Homework 5

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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] "Poa"            "Dichelostemma"  "Serenoa"         "Janusia"
##   [5] "Poa"            "Smilax"         "Carpinus"        "Corylus"
##   [9] "Vulpia"         "Rhus"           "Rhynchosia"      "Trachelospermum"
##  [13] "Fagus"          "Toxicodendron"  "Uvularia"        "Morelotia"
##  [17] "Diervilla"      "Cardamine"      "Ambrosia"        "Hesperostipa"
##  [21] "Pedicularis"    "Cryptantha"     "Sedum"           "Bouteloua"
##  [25] "Eupatorium"     "Oldenlandia"    "Polygala"        "Fragaria"
##  [29] "Potentilla"     "Lonicera"       "Cirsium"         "Smilax"
##  [33] "Pilea"          "Viola"          "Erythroxylum"    "Andropogon"
##  [37] "Elymus"         "Nyssa"          "Artemisia"       "Oxalis"
##  [41] "Acer"           "Gaultheria"     "Desmanthus"      "Mimulus"
##  [45] "Sporobolus"     "Rubus"          "Diodia"          "Coreopsis"
##  [49] "Amelanchier"    "Turnera"        "Carex"           "Viola"
##  [53] "Pediocactus"    "Linum"          "Betula"          "Cirsium"
##  [57] "Ostrya"         "Arisaema"       "Machaeranthera"  "Machaeranthera"
##  [61] "Ledum"          "Desmodium"      "Ipomoea"         "Pedicularis"
```

```
##  [65] "Lonicera"        "Physalis"        "Gaura"           "Thuja"
##  [69] "Physalis"        "Acacia"          "Athyrium"        "Echinacea"
##  [73] "Gilia"           "Symphoricarpos"  "Pseudoroegneria" "Saxifraga"
##  [77] "Axonopus"        "Trientalis"      "Quercus"         "Bouteloua"
##  [81] "Acer"            "Galium"          "Petasites"       "Bromus"
##  [85] "Vaccinium"       "Quercus"         "Carex"           "Nyssa"
##  [89] "Bouteloua"       "Smilax"          "Carex"           "Galactia"
##  [93] "Solidago"        "Galium"          "Medeola"         "Carex"
##  [97] "Acer"            "Arctostaphylos"  "Fraxinus"        "Campsis"
```

Question 2:

```
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] "Onoclea sensibilis"        "Astragalus plattensis"
##    [3] "Schedonnardus paniculatus" "Sorghastrum nutans"
##    [5] "Paronychia virginica"      "Hesperostipa comata"
##    [7] "Dichanthelium sphaerocarpon" "Lespedeza violacea"
##    [9] "Amorpha canescens"         "Rubus occidentalis"
##   [11] "Stillingia sylvatica"      "Betula occidentalis"
##   [13] "Tragia urens"              "Betula sp"
##   [15] "Dryas octopetala"          "Elaeagnus umbellata"
##   [17] "Ostrya virginiana"         "Carex sp"
##   [19] "Ipomoea sp"                "Dichanthelium ovale"
##   [21] "Strophostyles umbellata"   "Pediomelum argophyllum"
##   [23] "Populus tremuloides"       "Euonymus sp"
##   [25] "Oxalis sp"                 "Elymus sp"
##   [27] "Amyris elemifera"          "Galium aparine"
##   [29] "Xyris caroliniana"         "Carex sp"
##   [31] "Toxicodendron radicans"    "Vaccinium vitis"
##   [33] "Carex duriuscula"          "Lithospermum sp"
##   [35] "Rhododendron sp"           "Maianthemum sp"
##   [37] "Tragopogon dubius"         "Carex spp"
##   [39] "Cypripedium sp"            "Quercus velutina"
##   [41] "Coccoloba microstachya"    "Maianthemum canadense"
##   [43] "Urochloa maxima"           "Nama hispidum"
##   [45] "Lindera benzoin"           "Betula papyrifera"
##   [47] "Carex crinita"             "Paspalum setaceum"
##   [49] "Smilax glauca"             "Galactia mollis"
##   [51] "Smilax rotundifolia"       "Oryzopsis sp"
##   [53] "Penstemon whippleanus"     "Fraxinus nigra"
##   [55] "Chapmannia floridana"      "Acalypha monococca"
```

```
##  [57] "Lonicera japonica"        "Gutierrezia sarothrae"
##  [59] "Ilex montana"             "Vaccinium uliginosum"
##  [61] "Dactylis glomerata"       "Galactia regularis"
##  [63] "Smilax bona"              "Draba streptocarpa"
##  [65] "Chamerion angustifolium"  "Sida rhombifolia"
##  [67] "Symphyotrichum ericoides" "Rubus sp"
##  [69] "Sphaeralcea coccinea"     "Populus tremuloides"
##  [71] "Galium circaezans"        "Opuntia macrorhiza"
##  [73] "Ambrosia psilostachya"    "Verbesina alternifolia"
##  [75] "Aristida purpurea"        "Festuca altaica"
##  [77] "Echinocereus viridiflorus" "Poa cuspidata"
##  [79] "Schizachyrium scoparium"  "Polygonum virginianum"
##  [81] "Fraxinus americana"       "Rubus sp"
##  [83] "Vitis rotundifolia"       "Chamaesyce prostrata"
##  [85] "Poa pratensis"            "Diospyros virginiana"
##  [87] "Carpinus caroliniana"     "Dryopteris intermedia"
##  [89] "Carex sp"                 "Acer saccharum"
##  [91] "Chamaesyce maculata"      "Fagus grandifolia"
##  [93] "Aristolochia serpentaria" "Mitchella repens"
##  [95] "Galium virgatum"          "Lepidium sp"
##  [97] "Saxifraga nelsoniana"     "Fraxinus americana"
##  [99] "Hypoxis juncea"           "Physalis heterophylla"
```

Question 3

```r
## Creates data frame n_1 that counts the number of sample_areas with a size of 1 m2 in data_plant
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 sample_areas with a size of 1 and 10 m2 in data_pl
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 sample_areas with a size of 1, 10, and 100 m2 in
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()
```