RMarkdown_Tutorial_TK

TK51

2023-04-09

The Task

Use this example R script to practice compiling an R Markdown file, using the tutorial materials provided at: ourcodingclub.github.io Follow through the tutorial to make a well commented, easy to follow record of what is going on so that others can easily follow.

Preabmle

Loading packages

```
library(dplyr) # for data manipulation
library(pander) # to create pretty tables
```

Loading biodiversity data

Data exploration

This data is a publicly available dataset of occurrence records for many animal, plant, and fungi species, for 2000-2016 from the NBN Gateway

What is the species richness across taxonomic groups?

Constructing a table of species richness in each taxonomic group

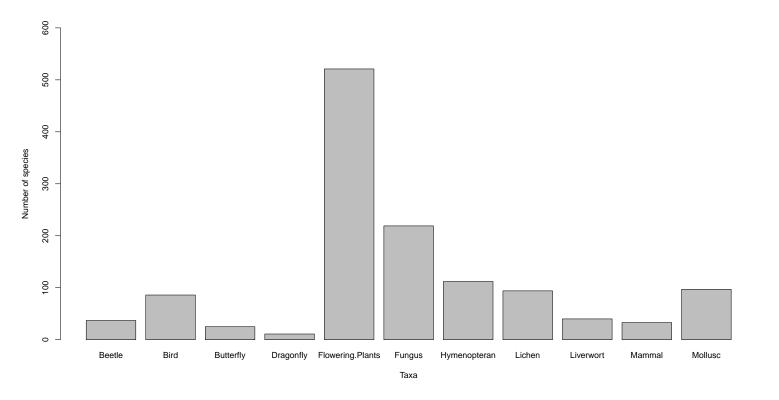
```
richness <-
  edidiv %>%
  group_by(taxonGroup) %>%
  summarise(Species_richness = n_distinct(taxonName))

pander(richness)
```

taxonGroup	Species_richness
Beetle	37
Bird	86
Butterfly	25
Dragonfly	11
Flowering.Plants	521
Fungus	219
Hymenopteran	112
Lichen	94
Liverwort	40
Mammal	33
Mollusc	97

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Creating a barplot of species richness in each taxonomic group



Determining what the most common species is in each taxonomic group

```
# Create a vector of most abundant species per taxa
max_abund <-
edidiv %>%
    group_by(taxonGroup) %>%
    summarise(taxonName = names(which.max(table(taxonName))))
max_abund
```

```
##
      <chr>>
                       <chr>>
##
  1 Beetle
                       Coccinella septempunctata
## 2 Bird
                       Turdus merula
##
   3 Butterfly
                       Maniola jurtina
##
   4 Dragonfly
                       Ischnura elegans
##
   5 Flowering.Plants Urtica dioica
                       Auricularia auricula-judae
##
   6 Fungus
   7 Hymenopteran
                       Bombus (Bombus) terrestris
##
##
   8 Lichen
                       Xanthoria parietina
   9 Liverwort
                       Lophocolea bidentata
## 10 Mammal
                       Sciurus carolinensis
## 11 Mollusc
                       Cornu aspersum
```

taxonName

A tibble: 11 x 2

taxonGroup

##

```
# Joining the two data frames together, using "taxonGroup" as the reference
richness_abund <- inner_join(richness, max_abund, by = "taxonGroup")</pre>
```

Renaming the headers of the tables, and viewing the data frame richness_abund <- rename(richness_abund, Most_abundant = taxonName, Taxon = taxonGroup) richness_abund</pre>

A tibble: 11 x 3 Taxon Species_richness Most_abundant ## <chr> <int> <chr> ## 1 Beetle 37 Coccinella septempunctata ## 2 Bird 86 Turdus merula ## 3 Butterfly 25 Maniola jurtina ## 4 Dragonfly 11 Ischnura elegans 521 Urtica dioica 219 Auricularia auricula-judae ## 5 Flowering.Plants ## 6 Fungus 112 Bombus (Bombus) terrestris ## 7 Hymenopteran ## 8 Lichen 94 Xanthoria parietina 40 Lophocolea bidentata ## 9 Liverwort 33 Sciurus carolinensis ## 10 Mammal ## 11 Mollusc 97 Cornu aspersum

pander(richness_abund)

Taxon	Species_richness	$Most_abundant$
Beetle	37	Coccinella septempunctata
Bird	86	Turdus merula
Butterfly	25	Maniola jurtina
Dragonfly	11	Ischnura elegans
Flowering.Plants	521	Urtica dioica
Fungus	219	Auricularia auricula-judae
Hymenopteran	112	Bombus (Bombus) terrestris
Lichen	94	Xanthoria parietina
Liverwort	40	Lophocolea bidentata
Mammal	33	Sciurus carolinensis
Mollusc	97	Cornu aspersum

library(knitr) kable(richness_abund)

Taxon	Species_richness	Most_abundant
Beetle	37	Coccinella septempunctata
Bird	86	Turdus merula
Butterfly	25	Maniola jurtina
Dragonfly	11	Ischnura elegans
Flowering.Plants	521	Urtica dioica
Fungus	219	Auricularia auricula-judae
Hymenopteran	112	Bombus (Bombus) terrestris
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Liverwort	40	Lophocolea bidentata
Mammal	33	Sciurus carolinensis
Mollusc	97	Cornu aspersum

Things to think about:

- Which bits of code need to be displayed in the final .html file?
- How can the formatting of the R markdown file be improved?

Experiment with other demo R scripts in the repo, or your own scripts for further practice!

- $\bullet \;\; RMarkdown_Demo_1.R$
- RMarkdown_Demo_2.R
- \bullet RMarkdown_Demo_3.R