Homework 5

Nathaniel Haulk

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```
library("devtools")

if(!require(neonDivData)) devtools::install_github("daijiang/neonDivData")

library("neonDivData")

library("tidyverse")
```

Question 1:

```
## Pulls the genus for each plant
data_plant$genus = sub(" .*", "", data_plant$taxon_name)

## Selects a random number 100 times between 1 and the length of data_plant
i = sample(1:nrow(data_plant), 100, replace=FALSE)

## Records the genus at the random
genus_samp = data_plant$genus[i]

## Prints out 100 genus
print(genus_samp)
```

```
##   [1] "Dupontia"       "Pediomelum"      "Rhynchosia"      "Opuntia"
##   [5] "Schizachyrium"  "Dichanthelium"   "Opuntia"         "Reynosia"
##   [9] "Boerhavia"      "Maianthemum"     "Vaccinium"       "Tragia"
##  [13] "Stylosanthes"   "Crossopetalum"   "Richardia"       "Bromus"
##  [17] "Carex"          "Pedicularis"     "Artemisia"       "Coccoloba"
##  [21] "Dichanthelium"  "Acer"            "Rosa"            "Plantago"
##  [25] "Symphoricarpos" "Boehmeria"       "Carex"           "Ambrosia"
##  [29] "Oenothera"      "Chamerion"       "Calamagrostis"   "Plantago"
##  [33] "Pinus"          "Leersia"         "Randia"          "Viola"
##  [37] "Solanum"        "Oxydendrum"      "Clarkia"         "Penstemon"
##  [41] "Dichanthelium"  "Tragopogon"      "Populus"         "Mycelis"
##  [45] "Symphoricarpos" "Sporobolus"      "Parthenocissus"  "Acalypha"
##  [49] "Claytonia"      "Dryopteris"      "Viola"           "Melilotus"
##  [53] "Doellingeria"   "Eriogonum"       "Rosa"            "Prosopis"
##  [57] "Melilotus"      "Arabis"          "Scleria"         "Viola"
##  [61] "Trientalis"     "Monarda"         "Astragalus"      "Saxifraga"
```

```
##  [65] "Asimina"        "Cryptotaenia"   "Plantago"       "Elymus"
##  [69] "Fagus"          "Frangula"       "Silene"         "Andropogon"
##  [73] "Carex"          "Erysimum"       "Bignonia"       "Anemone"
##  [77] "Heliotropium"   "Oxalis"         "Anemone"        "Carex"
##  [81] "Galactia"       "Pseudotsuga"    "Acer"           "Populus"
##  [85] "Lycopodium"     "Tridens"        "Microstegium"   "Sanguinaria"
##  [89] "Astragalus"     "Pityopsis"      "Symphoricarpos" "Quercus"
##  [93] "Vulpia"         "Acer"           "Polygonum"      "Serenoa"
##  [97] "Typha"          "Asimina"        "Arctostaphylos" "Bursera"
```

Question 2:

```r
data_plant$taxon_name2 = sub("(\\w\\s\\w+).*", "\\1", data_plant$taxon_name)

## Selects a random number 100 times between 1 and the length of data_plant
i = sample(1:nrow(data_plant), 100, replace=FALSE)

## Records the genus and species name at the random
taxon2_samp = data_plant$taxon_name2[i]

## Prints out data
print(taxon2_samp)
```

```
##    [1] "Carex spp"                "Senna bauhinioides"
##    [3] "Maianthemum canadense"    "Smilax tamnoides"
##    [5] "Serenoa repens"           "Saxifraga nelsoniana"
##    [7] "Viola sororia"            "Paronychia pulvinata"
##    [9] "Verbesina sp"             "Quercus velutina"
##   [11] "Smilax glauca"            "Carex sp"
##   [13] "Oligoneuron rigidum"      "Melilotus officinalis"
##   [15] "Saxifraga nelsoniana"     "Viola sp"
##   [17] "Acer rubrum"              "Hamamelis virginiana"
##   [19] "Artemisia tridentata"     "Xyris baldwiniana"
##   [21] "Lactuca serriola"         "Dichanthelium ovale"
##   [23] "Alliaria petiolata"       "Ipomoea hederacea"
##   [25] "Symphyotrichum sp"        "Justicia ovata"
##   [27] "Quercus alba"             "Vitis sp"
##   [29] "Liriodendron tulipifera"  "Nyssa sylvatica"
##   [31] "Smilax sp"                "Cornus sp"
##   [33] "Sassafras albidum"        "Arctagrostis latifolia"
##   [35] "Carex sp"                 "Menispermum canadense"
##   [37] "Chamaesyce polycarpa"     "Dalea aurea"
##   [39] "Opuntia macrorhiza"       "Croton setigerus"
##   [41] "Silene gallica"           "Acer saccharum"
##   [43] "Oxalis stricta"           "Pinus taeda"
##   [45] "Ambrosia artemisiifolia"  "Vaccinium uliginosum"
##   [47] "Lonicera japonica"        "Carex sp"
##   [49] "Celtis tenuifolia"        "Arnica cordifolia"
##   [51] "Prunus avium"             "Pictetia aculeata"
##   [53] "Elaeagnus umbellata"      "Astragalus missouriensis"
##   [55] "Rhododendron lapponicum"  "Vitis sp"
```

```
##  [57] "Medicago sativa"                  "Senna bauhinioides"
##  [59] "Tephrosia florida"                "Solidago canadensis"
##  [61] "Pityopsis aspera"                 "Krameria erecta"
##  [63] "Sporobolus contractus"            "Pascopyrum smithii"
##  [65] "Argythamnia candicans"            "Petasites frigidus"
##  [67] "Smilax rotundifolia"              "Polygonum viviparum"
##  [69] "Veronica officinalis"             "Alysicarpus vaginalis"
##  [71] "Sabal minor"                      "Andropogon capillipes"
##  [73] "Smilax rotundifolia"              "Elymus hystrix"
##  [75] "Asclepias verticillata"           "Mimosa microphylla"
##  [77] "Oeceoclades maculata"             "Toxicodendron radicans"
##  [79] "Sisyrinchium angustifolium"       "Atriplex canescens"
##  [81] "Bromus tectorum"                  "Vaccinium angustifolium"
##  [83] "Morus rubra"                      "Plantago patagonica"
##  [85] "Rubus chamaemorus"                "Aristida beyrichiana"
##  [87] "Solidago canadensis"              "Viola sp"
##  [89] "Yeatesia viridiflora"             "Anemone sp"
##  [91] "Desmodium incanum"                "Muhlenbergia sp"
##  [93] "Pseudognaphalium obtusifolium"    "Ledum groenlandicum"
##  [95] "Polygonum punctatum"              "Symphyotrichum ericoides"
##  [97] "Hexastylis arifolia"              "Viburnum sp"
##  [99] "Diervilla sp"                     "Tradescantia occidentalis"
```

Question 3

```r
## Creates data frame n_1 that counts the number of unique species at each sample_area with a size of 1
n_1 = data_plant %>%
  group_by(siteID) %>%
  filter(sample_area_m2 =="1") %>%
  summarise(richness_1m2 = n_distinct(taxon_name2))

## Creates data frame n_10 that counts the number of unique species at each sample_areas with a size of
n_10 = data_plant %>%
  group_by(siteID) %>%
  filter(sample_area_m2 %in% c("1","10")) %>%
  summarise(richness_10m2 = n_distinct(taxon_name2))

## Creates data frame n_100 that counts the number of unique species at each sample_areas with a size o
n_100 = data_plant %>%
  group_by(siteID) %>%
  filter(sample_area_m2 %in% c("1","10","100")) %>%
  summarise(richness_100m2 = n_distinct(taxon_name2))

## Joins n_1, n_10, n_100
n_all = left_join(n_1 ,n_10) %>%
  left_join(n_100)
```

```
## Joining, by = "siteID"
## Joining, by = "siteID"
```

```
## prints n_all
print(n_all)
```

```
## # A tibble: 47 x 4
##    siteID richness_1m2 richness_10m2 richness_100m2
##    <chr>         <int>         <int>          <int>
## 1 ABBY            188           228            261
## 2 BARR             71            87             91
## 3 BART             80           104            127
## 4 BLAN            268           313            378
## 5 BONA             72            88            100
## 6 CLBJ            413           477            517
## 7 CPER            185           222            241
## 8 DCFS            223           264            293
## 9 DEJU            152           183            198
## 10 DELA           303           391            457
## # ... with 37 more rows
```

Question 4

```
## creates n_all_longer that records site richness based off spatial scale.
n_all_longer = n_all %>%
  pivot_longer(!siteID, names_to = "spatial_scale", values_to = "richness")

## Prints dataframe
print(n_all_longer)
```

```
## # A tibble: 141 x 3
##    siteID spatial_scale  richness
##    <chr>  <chr>             <int>
## 1 ABBY   richness_1m2        188
## 2 ABBY   richness_10m2       228
## 3 ABBY   richness_100m2      261
## 4 BARR   richness_1m2         71
## 5 BARR   richness_10m2        87
## 6 BARR   richness_100m2       91
## 7 BART   richness_1m2         80
## 8 BART   richness_10m2       104
## 9 BART   richness_100m2      127
## 10 BLAN  richness_1m2        268
## # ... with 131 more rows
```

Question 5

```
## Graphs n_all_longer
ggplot(data = n_all_longer, aes(x = spatial_scale, y = richness,  group = siteID))+
  geom_point()+
  geom_line()
```