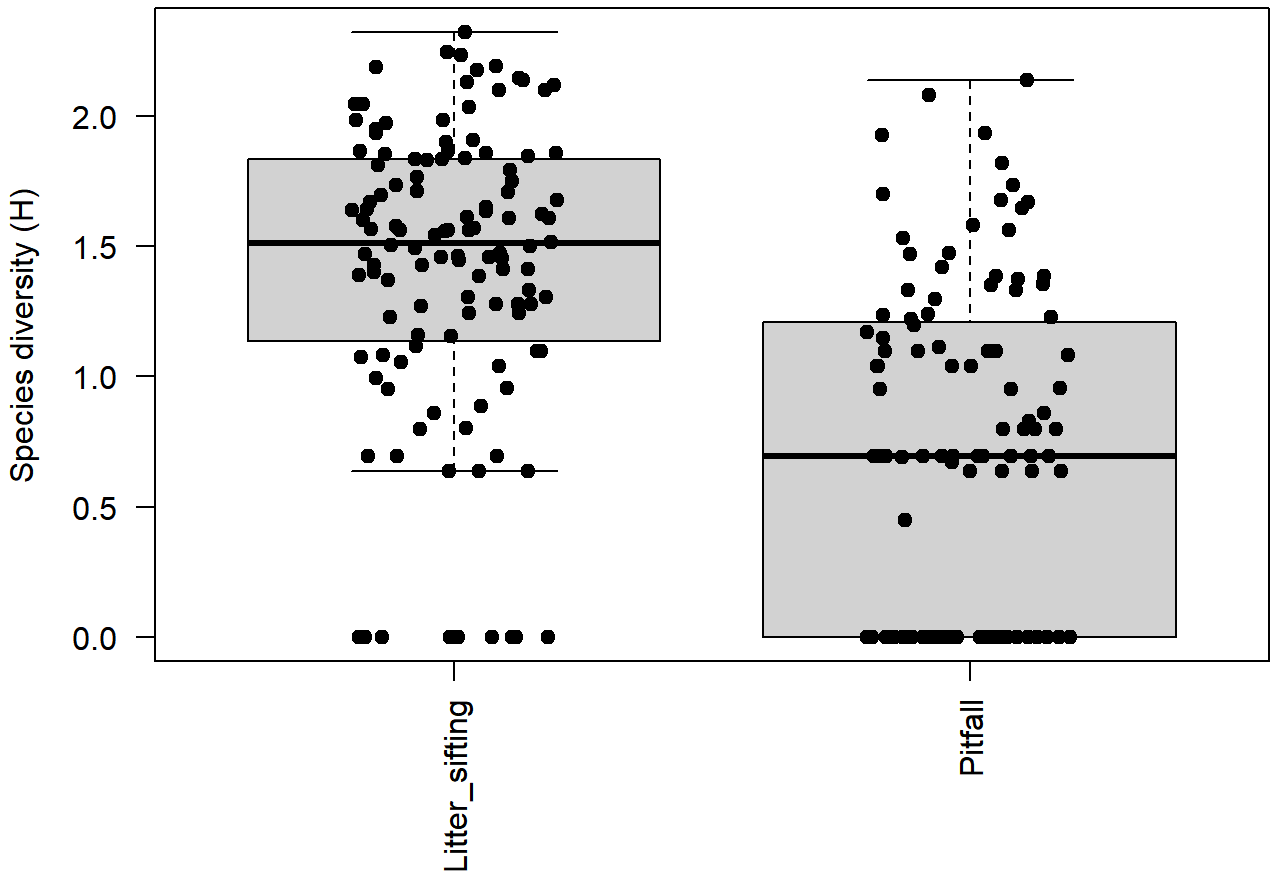
```
str(spider_new)
```

```
## 'data.frame':    231 obs. of  61 variables:
##  $ start.date     : chr  "5/19/2008" "5/19/2008" "5/19/2008" "5/19/2008" ...
##  $ end.date       : chr  "5/29/2008" "5/29/2008" "5/29/2008" "5/29/2008" ...
##  $ block          : Factor w/ 2 levels "Ridge","Valley": 1 1 1 1 1 1 1 1 1 1 ...
##  $ treatment      : Factor w/ 4 levels "Girdled","Hardwood",..: 1 1 1 1 1 1 1 1 1 1 ...
##  $ plot           : Factor w/ 8 levels "1","2","3","4",..: 5 5 5 5 5 5 5 5 5 5 ...
##  $ replicate      : int  1 1 2 2 3 3 4 4 5 5 ...
##  $ sampling.method: Factor w/ 2 levels "Litter_sifting",..: 1 2 1 2 1 2 1 2 1 2 ...
##  $ Agelenopsis    : num  0 0 0 0 0 0 0 0 0 0 ...
##  $ Agroeca        : num  0 2 0 1 0 3 0 3 0 0 ...
##  $ Amaurobius     : num  3 10 1 6 0 5 1 7 1 3 ...
##  $ Araniella      : num  0 0 0 0 1 0 0 0 0 0 ...
##  $ Callobius      : num  0 0 0 0 0 0 0 0 0 0 ...
##  $ Castianeira    : num  0 0 0 0 0 0 0 0 0 0 ...
##  $ Centromerus    : num  0 0 0 0 0 0 0 0 0 0 ...
##  $ Ceraticelus    : num  5 0 1 0 3 0 2 0 0 0 ...
##  $ Ceratinella    : num  4 0 0 1 5 0 2 0 3 1 ...
##  $ Ceratinops     : num  0 0 0 0 0 0 0 0 0 0 ...
##  $ Ceratinopsidis : num  0 0 0 0 0 0 0 0 0 0 ...
##  $ Ceratinopsis   : num  0 0 0 0 0 0 0 0 0 0 ...
##  $ Cicurina       : num  0 0 0 1 0 0 0 1 0 0 ...
##  $ Clubiona       : num  0 0 0 0 0 0 0 0 0 0 ...
##  $ Collinsia      : num  4 0 0 0 6 0 30 0 10 0 ...
##  $ Coras          : num  0 0 0 0 0 0 0 0 0 0 ...
##  $ Cryphoeca      : num  0 0 0 0 0 0 0 0 0 0 ...
##  $ Dictyna        : num  0 0 0 0 0 0 0 0 0 0 ...
##  $ Emblyna        : num  0 0 0 0 0 0 0 0 0 0 ...
##  $ Eperigone      : num  0 0 0 0 1 0 0 0 0 0 ...
##  $ Eris           : num  0 0 0 0 0 0 0 0 0 0 ...
##  $ Habronattus    : num  0 0 0 0 0 0 0 0 0 0 ...
##  $ Hahnia         : num  0 0 0 0 0 0 0 0 0 0 ...
##  $ Helophora      : num  0 0 0 0 0 0 0 0 0 0 ...
##  $ Hogna          : num  0 0 0 0 0 0 0 0 0 0 ...
##  $ Lathys         : num  0 0 0 0 0 0 0 0 0 0 ...
##  $ Macrargus      : num  0 0 0 0 0 0 0 0 1 0 ...
##  $ Meioneta       : num  0 0 0 4 1 0 0 0 0 0 ...
##  $ Microneta      : num  0 0 1 0 1 0 1 0 0 0 ...
##  $ Naphrys        : num  0 0 0 0 0 0 0 0 0 0 ...
##  $ Neoantistea    : num  0 0 0 0 0 0 0 0 0 0 ...
##  $ Neon           : num  1 0 0 0 1 0 0 0 0 0 ...
##  $ Ozyptila       : num  1 0 0 0 0 0 0 0 0 0 ...
##  $ Pardosa        : num  0 0 0 2 0 1 0 1 0 1 ...
##  $ Pelegrina      : num  0 0 0 0 0 0 0 0 0 0 ...
##  $ Phidippus      : num  0 0 0 0 0 0 0 0 0 0 ...
##  $ Pholcomma      : num  0 0 0 0 0 0 0 0 0 0 ...
##  $ Phrurotimpus   : num  4 0 0 0 0 0 3 0 0 0 ...
##  $ Pirata         : num  1 3 0 0 0 2 0 6 1 1 ...
##  $ Pocadicnemis   : num  0 0 0 0 0 0 0 0 0 0 ...
##  $ Robertus       : num  0 0 0 0 0 0 0 0 0 0 ...
##  $ Scylaceus      : num  0 0 0 0 0 0 0 0 0 0 ...
##  $ Sisicottus     : num  0 0 0 0 0 0 0 0 0 0 ...
##  $ Sisicus        : num  0 0 0 0 0 0 0 0 0 0 ...
```

```
##  $ Tapinocyba     : num  0 0 1 0 7 0 4 0 3 0 ...
##  $ Tenuiphantes   : num  2 0 1 1 1 0 0 0 2 1 ...
##  $ Trochosa       : num  0 0 0 0 0 0 0 0 0 0 ...
##  $ Wadotes        : num  0 0 0 0 0 0 0 0 0 0 ...
##  $ Walckenaeria   : num  0 0 1 0 0 0 0 0 0 0 ...
##  $ Xysticus       : num  0 0 0 0 0 0 0 0 0 0 ...
##  $ Zelotes        : num  0 0 0 0 0 0 0 0 0 0 ...
##  $ totabund       : num  25 15 6 16 27 11 43 18 21 7 ...
##  $ sp.rich        : int  9 3 6 7 10 4 7 5 7 5 ...
##  $ sh.div         : num  2.044 0.861 1.792 1.667 1.973 ...
```

```
spider_new$sampling.method <- as.factor(spider_new$sampling.method)
spider_new$sh.div <- diversity(spider_new[,8:58], index = "shannon")

par(mar=c(6,4,2,2))
boxplot(sh.div ~ sampling.method, data = spider_new, xlab = "", ylab = "Species diversity (H)",
cex.axis = 1, las = 2)
stripchart(sh.div ~ sampling.method, data = spider_new, pch = 19, add = TRUE, vertical = TRUE, m
ethod = "jitter", jitter = 0.2) +
  theme(axis.text.x = element_text(angle = 0, hjust = 0.5))
```




```
## NULL
```

7. Fit a regression modeling spider genera diversity as a function of treatment and sampling method. You will need to use materials from previous lectures and activities to determine the appropriate structure of the model. Provide the model summary.

```
lm_spider <- lm(spider_new$sh.div ~ treatment + sampling.method, data=spider_new)
summary(lm_spider)
```

```
##
## Call:
## lm(formula = spider_new$sh.div ~ treatment + sampling.method,
##     data = spider_new)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -1.46308 -0.48672  0.07325  0.39217  1.61772
##
## Coefficients:
##                         Estimate Std. Error t value Pr(>|t|)
## (Intercept)              1.46308    0.08536  17.141  < 2e-16 ***
## treatmentHardwood        0.15485    0.10962   1.413   0.1592
## treatmentHemlock        -0.10477    0.10818  -0.968   0.3339
## treatmentLogged         -0.26699    0.10864  -2.457   0.0147 *
## sampling.methodPitfall -0.67548    0.07706  -8.765 4.52e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.5851 on 226 degrees of freedom
## Multiple R-squared:  0.2928, Adjusted R-squared:  0.2803
## F-statistic: 23.39 on 4 and 226 DF,  p-value: 3.384e-16
```

```
lm_spider_inter <- lm(spider_new$sh.div ~ treatment * sampling.method, data=spider_new)
summary(lm_spider_inter)
```

```
##
## Call:
## lm(formula = spider_new$sh.div ~ treatment * sampling.method,
##     data = spider_new)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -1.42019 -0.42993  0.03929  0.40449  1.29452
##
## Coefficients:
##                                        Estimate Std. Error t value Pr(>|t|)
## (Intercept)                             1.42019    0.09895  14.352  < 2e-16
## treatmentHardwood                       0.42312    0.13994   3.024  0.00279
## treatmentHemlock                        0.09169    0.13994   0.655  0.51301
## treatmentLogged                        -0.56017    0.13994  -4.003 8.52e-05
## sampling.methodPitfall                 -0.58664    0.14242  -4.119 5.36e-05
## treatmentHardwood:sampling.methodPitfall -0.57428    0.20340  -2.823  0.00518
## treatmentHemlock:sampling.methodPitfall  -0.40128    0.20051  -2.001  0.04657
## treatmentLogged:sampling.methodPitfall    0.60731    0.20141   3.015  0.00286
##
## (Intercept)                            ***
## treatmentHardwood                      **
## treatmentHemlock
## treatmentLogged                        ***
## sampling.methodPitfall                 ***
## treatmentHardwood:sampling.methodPitfall **
## treatmentHemlock:sampling.methodPitfall  *
## treatmentLogged:sampling.methodPitfall   **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.542 on 223 degrees of freedom
## Multiple R-squared:  0.4012, Adjusted R-squared:  0.3824
## F-statistic: 21.34 on 7 and 223 DF,  p-value: < 2.2e-16
```

8. Write 1-2 sentences interpreting the results.

The mean Shannon diversity index is 1.46 ($p < 0.001$), indicating statistical significance. Although the mean diversity index increased 0.155 under the Hardwood treatment (i.e., spider diversity), the increase was not statistically significant (p=0.159).