

Tutorial notebook

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Reading in data

Before beginning the analysis, let's get the data into R. Assuming R is installed on your computer, the first thing we want to do is create a workspace.

The first objective is to convert the ascii community data file to an R object.

```
> # raw_data_file <- 'data/raw/1992-01-01/bryceveg.R' # relative to where the
> # project .Rproj file is!
> raw_data_file <- "../data/raw/1992-01-01/bryceveg.R" # relative to where the .Rmd file is!
> veg <- read.table(raw_data_file, header = TRUE, row.names = 1)
```

Data set characteristics

Now that we've got the data into a data frame, we can examine the characteristics of the distribution of the data. First, we need to know there are 160 plots and 169 species in the data set. R could tell us that if we asked:

```
> dim(veg) # to get the dimensions of the data set
```

```
## [1] 160 169
```

```
> names(veg) # to get the columns names (species in our case)
```

```
## [1] "junost" "ameuta" "arcpat" "arttri" "atrcan" "berfre"
## [7] "ceamar" "cerled" "cermon" "chrdep" "chrnau" "chrpar"
## [13] "chrvis" "eurlan" "juncom" "pacmyr" "pruvir" "purtri"
## [19] "quegam" "rhutri" "ribcer" "roswoo" "samcoe" "shearg"
## [25] "sherot" "symore" "arcuva" "artarb" "artfri" "artpyg"
## [31] "atrcon" "berrep" "ericor" "gutsar" "tetcan" "agrcri"
## [37] "agrdas" "agrscr" "agrsmi" "bougra" "broano" "brocil"
## [43] "broine" "carrss" "elysal" "fesovi" "hiljam" "junbal"
```

```
## [49] "koenit" "muhmon" "muhric" "oryhym" "orymic" "phlpra"
## [55] "poacom" "poafen" "poanev" "poapra" "sithys" "sticom"
## [61] "stilet" "stipin" "achmil" "agogla" "anemul" "antros"
## [67] "antros.1" "apoand" "arahol" "arapen" "arefen" "artcar"
## [73] "artlud" "astagr" "astchi" "astcon" "asthum" "astken"
## [79] "astmeg" "astmis" "astten" "balsag" "calnut" "caschr"
## [85] "caslin" "chadou" "cirneo" "compal" "corkin" "creint"
## [91] "crycon" "cypur" "dessop" "drasub" "echtri" "eriala"
## [97] "erican" "erieat" "erifla" "eripan" "eripum" "erirac"
## [103] "erisub" "eriumb" "eupfen" "euplur" "euprob" "fraves"
## [109] "genaff" "gerfre" "gerric" "gilcon" "haparm" "heddru"
## [115] "hymaca" "hymfil" "hymric" "ipoagg" "irimis" "ivesab"
## [121] "leppun" "lesint" "leueri" "ligpor" "linkin" "linlew"
## [127] "litinc" "litmul" "lotuta" "lupkin" "lupser" "lyggra"
## [133] "lygspe" "macgri" "molpar" "oenbra" "oencae" "oencor"
## [139] "oenfla" "oenlav" "opueri" "orofas" "pedcan" "pedsim"
## [145] "pencae" "pencom" "penlei" "penuta" "phllon" "phycha"
## [151] "potcon" "potcri" "potgra" "pteand" "pyrvir" "salibe"
## [157] "sclwhi" "senmul" "sphcoc" "stapin" "steten" "strcor"
## [163] "swerad" "taroff" "thafen" "towmin" "tradub" "valacu"
## [169] "vicame"
```

```
> row.names(veg) # to get the row names (plots in our case)
```

```
## [1] "bcnp_1" "bcnp_2" "bcnp_3" "bcnp_4" "bcnp_5" "bcnp_6" "bcnp_7"
## [8] "bcnp_8" "bcnp_9" "bcnp_10" "bcnp_11" "bcnp_12" "bcnp_13" "bcnp_14"
## [15] "bcnp_15" "bcnp_16" "bcnp_17" "bcnp_18" "bcnp_19" "bcnp_20" "bcnp_21"
## [22] "bcnp_22" "bcnp_23" "bcnp_24" "bcnp_25" "bcnp_26" "bcnp_27" "bcnp_28"
## [29] "bcnp_29" "bcnp_30" "bcnp_31" "bcnp_32" "bcnp_33" "bcnp_34" "bcnp_35"
## [36] "bcnp_36" "bcnp_37" "bcnp_38" "bcnp_39" "bcnp_40" "bcnp_41" "bcnp_42"
## [43] "bcnp_43" "bcnp_44" "bcnp_45" "bcnp_46" "bcnp_47" "bcnp_48" "bcnp_49"
## [50] "bcnp_50" "bcnp_51" "bcnp_52" "bcnp_53" "bcnp_54" "bcnp_55" "bcnp_56"
## [57] "bcnp_57" "bcnp_58" "bcnp_59" "bcnp_60" "bcnp_61" "bcnp_62" "bcnp_63"
## [64] "bcnp_64" "bcnp_65" "bcnp_66" "bcnp_67" "bcnp_68" "bcnp_69" "bcnp_70"
## [71] "bcnp_71" "bcnp_72" "bcnp_73" "bcnp_74" "bcnp_75" "bcnp_76" "bcnp_77"
## [78] "bcnp_78" "bcnp_79" "bcnp_80" "bcnp_81" "bcnp_82" "bcnp_83" "bcnp_84"
## [85] "bcnp_85" "bcnp_86" "bcnp_87" "bcnp_88" "bcnp_89" "bcnp_90" "bcnp_91"
## [92] "bcnp_92" "bcnp_93" "bcnp_94" "bcnp_95" "bcnp_96" "bcnp_97" "bcnp_98"
## [99] "bcnp_99" "bcnp100" "bcnp101" "bcnp102" "bcnp103" "bcnp104" "bcnp105"
## [106] "bcnp106" "bcnp107" "bcnp108" "bcnp109" "bcnp110" "bcnp111" "bcnp112"
## [113] "bcnp113" "bcnp114" "bcnp115" "bcnp116" "bcnp117" "bcnp118" "bcnp119"
## [120] "bcnp120" "bcnp121" "bcnp122" "bcnp123" "bcnp124" "bcnp125" "bcnp126"
## [127] "bcnp127" "bcnp128" "bcnp129" "bcnp130" "bcnp131" "bcnp132" "bcnp133"
## [134] "bcnp134" "bcnp135" "bcnp136" "bcnp137" "bcnp138" "bcnp139" "bcnp140"
## [141] "bcnp141" "bcnp142" "bcnp143" "bcnp144" "bcnp145" "bcnp146" "bcnp147"
## [148] "bcnp148" "bcnp149" "bcnp150" "bcnp151" "bcnp152" "bcnp153" "bcnp154"
## [155] "bcnp155" "bcnp156" "bcnp157" "bcnp158" "bcnp159" "bcnp160"
```

Transformation of Vegetation Data

```
> cover <- veg # to create a copy of the veg data frame
> cover[veg == 1] <- 3 # to convert class 1 to midpoint of 3.0 percent
> cover[veg == 2] <- 15 # to convert class 2 to midpoint of 15.0 percent
```

```

> cover[veg == 3] <- 37.5 # to convert class 3 to midpoint of 37.5 percent
> cover[veg == 4] <- 62.5 # to convert class 4 to midpoint of 62.5 percent
> cover[veg == 5] <- 85 # to convert class 5 to midpoint of 85.0 percent
> cover[veg == 6] <- 97.5 # to convert class 6 to midpoint of 97.5 percent
> cover[1:15, 1:10]

```

```

##      junost ameuta arcpat arttri atrcan berfre ceamar cerled cermon
## bcnp__1      0   0.0   3.0   0.0     0     0   0.5   0.0     0
## bcnp__2      0   0.5   0.5   0.0     0     0   0.0   0.0     0
## bcnp__3      0   0.0   3.0   0.0     0     0   0.5   0.0     0
## bcnp__4      0   0.5   3.0   0.0     0     0   0.5   0.0     0
## bcnp__5      0   0.0  62.5   0.0     0     0   0.5   0.0     0
## bcnp__6      0   0.5   3.0   0.0     0     0   3.0   0.0     0
## bcnp__7      0   0.0  62.5   0.0     0     0   3.0   0.0     0
## bcnp__8      0   0.0  15.0   0.0     0     0   0.0   0.0     0
## bcnp__9      0   0.0   0.0   0.0     0     0   0.0   0.0     0
## bcnp_10      0   0.0  85.0   0.0     0     0   0.5   0.0     0
## bcnp_11      0   0.0  15.0   0.0     0     0   0.5   0.5     0
## bcnp_12      0   0.0  15.0   0.5     0     0   0.5   0.0     0
## bcnp_13      0   0.0   0.5   0.0     0     0   0.5   0.0     0
## bcnp_14      0   0.0  37.5   0.0     0     0   0.5   0.0     0
## bcnp_15      0   0.5  62.5   0.0     0     0   0.5   0.0     0
##      chrdep
## bcnp__1      0
## bcnp__2      0
## bcnp__3      0
## bcnp__4      0
## bcnp__5      0
## bcnp__6      0
## bcnp__7      0
## bcnp__8      0
## bcnp__9      0
## bcnp_10      0
## bcnp_11      0
## bcnp_12      0
## bcnp_13      0
## bcnp_14      0
## bcnp_15      0

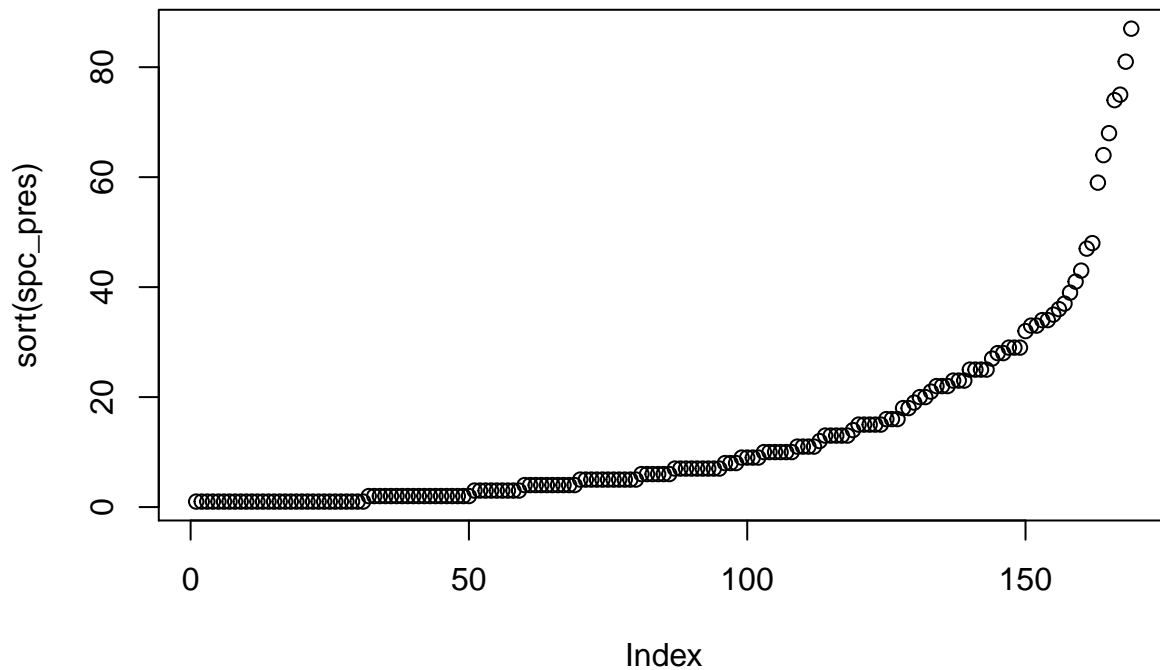
```

How many plots does each species occur in?

```

> # to get number of presences for each species. Note that the first part of
> # the function call (veg>0) evaluates to TRUE/FALSE or 1/0), and it is the
> # sum of ones and zeros that gets calculated.
> spc_pres <- apply(veg > 0, 2, sum)
>
> # to see a plot of the cumulative empirical density function (CEDF) for
> # species presences
> plot(sort(spc_pres))

```



Old stuff

R Markdown

This is an R Markdown document. Markdown is a simple formatting syntax for authoring HTML, PDF, and MS Word documents. For more details on using R Markdown see <http://rmarkdown.rstudio.com>.

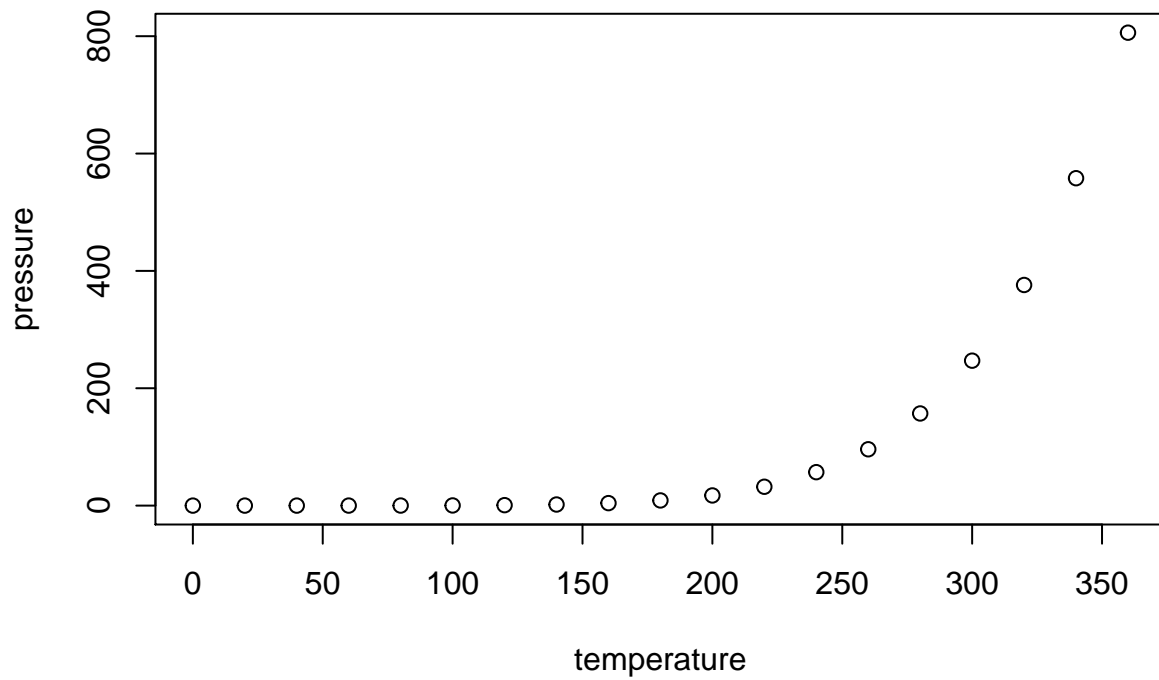
When you click the **Knit** button a document will be generated that includes both content as well as the output of any embedded R code chunks within the document. You can embed an R code chunk like this:

```
summary(cars)
```

```
##      speed      dist
##  Min.   : 4.0    Min.   : 2.00
##  1st Qu.:12.0    1st Qu.: 26.00
##  Median :15.0    Median : 36.00
##  Mean   :15.4    Mean    : 42.98
##  3rd Qu.:19.0    3rd Qu.: 56.00
##  Max.   :25.0    Max.    :120.00
```

Including Plots

You can also embed plots, for example:



Note that the `echo = FALSE` parameter was added to the code chunk to prevent printing of the R code that generated the plot.